

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 18, 2005, 16:30:41; Search time 20847.7 Seconds  
(without alignments)  
5315.550 Million cell updates/sec

Title: US-09-611-257a-24  
Sequence: 1 MLEHVRPCVTRTPPLRGSR.....KDTLSGLSLSDPTDMDPZ 2287

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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Database :

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14: gb\_vl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	DB ID	Description
1	12024	100.0	7540	6	AX068898 Sequence
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3	11980	99.6	7542	10	AF027984 Rattus no
4	11829	98.3	7285	6	BD224079 T-type ca

5	11829	98.3	7286	10	AF125161	AF125161 Rattus no
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8	11489	95.5	7527	10	BC057399	BC057399 Mus muscu
9	11088	92.2	7274	9	AF126966	AF126966 Homo sapi
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11	11066.5	92.0	7741	6	AR201015	AR201015 Sequence
12	11037.5	91.8	7253	9	AF126965	AF126965 Homo sapi
13	10948.5	91.0	6822	6	AR201014	AR201014 Sequence
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17	10914.5	90.7	6766	9	AF227745	AF227745 Homo sapi
18	10902	90.6	6855	9	AF227751	AF227751 Homo sapi
19	10898	90.6	6801	9	AF227748	AF227748 Homo sapi
20	10891	90.5	6921	9	AF227750	AF227750 Homo sapi
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22	10845.5	90.2	7648	9	AF134985	AF134985 Homo sapi
23	10631.5	88.4	7030	6	C0724231	C0724231 Sequence
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25	8137	67.7	5475	9	AB012043	AB012043 Homo sapi
26	7256.5	60.3	4903	9	AK129294	AK129294 Mus muscu
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ALIGNMENTS

RESULT 1	AX068898	7540 bp	DNA	linear	PAT 25-JAN-2001
LOCUS	AX068898	Sequence 23 from Patent WO0102561.			
DEFINITION	AX068898				
ACCESSION	AX068898				
VERSION	AX068898.1	GI:12578748			
KEYWORDS					
SOURCE					
ORGANISM	Rattus sp.				
	Rattus sp.				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
	Rattus.				
REFERENCE	1	Snutch, T.P. and Baillie, D.L.			
AUTHORS					
TITLE		Mammalian calcium channels and related probes, cell lines and			
JOURNAL		methods Patent: WO 0102561-A 23 11-JAN-2001;			
FEATURES		Neuromed Technologies, Inc. (CA)			
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		/mol_type="unassigned DNA"			
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ORIGIN  
Alignment Scores: 0  
Pred. No.: 12024.00  
Score: Length: 7540  
Matches: 2286

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.97% Indels: 0  
DB: 6 Gaps: 0

US-09-611-257a-24 (1-2287) x AX068898 (1-7540)

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QY 21 ProSerSerAspProProGlyProArgLeuAlaArgGlyTyrThrArgArgMetGlu 40  
DB 445 CCTCTTGGAGACCCCGGGGGCCCGGGCTGGCCAGAGATGAGACAGAGAGAGATGAG 504  
QY 41 ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrCysProGly 60  
DB 505 CGGCGCGCAGAGTGGGACAGCCCGTAGCTTCACGCACTCAACGACTGTCCGGGG 564  
QY 61 ProGlyAlaAlaGlyValGlySerThrGlyLysAspProGlySerAlaAspSerGluAla 80  
DB 555 CGGGGGCGCGGAGGGCGGCTGCGACGGAAGAACCGGGGCAAGCGGACTCCAGGGCG 624  
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QY 101 ArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgLysMet 120  
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DB 745 CTGGTCATCTTCTCAACTGTGTGACTCTGGGTATGTTCAAGCCGATGAGGACATGCG 804  
QY 141 CysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePhe 160  
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QY 161 AlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeu 180  
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QY 181 GlyAspThrTyrAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer 200  
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DB 1645 CTGTGCTGTGTGTGATTGTCACAGCAATCTCCAGAGCAAAACAGCGGAGAGTCAAGCTG 1704  
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 1 (bases 1 to 6942)  
 McRory, J.E., Santti, C.M., Hamming, K.S., Mezeyova, J., Sutton, K.G.,  
 Baillie, D.L., Stee, A. and Snutch, T.P.  
 Molecular and functional characterization of a family of rat brain  
 T-type calcium channels  
 J. Biol. Chem. 276 (6), 3999-4011 (2001)  
 JOURNAL  
 MEDLINE  
 PUBMED  
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 11073957  
 2 (bases 1 to 6942)  
 Snutch, T.P., McRory, J.E. and Hamming, K.S.  
 Direct Submission  
 Submitted (27-JUL-2000) Biotechnology Laboratory, University of  
 British Columbia, 6174 University Blvd., Vancouver, BC V6T1Z3,  
 Canada  
 3 (bases 1 to 6942)  
 Snutch, T.P., McRory, J.E. and Hamming, K.S.  
 Direct Submission  
 Submitted (29-NOV-2000) Biotechnology Laboratory, University of  
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 Canada  
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1200 lYArgSerSerAlaSerGlnHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuA 1220
3616 GCCGAGGCTGTGCTGTGAGCACCAAGACTGTAAATGGCAAGTGGCTTCAAGGGCTTTTGG 3675
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Db	4756	GTAAGGAGAGAGATGGCCCGAAGCCAGTGCAGAACCTTACTACTGACTGAGAT	4815
Qy	1600	heArgleuLeuValHlshlsleuCystrhSerHlsTyrlleuAspLeuPheHlthrglyl	1620
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Qy	1620	allleGlyLeuAsnValValThrMetAlaMetGlnHlsTyrglnlnProGlnlleLeuA	1640
Db	4876	TCATGGGCTGAACCTGGTCACTATGGCCATGAACATTACCAAGAGCCCAAGATCCGG	4935
Qy	1640	spglualaleuylsileCysAsnTyrllePheThrValHllepheValPheGlnSerValP	1660
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Qy	1660	heLyLeuValAlaPheAlaPheArgArgrPheGlnAspArgTrpAsnGlnleuAspL	1680
Db	4996	TCAAACTTGCGCTTGGCTTCCGCCCTTCTTCTTCAGAGACAGGTGGAACAGCTGAGCC	5055
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Qy	2020	hrTrpGlyAlaHleProLysLeuProProProGlyArgSerProleuAlaGlnArgProL	2040
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Qy	2260	erThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerA	2280
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QY 2280 BPProThraspethappro 2286  
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RESULT 3  
RNCALG 7542 bp mRNA linear ROD 24-OCT-1998  
LOCUS RNCALG  
DEFINITION Rattus norvegicus low voltage-activated, T-type calcium channel  
alpha subunit (CACNALG) mRNA, complete cds.  
AF027984  
AF027984.1 GI:3786350

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
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AUTHORS  
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REMARK  
COMMENT  
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source

1 (baees 1 to 7542)  
Perez-Reyes, E., Cribbs, L.L., Daud, A., Lacerda, A.E., Barclay, J.,  
Williamson, M.P., Fox, M., Rees, M. and Lee, J.H.  
Molecular characterization of a neuronal low-voltage-activated  
T-type calcium channel  
Nature 391 (6670), 896-900 (1998)  
98154730  
2 (baees 1 to 7542)  
Cribbs, L.L., Yang, J., Daud, A., Lee, J.-H. and Perez-Reyes, E.  
Direct Submision  
Submitted (02-OCT-1997) Physiology, Loyola University Medical  
Center, 2160 South First Avenue, Maywood, IL 60153, USA  
3 (baees 1 to 7542)  
Cribbs, L.L., Yang, J., Daud, A., Lee, J.-H. and Perez-Reyes, E.  
Direct Submision  
Submitted (22-OCT-1998) Physiology, Loyola University Medical  
Center, 2160 South First Avenue, Maywood, IL 60153, USA  
Sequence update by submitter  
On Oct 24, 1998 this sequence version replaced gi:2921748.  
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ORIGIN  
Alignment Scores:  
Pred. No.: 0 Length: 7542  
Score: 11980.00 Matches: 2283  
Percent Similarity: 99.78%  
Best Local Similarity: 99.78% Mismatches: 3  
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US-09-611-257a-24 (1-2287) x RNCALG (1-7542)

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Db 1045 TCAGGCGCATTAACCGGGTGCCAGACATGCGCATTCGTCAATTACTGCTGGACACT 1104  
QY 240 euProMetLeuGIyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGIyIleV 260  
Db 1105 TGCCATATGCTGGGCAACGTCCTGCTGCTGTCTTGTCTTTCATCTTTGGCATCG 1164  
QY 260 aIGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGlnAsnPhes 280  
Db 1165 TGGGCGTCACAGCTGTGGGAGAGACTGCTTCGCAACGGGTGCTTCTCCCGAGAACTTCA 1224  
QY 280 eTLeuProLeuSerValAspLeuGluProTyrrTyrrGlnThrGlnAsnGlnAspGIuSerP 300  
Db 1225 GCGTCCCCCTGAGCGGTGAGCCTGAGCCCTTATTACAGACAGAGATGAGAGCGAGAGCC 1284  
QY 300 rOPheIleCysSerGIuProArgGIuAsnGlyMetArgSerCysArgSerValProThrL 320  
Db 1285 CTTTCATCTGCTCTCAGCCCTCGGAGAGATGSCATAGATCTCGCAGAGGTGCCCAAC 1344  
QY 320 euArgGIyGIuGIyGIyGIyGIyProProCysSerLeuAspTyrrGlnThrTyrrAsnSers 340  
Db 1345 TGCGGTGGGAAAGCGGTGGTGCCACCTCGAGCTGGACTATGAGACCTATACAGTT 1404  
QY 340 eSerSerAsnThrThrCysValAsnTrpAsnGlnTyrrTyrrThrAsnGlySerAlaGIyGlnH 360  
Db 1405 CCAGAGAACACCACTGTGTCAACTGAAACCAAGTACTATACCAACTGCTCGGGCGAGC 1464  
QY 360 iAsnProPheLeysGIyAlaIleAsnPheAspAsnIleGIyTyrrAlaTrpIleAlaIleP 380  
Db 1465 ACAACCCCTTCAAAAGCGCCATCAACTTGAACAATTGGCTATGCTGGATCGCATCT 1524  
QY 380 heGlnValIleThrLeuGlnGlyTyrrValAspIleMetTyrrPheValMetAspAlaHis 400  
Db 1525 TCCAGGTATCATCACGTGAGGGGTGGGTGCATCATGATGATTCGTATGAGCGCTCACT 1584  
QY 400 ePheThrAsnPheIleTyrrPheIleLeuLeuIleIleValGIySerPhePheMetIleA 420  
Db 1585 CCTTCTACAACTTCATCTACTTCATTCATCATCATCGTGGGCTCTTCTTCATGATCA 1644  
QY 420 snLeuCysLeuValValIleAlaThrGlnPheSerGIuThrLysGlnArgGIuSerGlnL 440  
Db 1645 ACCTTGCTGCTGGTGTGATGTCGACGAGTCTCCGAGACCAAAAGCGGAGATCGAC 1704  
QY 440 euMetArgGIuGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerg 460  
Db 1705 TGATCGGAGAGAGCGGTGATCGATCTCTGTCATAGTACACCTTGCAAGACTTCTCTG 1764  
QY 460 lInProGIySerCysTyrrGIuGIuLeuLeuLysTyrrLeuValTyrrIleLeuArgLysAlaA 480  
Db 1765 AGCCAGGAGAGCTGATAGAGAGCTACTCAAGTACCTGGTGTACATCTCCGAAAGAG 1824  
QY 480 lAArgArgLeuAlaGlnValSerArgAlaIleGIyValArgAlaGIyLeuLeuSerSerp 500  
Db 1825 CCCGAAAGCTGGCCAGAGTCTCTAGGCGCTATAGGCGTCCGGCTGCTCGACAGACC 1884  
QY 500 roValAlaArgSerGIyGlnGluProGlnProSerGIySerCysThrArgSerHisArgA 520  
Db 1885 CAGTGGCCCGTGTGTGGGAGAGAGCCCAAGCCAGGTGAGAGCTGCTGCTCACACCGTC 1944  
QY 520 rGLeuSerValHisIleLeuValHisIleHisIleHisIleHisIleHisIleHisIleHis 540  
Db 1945 GTCTGTGTGTCCACCACTGTGTCCACCAACCATCACCAACCATCACCACTACCACTGG 2004

QY 540 lYAenGIyThrLeuArgValProArgAlaSerProGIuIleGlnAspArgAspAlaAsnG 560  
Db 2005 GTAATGGAGCCCTAGAGATTCCCGGGCCAGCCAGAGATCCAGAGACGAGATCCCAT 2064  
QY 560 lYSerArgArgLeuMetLeuProProSerThrProThrProSerGIyGIyProProA 580  
Db 2065 GGTCTCGCGGCTCATGCTACACACCCCTCTTACACCACACTCCCTCTGGGGGCCCTCGA 2124  
QY 580 rGGIyAlaGIuSerValHisSerPheTyrrHisAlaAspCysHisLeuGluProValArgC 600  
Db 2125 GGGGTGGAGTCTGTACACAGCTTCTTACAGTGTACTGTCACTTGACACTTGAGCCAGTCCGTT 2184  
QY 600 ySglnAlaProProProArgCysProSerGIuAlaSerGIyArgThrValGIySerGIyL 620  
Db 2185 GCCAGGACCCCTCCAGAGTCCCATCGAGAGCATGTGGTAGGACGTGGGTGTGGGA 2244  
QY 620 ySValTyrrProThrValHisThrSerProProGIuIleLeuLysAspLysAlaLeuV 640  
Db 2245 AGGTGTACCCCATGTGCATTCAGCCCTCCACAGAGATATGAAAGATTAAGCACTAG 2304  
QY 640 aIGlyValAlaProSerProGIyProProThrLeuThrSerPheAsnIleProProGIyP 660  
Db 2305 TGGAGGTGGCCCAAGCCCTGGAGCCCCCACTTCACCAAGCTTCAACAATCCACCTGGAGC 2364  
QY 660 rOPheSerSerMetHisLysLeuLeuGIuThrGlnSerThrGlyAlaCysHisSerSerc 680  
Db 2365 CTTTCAGTCCATCATCAGACTGCTCGAGACACAGATAGGGAGCCTGCCATATGCTCT 2424  
QY 680 ySlySllSerSerProCysSerLysAlaAspSerGIyAlaCysGIyProAspSerCysP 700  
Db 2425 GCAAAATCTCCAGCCCTTGTGCTCCAAAGCAGACAGTGAAGCCTGGGGCGGACAGTTGTC 2484  
QY 700 roTyrrCysAlaArgThrGIyAlaGIyGIuProGIuSerAlaAspHisValMetProAsps 720  
Db 2485 CTAAGTGTCCCGACAGAGACAGAGAGCCAGAGTCCGTGACCAATGCTATGCTGTAAGT 2544  
QY 720 eTAspSerGIuAlaValTyrrGIuPheThrGlnAspAlaGlnHisSerAspLeuArgAsp 740  
Db 2545 CAGACAGAGAGCGTGTATGATGATTCACACAGACGCTCAGACATCGGAGATCCCGGGATC 2604  
QY 740 roHisSerArgArgArgGlnArgSerLeuGIyProAspAlaGIuProSerSerValLeuA 760  
Db 2605 CCCACAGCCGGCGGACAGGGAGCCTGGGCCAGATGACAGACCCTAATGCTGTGTGG 2664  
QY 760 lAPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrrPheGIyA 780  
Db 2665 CTTTCTGAGGCTATCTGTGACATTCGGAAGATCGTATGATGCAATATCACTTTTGGCC 2724  
QY 780 rGGIyIleMetIleAlaIleLeuValAsnThrLeuSerMetGIyIleGIuTyrrHisGIuG 800  
Db 2725 GGGGAATCATGATCGCCATCTGGTCAATACACTCACATGGGCATCGAGTACACAGAGC 2784  
QY 800 lInProGIuGIuLeuThrAsnAlaLeuGIuIleSerAsnIleValPheThrSerLeuPheA 820  
Db 2785 AGCCGAGAGACTCACCAAGCCCTGGAAATCACAAACATCGTTCACACAGCCTCTTGC 2844  
QY 820 lALeuGIuMetLeuLeuLysLeuLeuValTyrrGIyProPheGIyTyrrIleLysAsnProT 840  
Db 2845 CTTTGAAGATGCTCTGAAGCTGCTTGTCTACAGGTCCCTTTGGCTACATTAGAAATCCT 2904  
QY 840 yRAenIlePheAspGIyValIleValIleSerValTrpGIuIleValGIyGlnGlnG 860  
Db 2905 ACAACATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2964  
QY 860 lYGIyGIyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgP 880  
Db 2965 GAGGTGCGCTGTCTGTCTGTGGAGCCTTCCGCTGATGCGGGTCTTAAGCTGTGTGGCT 3024  
QY 880 heLeuProAlaLeuGIuArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaT 900  
Db 3025 TCTGTGGGCGCTTCAGCGCCAGCTCGTGTGCTCATGAAAGACCATGAGACAGTGGCCA 3084  
QY 900 hrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGIyMetHisLeuP 920



Db ||||| 3085 CCTTCGCAATGCTCCCATGCTGTTTCATCTTCATCTTCAGCATCTCCGGGCATGCATCTCT 3144  
Qy ||||| 920 hGg1CYbAtySPhealaseRg1uArGAspG1yAsPthLeuProAspAryLysAsnPhea 940  
Db ||||| 3145 TTGGTTGCAGAGTTCGATCTGAAAGGGAATGGGACAGCTTGGCCAGCCGGAAGAAATTTGG 3204  
Qy ||||| 940 SPSeLeuLeuTPa1a1eValThrValPheGln1LeuThrg1uAspTPaAsL 960  
Db ||||| 3205 ACTCCCTGCTGGGCATGCTGCTCATGCTTTTCAGATTCTGACTCAGAAAGCTGGAAAT 3264  
Qy ||||| 960 yValLeuTyRang1yMe1a1aseThSereTPa1a1aleuTyRPhel1eAlL 980  
Db ||||| 3265 AAGTCCCTTACAAAGCATGGCTCCACATCGCTTGGGCTGCTCTTACTTCATGCGCC 3324  
Qy ||||| 980 eumethrPheG1yAsnTyRValLeuPheAsnLeuVala1a1eVala1G1uG1yP 1000  
Db ||||| 3325 TCATGACTTTGGCACTATGCTCTTTTAACTGCTGCTGGCCATTTCTTGGAAAGAT 3384  
Qy ||||| 1000 heG1na1aG1uG1yAspA1aThrLySereG1uSereG1uProAspPheSereProSery 1020  
Db ||||| 3385 TCAGGCAAGGAGATGACCAAGCTGAGTCAGAGCTGATTTCTTTTCCGCCAGTG 3444  
Qy ||||| 1020 a1AspG1yAspG1yAspAryLysLySarg1eua1aleuVala1aleuG1yG1uH1a1AG 1040  
Db ||||| 3445 TGGATGATGATGGGGAAGAAAGAGCGCTTGGCTGGCTTGGGAGAAACAGCGG 3504  
Qy ||||| 1040 JuLeuArgLySereLeuLeuProProLeu1e1eH1eThra1a1aThrProMetSereH 1060  
Db ||||| 3505 AACTACGAAGAGCCCTTTTGGCACTCCCTCATCTCATACAGCTGGGACACCAATGTCAC 3564  
Qy ||||| 1060 1aSProLySereSereThng1yValG1yG1uH1a1eug1ySereG1ySereArgThS 1080  
Db ||||| 3565 ACCCAAGAGCTCACACAGAGTGCGGGGGAAGACAGCTGGCTCTGGCTCCGACGTAACA 3624  
Qy ||||| 1080 eRSereRg1ySera1aG1uProG1yAla1aH1eH1eG1uMetLyCySPProProSereA 1100  
Db ||||| 3625 GTAGCAGTGCGCTCGCTGAGCCTCGAGCTGCCACCATGAGTAAGTAATGCCCAAGTG 3684  
Qy ||||| 1100 1aRgSereProH1aseRProTPSera1a1aseSereTPThrSereArgSers 1120  
Db ||||| 3685 CCGGAGCTCCCGCAAGTCCCTGAGTGGGCAAGCACTGACCAAGAGCGCTTCCA 3744  
Qy ||||| 1120 eArGAsnSereLeuG1yArg1a1aProSereLeuLySarg1ySereProSereG1yG1uArgA 1140  
Db ||||| 3745 GCGAGAAAGCCTGGGCGGGGCCCCAGCCTTAAAGGGAAGAGCCGAGCGGAGCGAG 3804  
Qy ||||| 1140 rGSereLeuSereG1yG1uG1yG1uSereG1uAspG1uG1uSereSereG1uG1uA 1160  
Db ||||| 3805 GGTCCCTGCTGCTCGAGAGGCGCAGAGAGTCAGAGTGAAGAGAAAGTTCAAGAAAGAG 3864  
Qy ||||| 1160 SPArG1aseRProa1aG1ySereAspH1aRgH1aRgG1ySereLeuG1uArg1uAlaL 1180  
Db ||||| 3865 ACCGGGCGAGCCAGAGGAGGAGTGAACCATGCCACAGGGGCTCTTGGAACTGAAGCCA 3924  
Qy ||||| 1180 ySereSerePheAspLeuProAspThrLeuG1nVal1ProG1yLeuH1eSarg1Thra1aseRg 1200  
Db ||||| 3925 AGAGTTCCTTGAACCTGCCGACACTCTGCAAGGAGCGGGGCTGCACCGCAGCGCAGCG 3984  
Qy ||||| 1200 1yArGereSera1aseRg1uH1eG1naSPCySaBeng1yLySera1aseRg1yArG1eua 1220  
Db ||||| 3985 GCGGAGCTCTGCTCTGAGACCAAGACTGTATATGCAAGTGGCTTCAAGGGCGCTTTGG 4044  
Qy ||||| 1220 1aRgThrLeuAryGThrAspAspProG1nLeuAspG1yAspAspAspAspAspG1uG1yA 1240  
Db ||||| 4045 CCGGACACTGAAGACTGATGAACCCCACTGGATGGAGTGAATGACAAAGTGAAGGAA 4104  
Qy ||||| 1240 anLeuSereLySg1yG1uArg1eG1na1aTPValaRgSereArgLeuProa1aCySPsa 1260  
Db ||||| 4105 ATCTGAGCAAAAGGGAAGCATACAAAGCCTGGGTCAATCCGGCTTCTGCGCTTGCC 4164  
Qy ||||| 1260 rGg1uArGAspSereTPSera1aTy1LePheProProG1nSereArgPhArgLeuLeuc 1280

Db ||||| 4165 GAGAGCAGATTCCTGGCTGCTATATCTTTCCTCCTCAAGCAAGTTCGCTCTCTGT 4224  
Qy ||||| 1280 yH1eArg1e1eThrH1eLySMeC PheAspH1eVal1a1eLeuVal1e1ePheLeua 1300  
Db ||||| 4225 GTCAACCGATATCACCCCAAGATGTTGACCAAGTGGTCTCTCTCATCTTCCTCCA 4284  
Qy ||||| 1300 sRGCy1eThr1e1a1aMetG1uArgProLyS1eAspProH1aseR1aG1uArg1eP 1320  
Db ||||| 4285 ACTGTATACCAATGCTATGAGCGCCCAAAATTAAGCCCAAGCGCTGAAGCCATCT 4344  
Qy ||||| 1320 heLeuThrLeuSereAsnTyR1ePheThra1aValPheLeuA1aG1uMetThra1aLySv 1340  
Db ||||| 4345 TCCTAACCCTCCCAATCATCATCTTCAAGGCACTTTCTTACTGTAATTAAGACGAAAG 4404  
Qy ||||| 1340 a1Vala1aleuG1yTPCySPheG1yG1uG1na1aTyRLeuArgSereTPaAsnValL 1360  
Db ||||| 4405 TGGGCACTGGGCTGGTGGCTTGGGAGAGCGGCTTACCTGGCGAGAGCTGAATGTC 4464  
Qy ||||| 1360 eUAspG1yLeuLeuValLeu1eSereVal11eAsp1eLeuValSereMetValSereAspS 1380  
Db ||||| 4465 TGGAGCGCTTGGATGCTCATCTCGTATGACATCTGGTCTTCATGGATCTCGACA 4524  
Qy ||||| 1380 eRg1yThrLyS1eLeuG1yMeCLeuAryVal1eUArgLeuLeuArgThrLeuArgProL 1400  
Db ||||| 4525 GCGGACCAAGATCCTTGGCATGCTGAGGGTGCTGGCTGCTGGGACCTGCGCCAC 4584  
Qy ||||| 1400 eUArgVal11eSeraRga1aG1nG1yLeuLyLeuValValG1uThrLeuMetSereL 1420  
Db ||||| 4585 TCAGGATCATCAGCGGCGCCAGGAGCTGAGCTGGTGTAGAGCTGAGTGCATGCC 4644  
Qy ||||| 1420 eUlySPro1eG1yAsn1eVal11eCySPa1aPhePhe1e1ePheG1yLeL 1440  
Db ||||| 4645 TCAAAACCAATGGCAACATGTGTCAATGCTGCTCTTCAATTTTGGAAATTC 4704  
Qy ||||| 1440 eUG1yValG1nLeuPheLySg1yLySPhePheValCySG1nG1yG1uAspThraRgaSn 1460  
Db ||||| 4705 TCGGGGTGAGCTCTTCAAGAGGAAGTTCTTGATGTGATGAGGTGAGGACACAGGAACA 4764  
Qy ||||| 1460 1eThrAsnLySereAspCySa1aG1uA1aseR1yArgTPValaRgH1eLyTyRAsn 1480  
Db ||||| 4765 TCACTAACAAATCCGACTGCTGAGGACGACGATGAGGTCCGCGCAAGTCAACT 4824  
Qy ||||| 1480 heAspAsnLeuG1yG1na1aleuMetSereLeuPheValLeuA1aseR1yAspG1yTPV 1500  
Db ||||| 4825 TTGACAACTGGGCGAGGCTGTGATGCTCTGTGTGTGCTGCTCCCAAGAAAGTTGG 4884  
Qy ||||| 1500 a1Asp1eMetTyRAspG1yLeuAspA1aValG1yValaSPG1nG1nPro1leMetAsnH 1520  
Db ||||| 4885 TTGACATCATGTATGATGGGCTGGATGCTGTGGGTGGAATCAAGCAAGCCCATCATGAACC 4944  
Qy ||||| 1520 1aSPnProTPMeCLeuLeuTyRPhel1eSerePheLeuLeu1eVala1aPhePheValL 1540  
Db ||||| 4945 ACAACCCCTGAGATGCTGATACCTTCACTCTCTCTCAATCGGCGCTTCTTGTGCC 5004  
Qy ||||| 1540 eUAsnMetPheValG1yVal1a1aG1uAsnPhel1eLySPCySarg1nH1eG1nG1uG 1560  
Db ||||| 5005 TGAACATGTTTGTGGCGGTGGTGGAGAACTTCCATTAAGTGAAGACAGCCAGGAAG 5064  
Qy ||||| 1560 1uG1uG1uA1aRgArGArG1uG1uLyArG1euaRgArG1eug1uLyLySArGArG 1580  
Db ||||| 5065 AGGAGAGGCGAGCGCGCTGAGAGAGCACTACGAGAGCTGAGAGAAAGAGAGGA 5124  
Qy ||||| 1580 eR1ySg1uLySg1uMetA1aG1uA1aG1nCySaLySPProTyR1ySereAspTyRAsp 1600  
Db ||||| 5125 GTAAAGAGAAGAGATGGCGCAAGCCAGTGAAGCGCTTCACTCTGACTCAAGAT 5184  
Qy ||||| 1600 heArgLeuLeuValH1eH1eS1eUcySPThSereH1eTyRLeuAspLeuPhe1eThng1yV 1620  
Db ||||| 5185 TCGGCTCTTGTCAACCACTGTGTACAGGACACTTGAACCTTTCATCACTGGAG 5244  
Qy ||||| 1620 a11eG1yLeuAsnVal1a1ThrMetA1aMetG1uH1eTyR1nG1nProG1n1eLeua 1640  
Db ||||| 5245 TCATCGGCTGAACGTGTGCTCATGTGCAATGAACATTACAGAGAGCCCAAGATCTTGG 5304

QY	1640	spgLuAlaLeuuyrIIeCySaenTyrrIIepheThrValIIlepheValIphegiuserValP	1660
Db	5305	ACGAGGCTCTGAAGATTCGCAATTAACATCTTTACCGTCACTTGTGCTTGAGTCAAGTTT	5364
QY	1660	heLyLeuValAlaPheAlaPheArgArGPhePheGlnAspArgTrpAsnGlnLeuAspL	1680
Db	5345	TCAAACTGTGGCCCTTTGGCTTCCGCCGTTTCTTCCAGGACAGGAGGAAACGACTGGACC	5424
QY	1680	euaAlaIleValLeuLeuSerIIleMetGlyIleThrLeuGlnGluIleGluValAsnLeuS	1700
Db	5425	TGGCAATGTGCTGTGCTTCATCATGGGATCACACTGGAGAGATGAGGTCATTCGT	5484
QY	1700	eLeuProIleAsnProThrrIleIleArgIleMetArCyValLeuArgIleAlaArgValL	1720
Db	5485	CCCTGCCCATCAACCCACCATCATCCGTATCATAGGGGTCTCCGCAITGCTCAGATTC	5544
QY	1720	eulLyLeuLeuLySMeAlaValGlyMeArGAlaLeuLeuHISThrValMetGlnAlaL	1740
Db	5545	TCAAGCTGTTGAAGATGGCTGTGGGCAATGGGGCACTGCTGCACAGGGATGCAGGCC	5604
QY	1740	eupProGlnValGlyAsnLeuGlyIleLeuLeuPheMetLeuLeuPheHeIIePheAlaAlaL	1760
Db	5605	TGCCCAAGTGGGGAACCTGGGACTTCTTCATGTATGTTTTTCATCTTTGCAGGCTC	5664
QY	1760	eugIYValGluLeuPheGlyAspLeuGluCySaSpGluThrHISProCySgIleGluLeuG	1780
Db	5665	TGGGGGTGAGGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCTTGTGAGGGCTTGG	5724
QY	1780	IYArgHISAlaThrPheArgAsnPheGlyMeAlaPheLeuThrLeuPheArgValISerT	1800
Db	5725	GTCCGCAATGCCACTTTAGGAACCTTGGTATGGCTTCTGCACCTCTTCCAGTCTCCA	5784
QY	1800	hGGLYAspAsnTrpAsnGlyIleMetLyAspProSerArGPcySaSpGlnGlnIleuSerT	1820
Db	5785	CTGGGAGACAACCTGATGTATTATGAAGAGACACCTCCGGGACTGTGACCGAGGTCCA	5844
QY	1820	hrcySArThrAsnThrrAlIleSerProIleTyPheValSerPheValLeuThrrAlaGlnP	1840
Db	5845	CTGTCTCAACAACCTGTCACTCCCTATCTACTTTGTGTCTTGTGCTGAGGGCCCAAGT	5904
QY	1840	heValLeuValAsnValValIleAlaValLeuMetLyHISLeuGlnIleuSerAsnLySg	1860
Db	5905	TGTGTGTGGTCAACGTGGTCAATAGCTGTGTGATGAAGCACTGGAAGAAACACCAAG	5964
QY	1860	IYAlaLyGlnGlnValaGluLeuGlnValaGluLeuGlnIleuGlnIleuMetLySThrLeuSerP	1880
Db	5965	AGGCCAAGAGAGAGCCGAGCTCGAGGCCGAGCTGAGCTGAGATGAAGAGCTCAAGC	6024
QY	1880	roGlnProHISerProLeuGlyIleSerProPheLeuTrpProGlyValaGlnIleValAsnS	1900
Db	6025	CGCAGCCCACTCCCGCGTGGGCAAGCCCTTCTGTGGCCCGGGGTGAGGGGTGCACACA	6084
QY	1900	eTrHrAspSerProLySProGlyValaProHISThrThrrAlaHISIleGlyAlaAlaSerG	1920
Db	6085	GTACTGACAGCCCTTAAGCCTGGGGCTCCACACACACTGCCCCACATGGAAGAGGCTCGG	6144
QY	1920	IYPheSerLeuGlnHISProThrMetValProHISProGlnGlnValaProValaProluG	1940
Db	6145	GCTTCTCCCTTGAGACCCCAAGATGTACCCACCCCGAGGAGGATGCGAGTCCCTCAG	6204
QY	1940	IYProAspLeuLeuThrrValaArgLySergIYValSerArGThrrHISerLeuProAsnA	1960
Db	6205	GACCGAGACTGCTGACTGTGAGAGAACTGTGTGTACGCCGAGCGGACTCTCGCCCAATG	6264
QY	1960	spSerTyMeCySaArgaGngIySerThrrAlaGluArgSerLeuGlnYHISArgGlyTrpG	1980
Db	6265	ACAGCTACATGTGCGCAATGGAGAGACTGTGAAGATCCCTAGAGACAGAGGGCTGGG	6324
QY	1980	IYLeuProLyAlaGlnIleSerGlySerIleLeuSerValHISerGlnProAlaAspTrHIS	2000
Db	6325	GGCTCCCCCAAAAGCCAGTCAAGGCTCAATCTTGTGCTGTCACTCCCAACGACGACACCA	6384

QY	2000	ercySIIleLeuGlnLeuProLyAspValHISrTyLeuLeuGlnProHISrGlyAlaProT	2020
Db	6385	GCTGCATCTTACAGCTTCCCAAGATGTGACATATCTGTCTCCAGGCTCATGGGGCTCCA	6444
QY	2020	hrrTrpGlyAlaIleProLyLeuProProGlyIYArgSerProLeuAlaGlnArgProL	2040
Db	6445	CTTGGGGGCCCATCCCTTAACTACCCCACTGAGCCGCTCCCTTGCTCAGAGGGCTTC	6504
QY	2040	euarArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgG	2060
Db	6505	TCAGGCGCAGGACAGCAATTAAGACTGACTCTCTGAGATGTGCAAGGGCTGGGTAAGCCGG	6564
QY	2060	IuAspLeuLeuSerGluValSerGlyProSerCySProLeuThrrArgSerSerPheT	2080
Db	6565	AAAGCTGTGTCTGAGAGGTAGTGGGCCCTTCTGCTCCGTGACCCGGTCCATCTTCT	6624
QY	2080	rrpGlyIySerSerTleGlnValGlnGlnArgSerGlyIleGlnSerLyValSerLyS	2100
Db	6625	GGGGCGGGTCCAGCATCAGGTGCAGCAGCGTTCCGGCATCCAGAGCAAGTCTCCAAAGC	6684
QY	2100	ISIIeArgLeuProAlaProCySProGlyLeuGlnIleuProSerTrpAlaLyAspProProG	2120
Db	6685	ACATTCGCTGTGCAAGCCCTTGGCCAGGCTGTGAACCCAGCTGGGACCAAGAGACCTTCAG	6744
QY	2120	IuThrrArgSerSerLeuGlnLeuAspThrrGluLeuSerTrpIleSerGlyAspLeuLeuP	2140
Db	6745	AGACCAAGAGCACTTGAAGCTGGACAGGAGCTGAGCTGGATTTCCAGAGACTCTCTTC	6804
QY	2140	roSerSerGlnGlnGluProLeuPheProArgAspLeuLySlySlyCyTySerValaGluT	2160
Db	6805	CCAGCAGCCAGAGAAACCCCTGTTCACAGGACCTGAAGAAAGTGTATACAGTGTAGA	6864
QY	2160	hrgIleSerCySArArgArGPProGlyPheTrPLeuAspGlnGlnArgArgHISerIleA	2180
Db	6865	CCAGAGCTGCAGGCGCAGGCTTGAGTTCTGGCTAGATGAACAGCGAGACATCTCCATTG	6924
QY	2180	IaValSerCySLeuAspSerGlyIleSerGlnProArgLeuCySProSerProSerSerLeuG	2200
Db	6925	CTGTACAGTGTCTGGAACAGGGGCTCCCAACCCCGCTATGTCCAAAGCCCTCAAGCCTCG	6984
QY	2200	IYgIyGlnProLeuGlyIYProGlySerArGPolySlySlySlyLeuSerProProSerT	2220
Db	6985	GGGGCCAACTCTTGGGGGTCTCTGGAGCCGGCTTAAGAAAACCTAGCCCAACCAAGTA	7044
QY	2220	IleSerTleAspProProGlySerGlnIleYSerArGPProProCySArProGlyValaCysL	2240
Db	7045	TCTCTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCTCATGTGAGTCTGTGTCTGCC	7104
QY	2240	euarArgArgAlaProAlaSerAspSerLyAspProSerValSerSerProLeuAspS	2260
Db	7105	TCAGAGAGAGGGCGCCGGCCAGTGACTTAAGATCCCTGGGTCTCCAGCCCTTGACA	7164
QY	2260	eTrHrAlaAlaSerProSerProLySlyAspThrrLeuSerLeuSerGlyIleuSerSerA	2280
Db	7165	GCAGCGGCTGTCAACCTTCCCAAGAAAGACAGCTGAGTCTCTGTGTTGTCTTCTG	7224
QY	2280	spProThrrAspMetAspPro 2286	
Db	7225	ACCCACAGACATGAGACCC 7244	
RESULT 4			
LOCUS	BD224079	7285 bp	DNA linear PAT 17-JUL-2003
DEFINITION	T-type calcium channel.		
ACCESSION	BD224079		
VERSION	BD224079.1 GI:33033849		
KEYWORDS	JP 2002525077-A/2.		
SOURCE	Rattus sp.		
ORGANISM	Rattus sp.		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
Rattus.			
REFERENCE	1 (bases 1 to 7285)		

AUTHORS Li, M.  
TITLE T-type calcium channel  
JOURNAL Patent: JP 2002525077-A 2 13-AUG-2002;  
SOUTH ALABAMA MEDICAL SCIENCE FOUNDATION  
COMMENT OS Rattus sp. (rat)  
PN JP 2002525077-A/2  
PD 13-AUG-2002  
PF 26-AUG-1999 JP 2000570372  
PR 26-AUG-1998 US 60/098004,27-JAN-1999 US 60/117399 PI

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PC C12N15/09,A61K31/711,A61K45/00,A61K48/00,A61P3/10,C07K14/47,  
PC C07K16/18,  
PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12Q1/68,G01N33/  
PC 15,G01N33/50,  
G01N33/53,G01N33/53,G01N33/566,G01N33/577,G01N33/58,G01N33/68// PC  
C12P21/08  
PC C12N15/00,C12N5/00  
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Location/Qualifiers  
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Alignment Scores:  
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Score: 11829.00 Matches: 2270  
Percent Similarity: 97.72% Conservative: 1  
Best Local Similarity: 97.68% Mismatches: 15  
Query Match: 98.35% Indels: 38  
DB: 6 Gaps: 2

US-09-611-257A-24 (1-2287) x BD224079 (1-7285)

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QY 20 rGProSerSerAaPProGlyProArgLeuAlaRgLyTrPThrArgArgMecG 40  
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QY 40 LuRgAlaProArgSerArgAaPserProValAlaSerArgSerThrTh-CysAProG 60  
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QY 159 ePheAlaValGluMetValIlyLysMetValAlaLeuGlyIlePheGlyLysLysCysTy 179

DB 537 CTTTGTGCTGGAAATGNGTGAAGATGTGGCCTTGGGCATCTTGGAGAAATGTTA 596  
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DB 597 CTTGGAGACACTTGGAAACCGGCTGTGACTTTTCAATTCATTTGACGAGGAATGTGAGTA 656  
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DB 1377 GCTGATGCGGAGAGCGGTGTACGATTCCTGTCCATGTATACCACTTGGCAAGCTTTC 1436  
QY 459 rGluProGlySerCysTrpGlyGlyLeuLeuLysTrpLeuValTrpIleLeuAaRgAla 479  
DB 1437 TGAAGCAGGAGCTGTATGAGAGTACTCAAGTCTGTGTATCATCTTCCGAAAGC 1496  
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Db	6057	CAATGGAGCACCTGCTGAGAGATCCCTTAGACACAGGGGCTCCGAGCCCAAGCCCA	6116
QY	1985	nSerGlySerIleLeuSerValHisSerGlnProIaAsPThrSerCyAlleLeuGlnLe	2005
Db	6117	GTACAGGCTCATCTGTGCTCCGTTCACTCCACACAGACACACAGCTGATCTTACAGCT	6176
QY	2005	uProIyAspValHisTYrLeuLeuGlnProHisGlyAlaPThrTTPGjYAlaIlePr	2025
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Db	6297	AATTAAGACTGACTCCCTGGATGTGAGGGCTGGGTACCGGAAAGACTGTGTGACA	6356
QY	2065	uValSerGlyProSerCySspProleuThraSserSerSerPheTTPGjYgIySerSer11	2085
Db	6357	GGTGAAGTGGCCCTCTGCTGCTGACCCGCTCTCATCTCTTGGGGGGGTGAGCAT	6416
QY	2085	eGlnValGlnGlnArSserGjYIleGlnSerIySAlSerIySHIsIleArGLeuProAl	2105
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QY	2105	aBroCySspProGjYLeuGlnuProSerTTPAlaIyAspProPProGjuthraSserSer1e	2125
Db	6477	CCCTTGCCACAGGCTCGAACCAGGCTGGGCAAGGACCTTCAGAGACCAAGACAGCTT	6536
QY	2125	uGluLeuAspThraGluLeuSerTTP1eSerGlyAspLeuLeuProSerSerGlnGluG1	2145
Db	6537	AAAGCTGACACAGGAGCTGAGTTCATTCAGAGACCTCCCTTCCACAGACCAAGAA	6596
QY	2145	uProIeuaPheProArSspLeuLeuIySAsCyArSserValGluThraGlnSerCyArAr	2165
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QY	2165	gArGProGjYpHeTTPLeuaSspGluGlnArGArHisSerIleAlaValSerCySLeuaS	2185
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QY	2185	pSerGlySerGlnProArGLeuCySProSerProSerSerIeugIyGlnProLeuG1	2205
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QY	2205	yG1YProGjYSerArGProIySAlSylSLeuSerProPProSerIleSerIleAsPProPr	2225
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QY	2245	oAlaSerAspSerIyAsPProSerValSerSerProleuaSspSerThraAlaISerPr	2265
Db	6897	GGCCAGTGACTTAAGATCCCTCGGTCCAGCCCCCTTGAACACAGCGGCTCTCAC	6956
QY	2265	oSerProIySAlSAsPThraSserIeuaSerGjYLeuSerSerAsPProThraSspMeAs	2285
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DEFINITION	Rattus norvegicus T-type calcium channel isoform mRNA, complete		

ACCESSION	AF125161	cds.
VERSION	AF125161.1	GI:4633669
KEYWORDS		
SOURCE	Rattus norvegicus (Norway rat)	
ORGANISM	Rattus norvegicus	
REFERENCE		
AUTHORS	Zhang, H., Bhattacharjee, A., Hu, F., Zhang, M., Goewami, T., Wang, L., Wu, S., Berggren, P.O. and Li, M.	
TITLE	Cloning of a T-type Ca2+ channel isoform in insulin-secreting cells	
JOURNAL	Diabetes	
MEDLINE	20081696	
PUBMED	10615950	
REFERENCE	2 (bases 1 to 7286)	
AUTHORS	Zhang, H., Hu, F., Bhattacharjee, A., Zhang, M., Wu, S., Berggren, P. and Li, M.	
TITLE	Direct Submision	
JOURNAL	Submitted (01-FEB-1999) Pharmacology, University of South Alabama,	
FEATURES	Mobile, AL 36608, USA	
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	VLVAVVAVLIMKHLSESNKEAKERAELEAELEMKTLSPQPHSLPSSPLMPREVEY	
	NSPSPKPGAPHTTAHIGAASGFLSEPLTWPHPEEVPVPLGDLTLVRSGVSRTHS	
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	PHGAPTWGAIIPKLPPIPPERSPLAQRPLRRQAIRTDSDVOGLSGREDDLSEVSGPSCP	



ORIGIN

LTRSSFWGSGSTQVQDNKSCISKYSKAIRLRAPCPGLESPWAKDPPTRRSLLEDTLE  
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Alignment Scores:  
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Score: 11829.00 Matches: 2270  
Percent Similarity: 97.72% Conservative: 1  
Best Local Similarity: 97.68% Mismatches: 15  
Query Match: 98.35% Indels: 38  
DB: 10 Gaps: 2

US-09-611-257A-24 (1-2287) x AF125161 (1-7286)

QY 1 MetLeuProHieArg-VaIProArg-CyEValArgThrProProleuAArgGlySerAla 20  
DB 58 ATGCTCCCCACCGGGGGTCCCGGTTGGGTGAGACACTCTCTGAGGGGCTCCGCTC 117  
QY 20 rGProSerSerAProProGlyProAArgleuAlaArgGlyTTPThrArgArgMetG 40  
DB 118 GCCCTCTTCGACCCCGGGGGCCCGGCTGGCCAGAGATGAGCAGAGAGAGATG 177  
QY 40 lUaArgAlaProAArgSerAArgSerProValAlaSerArgSerThrThrCyAProG 60  
DB 178 AGCGGGCGCCGAGAGAGTCCGGGACAGCCCGTAGCTTCACGCACTCAACGACTGTC 237  
QY 60 lYProGlyAla-AlaGlyAla-GlySerThrGlyuYAspProGlySerAlaAspSerG 79  
DB 238 GGCCTGGGGCGCGCAGAGCGCGGGGTGACGAGAAAGAACCCGGGACGCGGACTCC 297  
QY 79 uAlaGlyGlyLeuProTyProAlaLeuAlaProValAlaPhePheTyLeuSerGlnAs 99  
DB 298 GCGGAGGGGCTCCGTAACCGGCGCTAGCCCGGGTGTCTTCTTCACTTGAGCCAG 357  
QY 99 pSerAArgProAArgSerTyCyAleuArgThrValCyAspProCTPheGlyuArgValSe 119  
DB 358 CAGCCCCCGCGAGGTGTGTCTCCGACGCTGTAAACCCGTGTTCAGAGGAGTCA 417  
QY 119 rMetLeuValAlaLeuLeuAsnCyValThrLeuGlyMetPheArgProCyGlnuAsp 139  
DB 418 TAGCTGTGTATCTTCTCAACTGTGTGACTGTGGGTGATGTTAGGCGGTAGAGCA 477  
QY 139 eAlaCyAspSerGlnArgCyAArgGlyLeuGlnAlaPheAspAspPheIlePheAlaP 159  
DB 478 TGCCTGTGACTCCACGCGCTGCGGATCTGCAAGGCTTCGATGACTTCTTCCCTT 537  
QY 159 ePheAlaValAlaGluMetValAlaLeuMetValAlaLeuGlyIlePheGlyLeuLysCy 179  
DB 538 CTCTGTGTGGAATGATGTGTGAAAGTGTGGCTTGGGCATCTTGGGAAAGTAA 597  
QY 179 rLeuGlyAspThrTTPAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGly 199  
DB 598 CCGGAGAGACACTTGGAAACCGGCTTGACTTTTCATTGTCAAGGAGTGTGAGTA 657  
QY 199 rSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 219  
DB 658 TTGGCTGTGACCTGCAAGACTCAGCTTCTCCGACGTCAAGACAGTCCGTGTGTCG 717  
QY 219 oLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAspTh 239  
DB 718 GCTCAGGGCATTAAACCGGGTGCACAGCATGCGCATCTCGTCACTTATCTGCGG 777  
QY 239 rLeuProMetLeuGlyAsnValLeuLeuLeuCyPhePheValPhePheIlePheGly 259  
DB 778 CTGGCTATGTCTGGCAACGCTCTGCTGTCTTCTTCTTTTCAATCTTGGCAT 837  
QY 259 eValAlaValAlaGlnLeuTrpAlaGlyLeuLeuArgAsnArgCyPheLeuProGlnuAs 279  
DB 838 CGTGGGGGTCCAGCTGTGGGCAAGACTGCTTCCGAACCATGCTTCTCCCGAGAACT 897  
QY 279 eSerLeuProLeuSerValAspLeuGluProTyTyGlnThrGluAsnGluAspGluSe 299

DB 898 CAGCTTCCCTCGACCGGTGACCTTGACCTTATTACAGACAGAGATGAGAGAG 957  
QY 299 rProPheIleCySerGlnProAArgGluAsnGlyMetArgSerCyAArgSerValProTh 319  
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DB 1018 ACTGGGTGGGAGAGCGGTGTGGGCCACCTCGACGTCTGACCTATGAGACTTATPACG 1077  
QY 339 rSerSerAsnThrThrCyValAsnTrpAsnGlnTyTyThrAsnCySerAlaGlyG 359  
DB 1078 TTCCAGCAACACCACTGTGTCACTGGAACCAAGACTATACCACTGTCTCGGGGGGA 1137  
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QY 379 ePheGlnValIleThrLeuGluGlyTTPValAspIleMetTyPheValMetAspAlaH 399  
DB 1198 CTTCAGGTCAATCAACATGAGAGGCTGGGTGACATCAATGTACTTGTATGAGACTCA 1257  
QY 399 sSerPheTyAsnPheIleTyPheIleLeuLeuIleIleValAlaGlySerPhePheMet 419  
DB 1258 CTCTCTTCAACCTTCAATCTTCACTTCTTCTTCTTCACTCGGGCTCTTCTTCAAT 437  
QY 419 eAsnLeuCyLeuValAlaIleAlaThrGlnPheSerGluThrGlyGlnArgGlySerG 439  
DB 1318 CAACCTGTGCTCGTGTGTGATGATGCCACGAGTTCTCCGAGCAAAACAGCGGAGATCA 1377  
QY 439 nLeuMetArgGlyGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe 459  
DB 1378 GCTGATGCGGAGACGCGTGTACATCTCTGTCCATGTCAATGTACACCTCGGCAAGCTTCTC 1437  
QY 459 rGluProGlySerCyTyTyGlyGluLeuLeuTyTyLeuValTyTyIleLeuArgGlyAl 479  
DB 1438 TTAGCCAGGACACTGTGATGAGAGACTTCAAGTACCTGTGTATCTTCCGAAAAC 1497  
QY 479 aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValaArgAlaGlyLeuLeuSerSe 499  
DB 1498 AGCCGGAAGCTGGCCAGGCTCTAGGCTATAGCGGTATAGCGGCGGCTGCTCAGCAG 1557  
QY 499 rProValAlaArgSerGlyGlnGluProGlnProSerGlySerCyTyThrArgSerThi 519  
DB 1558 CCAAGTGGCCCTAGTGGGCAAGAGCCCAAGCCAGTGCACCTCACTCGCTCACACCG 1617  
QY 519 gArgLeuSerValIleHieLeuValIleHieHieHieHieHieHieHieHieHieHie 539  
DB 1618 TGTCTGTGTGTCCACCACTGTGTCCACCACTCAACCACTCAACCACTCAACCACT 1677  
QY 539 uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAs 559  
DB 1678 GGGTAATGGGAGCTCAAGATTCCCGGGCCAGCCAGAGATCCAGGACAGGAGATCCAA 1737  
QY 559 nGlySerAArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProPr 579  
DB 1738 TGGGTCTCCCGGCTCATCTATCAACCACTCTTCAACCACTCTCTCTGGGGGCCCTTC 1797  
QY 579 oArgGlyAlaGlyuSerValHieSerPheTyThiAlaAspCyHieHieGlyProValAr 599  
DB 1798 GAGGGGTGGAGTGTGACAGACTTCTTACCAATGTGTGACTGCACTTGTGAGCAAGTCCG 1857  
QY 599 gCyGlnAlaProProProArgCyAspProSerGlnAlaSerGlyArgThrValGlySerG 619  
DB 1858 TTGCCAGGACCCCTTCCAGATGGCCATCGAGAGGATCTGTGTAGACTGTGGTATGTG 1917  
QY 619 yLysValTyProThrValHieThiSerProProProGluIleLeuLysAspLysAlaLe 639  
DB 1918 GAAAGGTATCCCACTAGTGCATATCAAGCCCTTCAACAGAAATCTGAAAGAAAGCACT 1977  
QY 639 uValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProG 659

Db	1978	AGTGGAGGTGGCCCCCAGCCCTGGGGCCCCCACCCTTCACACAGCTTCAACATCCACCTGG	2037
Qy	659	YProheserSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSer	679
Db	2038	GCCCTTCAGACTCATTGCAACAGAGCTCTTGAGAGACACAGATGAGGGAGGCTCCATAGCTC	2097
Qy	679	TCysAlaHisSerSerProCysSerLeuAlaAspSerGlyAlaCysGlyProAspSerCys	699
Db	2098	CTGGCAAAATCTCCAGCCCTTCTGCTCCAAAGGACAGACGTGAGAGCTCCGGGGCCGACAGTTG	2157
Qy	699	SPProLyrcysAlaAagThrnglyAlaGlyGluProGluSerLysAlaAspHisValMetProAs	719
Db	2158	TCCCTACCTGTGCCGAGACGGAGACGAGAGAGCAAGTCCGTGACCATGTCATGTCAGCTCGA	2217
Qy	719	pSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAs	739
Db	2218	CTCAACACACGAGAGGCTGTGTATGATTCACACAGGACCTCAGCACATGATGACCTCGGGGA	2277
Qy	739	pProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLe	759
Db	2278	TCCCCACAGCCGGCCGGACAGCGGAGGCTGGGCCCAATGACAGAGCTAGTTCGTGCTCT	2337
Qy	759	uAlaPheThrPaagLeuHisCysAspThrPheArgLysHisLeuAspSerLysTyrPheGlu	779
Db	2338	GCCCTTCTCGAGAGGCTGATCTGTGACACATCCGGAAGATCGAGTATACCAATACTTTGG	2397
Qy	779	YArgGlyLysMetLeuAlaLeuValaLysThrLeuSerMetGlyLeuGlyTyrHisGlu	799
Db	2398	CCGGGGGAAATCAGATCCGCATCTCTGGTCAATACATCAGATCGGACATCGAGTACACAGA	2457
Qy	799	uGlnProGluGluLeuThrAsnAlaLeuGluHisSerAsnHisLeuPheThrSerLeuPhe	819
Db	2458	GCAGGCCGAGGAGCTCACCAACGCCCTGGAATCAGCAACATCGCTTCACACAGCTCTTT	2517
Qy	819	eAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrHisLysAspPr	839
Db	2518	GCCCTTGGAGAGCTGCTGAACCTCTGTGTCACGCTCCCTTGGCTACATTAAGAAATCC	2577
Qy	839	CTYrAsnHisPheAspGlyValHisValaHisSerValTyrGluHisLeuGlyGlnGlu	859
Db	2578	CTACAAACATCTTGTATGTGTGTCATTTGTGTGTCATAGTGTGTGGAGATTTGTGGGCGACA	2637
Qy	859	ngLysGlyLysSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValaLar	879
Db	2638	GGGAGGTGGCCGTGCGGTGCTGCGGACCTTCGCTCGCTGATGCGGGGTGGAAGCTGTGCG	2697
Qy	879	gPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValaL	899
Db	2698	CTTCTCGCGCGCCCTGACAGCGGACGACCTGTGTGTCTCATGAAGACATGAGCAACGTGGC	2757
Qy	899	aThrPheCysMetLeuLeuMetLeuPheHisPheHisSerHisLeuGlyMetHisLeu	919
Db	2758	CACCTTCTGCAGTCTCTCTCATGCTTTATCTTCATCTTCAGCATCTCGGGGAGATGATCT	2817
Qy	919	uPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAspHis	939
Db	2818	CTTTGGTTGCAAGTTCGCATCTGGAACGGATGGGAGACAGCTTGCACAGCCGGAAGAAATTT	2877
Qy	939	eAspSerLeuLeuThrAlaHisLeuValThrValPheGlnHisLeuThrGlnGluAspThrAs	959
Db	2878	CGACCTCCCTGTGGGCGCATGCTACGTCTTTCAGATTCGATTCAGGAAGACTGGGA	2937
Qy	959	nLysValLeuTyrAsnGlyMetAlaSerThrSerSerThrAlaHisLeuTyrPheHisLeu	979
Db	2938	TAAAGTCTCTACAAACGGCATGGCTCCACATCGTCTTGGGCTGCTCTTACTTCATGCTC	2997
Qy	979	aLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValaHisLeuValaGluGlu	999
Db	2998	CCTCATGACTTTTGGCACTATAGTCTCTTTAACCCTGCTGGGAGGCATTTCTTGGAAAGG	3057
Qy	999	yPheGlnAlaGlu-----	1003
Db	3058	ATTCACAGAGGAGGAATTCGCAACGGGAAGATCGAGTGACAGTTAAGCTGATATCA	3117

QY	1004	-----GlyAspAlaThrLysSerGluSerGluProAspPhePn	1016
Db	3118	GCTCCCTGTCAACTCTCAGGAGGAGATGTCACCAAGTCTGAAGTCAAGAGCTTAATTTCTT	3177
QY	1016	eSerProSerValAspGlyAspGlyValAspArgLysArgLysAlaLeuValAlaLeuGly	1036
Db	3178	TTCCGCCAGGTGTGATGTATGTGGGACAGAAAGAGAGCGCTTGCGCTTGAGCTTTGGG	3237
QY	1036	YGLNH1aAlaGluLeuArgLysSerLeuLeuProIleLeu1aAla1aTh	1056
Db	3238	AGAACAGCGGAACTTACGAAAGAGCGCTTTGGACACCCCTCATCATCAGCTGCGTGCAG	3297
QY	1056	rPromSerSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuLysGlySer	1076
Db	3298	ACCAATGTCACTACCCCAAGAGCTTCACACAGGTGTGGGGAGAGCACTGGAGCTTGCTC	3357
QY	1076	rArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCy	1096
Db	3358	TCGACGTAACAGTACAGTGGGTCCTGAGCGCTGAGCGTCCACCATGATGATGAATC	3417
QY	1096	sProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe	1116
Db	3418	TCCCCCAAGTCCCGCAGCTCCCGCACATCTCTGAGTGGGCAAGCGTGGACAG	3477
QY	1116	rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSe	1136
Db	3478	CAGCGCGTCCACGACGAAACAGCGCTGGCGCGCGGCCGCCAGCGTAAAGCGAGAGCGCCGAG	3537
QY	1136	rGlyGlyLysArgArgSerLeuLeuSerGlyGlyGlyGlyGluSerGluAspGluGluSe	1156
Db	3538	CGGGAGCGGAGGTCCCTGCTGTCTGTGAGAGGGCGAGAGAGTACAGATAGAGAGGAAG	3597
QY	1156	rSerGluGluAspArgLysSerProAlaGlySerAspHisArgHisArgLysSerLeuGly	1176
Db	3598	TTCCAAAGAGGACCGGGCCAGCCACAGAGGACGTACATCGCCACAGGGGTTCTTTGGA	3657
QY	1176	uArgGluAlaLysSerSerPheAspLeuProAspThrLeuGluValProGlyLeuHisAr	1196
Db	3658	ACGTGAGGCCAAGAGTTCTTTTGACCTGCTGACACTCTCAGAGTGGCGGGGCTGCACCG	3717
QY	1196	qThrAlaSerGlyLysArgSerSerAlaSerGlyHisGlnAspCysAsnGlyLysSerAlaSe	1216
Db	3718	CACAGCCAGCGCGCGGAGCTCTGCTCTGTGAGCACCAAGACTGTATGTGCAAGTCGGCTTC	3777
QY	1216	rGlyArgLeuAlaArgThrLeuArgThrAspAspProGluLeuAspGlyLysAspAspAs	1236
Db	3778	AGGCGGTTTGGCCCCGACCCCTGAGAGACTGATGACCCCACTGGATGGGATATGACAA	3837
QY	1236	naSPGluGlyAsnLeuSerLysGlyLysArgGlyLeuAlaTrpValArgSerArgLeuPr	1256
Db	3838	TGAATGAGGAAATCTGTGCAAAAGGGAAACCAATACAAAGCTGGGTGCAATCCCGGCTTCC	3897
QY	1256	oAlaCysCysArgGlyLysArgAspSerTrpSerAlaTyrlLephProProGluInsArgPh	1276
Db	3898	TGCTCTTTCGCGAGAGGAGATTCCTGTGTGGCTTAATCTTCTCTCTCAGTCAAGCTT	3957
QY	1276	eArgLeuLeuCysHisArgGlyLeileThrHisLysMetPheAspHisValValLeuVal11	1296
Db	3958	TGCTCTCTCTGTGTACCGGATTCATCAACCAAGAGATTTTGACATCATGTGTCTCTCGTCAT	4017
QY	1296	eLephLeuAsnCysleileThrIleAlaMetGlyLysArgProLysIleAspProHisSerAl	1316
Db	4018	CATCTTCTCACTGTATCAACCATCGCTATGAGAGCGCCCAAAATTGAACCCCAACAGCC	4077
QY	1316	agLysArgIlePheLeuThrLeuSerAsenTyrlLephThrAlaValPheLeuAlaGluMe	1336
Db	4078	TGAGCGCATCTTCTGTACCCCTTCACATCACTCATCTTCAACGCGAGTCTTTCTAGCTGAAT	4137
QY	1336	rThValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrlLeuArgSerSe	1356
Db	4138	GACAGTAAAGTGTGTGCACCTGGCTGGTCTTTGGGAGACAGGCCCTACCTGTGCAGCAG	4197





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Pred. No.:	0
Score:	11673.00
Percent Similarity:	97.77%
Best Local Similarity:	97.73%
Query Match:	97.05%
DB:	6
	Gaps: 2
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QY	34 TTPThArgArgArgMetGluArgAlaProArgSerArgSerProValAlaSerArg 53
Db	2 TGGACAGAGAGAGATGGAGCGGCGCGCGAGAGTCCGAGACAGCCCGTAGCTTCAGCG 61
QY	54 SerSerThrThCysProGlyProGlyVala-AlaGlyVala-GlySerThrGluArgAsp 73
Db	62 AGGTCAACAGACTGTCCGGAGCCGGGGGCGGAGAGGCGCGGGGTCAAGGAAAGAAC 121
QY	73 roGlySerAlaAspSerGluAglGlyLeuProTyProAlaLeuAlaProValAlaP 93
Db	122 CGGGAGCGCGGAGACTCCGAGGGGAGGGGCTGCGTACCCGGCGCTAGCCCGGTGGTTT 181
QY	93 hepHeTyLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsp 113
Db	182 TCTTCTACTTGGACCAAGACAGCCGCCGAGAGCTGGTGTCTCCGACGGTCTGTAAAC 241
QY	113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db	242 CGTGGTTCAGAGGAGTCAAGTATGCTGTGATCTTCTTCACTGTGTAGCTGTGGTATGT 301
QY	133 hepArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 153
Db	302 TCAAGCGCGGTAGAGACATTTGCTGTGACTCCAGCGCTGCCGATCTTCAGGCGCTTCG 361
QY	153 spAspPheIlePheAlaPhePheAlaValIleGluMetValIleYMetValAlaLeuGlyI 173
Db	362 ATGACTTCATCTTTTGCTTTCTTGTCTGTGGAAATGCTGTAAAGTGTGGCTTGGGCA 421
QY	173 IePheGlyIleValCysTyLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
Db	422 TCTTTGGAGAAATGTTAACTGGGAGACACTGGAAACCGGCTTGACTTTTCACTGTCA 481
QY	193 IeAlaGlyMetLeuGlyTyLeuSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db	482 TTGCAGAGAGTCTGAGATTTGCTGTGACCTGCAGAAAGTCAAGCTTCCGCAATCAGGA 541
QY	213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db	542 CATTCGCTGTCTGGCAGCCGCTCAAGGGCACTTAACCGGGTCCAGAGATGGCACTTTCG 601
QY	233 aIThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db	602 TCACATTACTGCTGAGACACTTGGCTTAACTGTGGGCAAGTCTCTCTCTCTCTCTTTCG 661
QY	253 aIlePhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
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 DB 962 CCAACTGCTCTGTGGGCGAGACACACCCCTTCAAAGGCCCATCACTTTGACAACTTG 1021  
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DB 1802 TACTAAGGATTAACACTAGTGGAGGTGGCCCCAGGCTCTGGGCCCCCACTTCACCA 1861  
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 DB 1862 GCTTCAATATCCCACTGGGCGCTTCAGTCTCATGACAAAGTCTCTGGAGACACAGAGTA 1921  
 QY 673 hGlyValaCyHis8SerSerCyS8ValIleSerSerProCyS8SerValIAspSerGlyA 693  
 DB 1922 CCGAGCGCTCGCATAGCTCTCGCAAAATCTCCAGCCTTGTCTCCAAAGCGACAGTGGAG 1981  
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MMU012569			
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ACCESSION	AJ012569		
VERSION	AJ012569.1	GI:4584687	
KEYWORDS	alpha-1-G subunit; voltage-gated calcium channel.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
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AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1		
JOURNAL	Klugbauer, N., Marais, E., Lacinova, L. and Hofmann, F.		
MEDLINE	A T-type calcium channel from mouse brain		
PUBMED	Pflugers Arch. 437 (5), 710-715 (1999)		
REFERENCE	2 (bases 1 to 7625)		
AUTHORS	Klugbauer, N.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-NOV-1998) Klugbauer, N., Institut fuer Pharmakologie		
FEATURES	und Toxikologie, Technische Universitaet Muenchen, Biedersteiner		
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ORIGIN

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QY 79 uAlaGluGlyLeuProIyrrProAlaLeuAlaProValValPhePheTyrlLeuSerGlnas 99  
DB 249 GCGGAGGGGCTGCTTACCCTGCGCGCTGAGCCCCGGTGTCTTCTTACTTGAGCCAGGA 308  
QY 99 pSerArgProArgSerTrpCysLeuArgThrValCysasnProTrpPheGluArgValIse 119  
DB 309 CAGCGCGCCCGGAGAGCTGTGTCTCCGACGGTCTGTACCCGAGTTCGAGCGCAGTCCAG 368  
QY 119 rMetLeuValIleLeuLeuasnCysValThrLeuGlyMetCysaArgProCysGluaspI 139  
DB 369 CATGCTGTATTATCTCTCCCAACTGTGTGACTGTGGATATGTTCAAGCGCTGTGAGGACAT 428  
QY 139 eAlaCysaspSerGlnArgCysArgIleLeuGlnAlaPheaspPheIlePheAlaph 159  
DB 429 TGCGGTGACTCCCAAGCGCTGCGGATCTGCAAGGCTTCCAGACACTTCACTTTCCTT 488  
QY 159 ePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTy 179  
DB 489 CTTCGTGTGTGAATAATGGTGGTGAAGATGTGTGCTTTGGGATCTTTGGGAGAAATGTTA 548  
QY 179 rLeuGlyAspThrTrpAsnArgLeuaspPhePheIleValIleAlaGlyMetLeuGluTy 199  
DB 549 CCGTGGAGAACCTTGGAAACCGGCTTGACTTTTATATGTCATTCGTGGAGTGTGAGATA 608  
QY 199 rSerLeuaspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgPr 219  
DB 609 CTCCGTGCACTTCAGAAATGTCAAGCTTCTCCGCACTGACAGACACTCCGTGTGCGCAC 668  
QY 219 OlauArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuaspTh 239  
DB 669 GCTCAGGGCCATTAAACGGGGTGGCCAGACTCGCATTCCTGCATTAAGCTGAGATAC 728  
QY 239 rLeuProMetLeuGlyAsnValIleLeuLeuLysCysPhePheValPhePheIlePheGlyI 259  
DB 729 CTTCGCTATGCTGGGCAATGCTCGCTGCTGTTTCTTCGCTTTTTCATCTTTGGCAT 788  
QY 259 eValGlyValGluLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPh 279  
DB 789 GCTTGATGTTTACGCTGTGGGAGGGCTTACTTCGAACCGAATGCTTCCCTCGAGAAATT 848  
QY 279 eSerLeuProLeuSerValaAspLeuGluProTyrrTyrglnThrGluangluaspGluSe 299  
DB 849 CAGCTCCCGCTGAGTGTGACTTGGAGCTTACTACACAGACAGAAATGAGAGCAGAG 908  
QY 299 rProPheIleCysSerGlnProArgGluangluMetArgSerCysArgSerValProth 319  
DB 909 CCCCTTCACTGCTCTCAAGCTCGGAGAAACGAGATGCACTCGACAGACGTCGCCAC 968  
QY 319 rLeuArgGlyGlyGluGlyGlyGlyProProCysSerLeuaspTyrgluThrTyraSne 339  
DB 969 ACTGCGCGGGAGAGCGGTGTGTCTCACTCGGTGTGACATATGAGGCTTAAACAG 1028  
QY 339 rSerSerAsnThrThrCysValaAsnTrpAsnGlnTyrrTyrrThrAsnCysSerAlaGlyGI 359  
DB 1029 TTCAGCAATACCACTGTGTCAACTGGAACCAATATCAATCACTGTCTGACAGGCGGA 1088  
QY 359 uHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrrAlaTrpIleAlaI 379  
DB 1089 GCACAAACCCCTTCAAGGCGGCATCACTTTGACAAACATTTGGCTATGCTGGAATCGCAT 1148  
QY 379 ePheGlnValIleThrLeuGluGlyTyrrValAspIleMetTyrrPheValMetCAspAlaI 399  
DB 1149 CTTCAGGACTATCACTGAGGGGCTGGGTGACATCATCATCTTTGTGATGAGATGCTCA 1208  
QY 399 sSerPheTyraAsnPheIleTyrrPheIleLeuLeuIleIleValGlySerPhePheMetI 419

Db 1209 TTCCTTCTACACTTCACTTCACTTCTCTCACTCATCGGGCTCTTCTTCACTGAT 1268  
Qy 419 ebnleuCyseleuValIleAlaThrGlnPheSerGluThrLyseGlnArgGluSerG 439  
Db 1269 CAACCTGAGCTGGAGTGTATGACCAAGTTCTTGAGACCAAGCAACGGGAGGTCA 1328  
Qy 439 nleuMeCArgGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe 459  
Db 1329 GCTGATGGGGAGACAGCGTGTAGATCTCTGTCTCAATGTCTAGACCTCGCAAGCTTCTC 1388  
Qy 459 rgluProGlySerCyseTyrgLglnleuLeuLytyrIleuValTyrlleuAlaGlyVal 479  
Db 1389 TGAGCCAGGACACTGCTATGAGAGCTTCTCAAGTCACTGTGTATCATCTCTCGCAAAAC 1448  
Qy 479 aAlaArgAgluLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe 499  
Db 1449 AGCCCGCAGGCTGGCCAGAGCTCTTGGGCTGTAGCGGTGGGCTGGTGTCTGACAG 1508  
Qy 499 rProValAlaArgSerGlyGlnGluProGlnProSerGlySerCyseThrArgSerHisAr 519  
Db 1509 CCCAGTGGCCCGTGTGGGAGAGGCCAGCCAGCTGGGAGCTGCTCTGTTCACACCG 1568  
Qy 519 gArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHis 539  
Db 1569 TGGTCTGTGTCTCACACCTGTGTCCACACCATCAACACCAACATCACCATCAACACCT 1628  
Qy 539 uGlyAaNGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAs 559  
Db 1629 GGGTAATGGGACCTGAGAGTTCCCGGGCCAGCCCAAGATCAGAGACAGGAGATGCCAA 1688  
Qy 559 nGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProPr 579  
Db 1689 TGGGTCCCGCTGGCTATGTGTGCCACCACTTACCCCCACTCCCTCTGGGGGCCCTCC 1748  
Qy 579 oArgGlyAlaGluSerValHisSerPheTyrlleAlaAspCyseHisLeuGluProValAr 599  
Db 1749 GAGGGGTGGGAGTGTGTACACAGCTTCTACATGTGTGACTGTGACCTTGGAGGCACTGG 1808  
Qy 599 gCyseGlnAlaProProProArgCyseProSerGlyAlaSerGlyArgThrValGlySerG 619  
Db 1809 TTGCCAGGCCCCCTCCAGGTCCTCCATCGAGGAGCATCTGGAGCATGTGGGTAGTGG 1868  
Qy 619 yLyseValTyProThrValHisThrSerProProProGluIleLeuLyseAspLyAlaIe 639  
Db 1869 GAAGGTAATCCCACTGTGATACAGACCTTCCACCAAGAGATCTGAAGATTAAGCACT 1928  
Qy 639 uValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProG 659  
Db 1929 AGTGGAGGTGGCCCCAGCTGTGGCCCCCACCCTTCAACCTTCAACATCCACCTGG 1988  
Qy 659 yProPheSerSerMetHisLeuLeuGluGluThrGlnSerThrGlyValaCyseHisSerSe 679  
Db 1989 GCCCTTCAAGTTCATGACAAAGCTCTCGAGACACAGATACGGAGACCTTGCATAGCTC 2048  
Qy 679 rCyseLyseIleSerSerProCyseSerLyseAlaAspSerGlyAlaCyseGlyProAspSerCy 699  
Db 2049 CTTCGAAATATTCAGACCTTGTCTCCAAAGGACAGACAGTGGAGCGTGTGGCGGACGTTG 2108  
Qy 699 sProTyTyCyseAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValaMetProAs 719  
Db 2109 TCCCTACTGTGGCCGAGACAGAGAGGAGGAGCCAGATCCGCTGACCATATAATATGCTGTA 2168  
Qy 719 pSerAspSerGlnAlaValTyrgLupheThrGlnAspAlaGlnHisSerAspLeuArgAs 739  
Db 2169 CTGAGAGAGTGGCTGTATGATGATTCACAGAGAGCTCAGACACAGCACTTCCGGGA 2228  
Qy 739 pProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValle 759  
Db 2229 TCCCCAC---AGACGGGAGCGGCGGAGCGGCGGCGGCGGAGATGACAGGCTTGTGTGCT 2285  
Qy 759 uAlaPheTrpArgLeuIleCyseAspThrPheArgLyIleValAspSerLytyrPheG 779

Db 2286 GGCCTTCTGAGGCGTGTGTGACATTCGGAAGATCGATAGCAAAATCTTGG 2345  
Qy 779 yArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrlleHisG 799  
Db 2346 CCGGGGAATCATGATCGCTATCTGTGTCAATACCTTCAGCATGGGCACTAGATACACGA 2405  
Qy 799 uGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPh 819  
Db 2406 GAGGCCGAGAGGCTCACCAAGCCCTGGAATACAGACATCGTCTTCCACAGCTCTT 2465  
Qy 819 eAlaLeuGluMetLeuLeuLyseLeuValTyrgLuproPheGlyTyrlleLyseAsnBr 839  
Db 2466 CCGCTTGGAGATGCTGTGAAGCTCTGTACAGGTCCCTTCGGCTACATTAAGATTC 2525  
Qy 839 oTyrlleAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnI 859  
Db 2526 CTACAAACATCTTGTATGGGCTATGTGTCTATCAGCGTGGGAGATGTGGCGCAGCA 2585  
Qy 859 nGlyGlyGlyLeuSerValIleuArgThrPheArgLeuMetArgValIleuLyseLeuValAr 879  
Db 2586 GGGAGGTGGCTGT 2645  
Qy 879 gPheLeuProAlaLeuGlnArgGlnLeuValIleuMetLystrMetAspAsnValAl 899  
Db 2646 CTTCCTGCGGACATGACAGCGGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2705  
Qy 899 aThrPheCyseMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisIle 919  
Db 2706 CACCTTGTGCATGCTGTATCTATCTCTTCACTTTCACATCTTCGAGATCTGGGATGACCT 2765  
Qy 919 uPheGlyCyseLysePheAlaSerGluArgAspGlyAspThrLeuProAspArgLyseAsnPh 939  
Db 2766 TTTTGGTGTCAAGT 2825  
Qy 939 eAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnIleuAspTrpAs 959  
Db 2826 TGAATCTCTGTCTGTGGCCATGTGTCACTCTTTAGATTTGATGATCAGAAAGATCGAA 2885  
Qy 959 nLyseValLeuTyrlleAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrlleAla 979  
Db 2886 TTAAGTCTTTTACAAAGGATGGCTCCAGTCACTTGTGGCTGTCTTATCTTCACTTCC 2945  
Qy 979 AleuMetThrPheGlyAsnTyrlleValIleuPheAsnLeuLeuValAlaIleuValGluG 999  
Db 2946 CCTCATGACTTTTGGACATGACTGTCTTTTAACTGTGTGTGTGTGTGTGTGTGTGTGT 3005  
Qy 999 yPheGlnAlaGlu-----GlyAspAlaThrLyseSerGluSerGluProAspPhePh 1003  
Db 3006 TTTTCCAGGAGAGAAATCGGCAACGGGAAAGTACAGTGGACATTAAGCTGTATTCA 3065  
Qy 1004 -----GlyAspAlaThrLyseSerGluSerGluProAspPhePh 1016  
Db 3066 GCTGCTGTCAACTCCAGGGGGAGATGCCACCAAGTCTGAAGTCAAGACCTGATTTCTT 3125  
Qy 1016 eSerProSerValAspGlyAspGlyAspArgLyseLyseAlaLeuValAlaLeuG 1036  
Db 3126 TTGCGCCAGTGTGAGT 3185  
Qy 1036 yGluHisAlaGluLeuArgLyseSerLeuLeuProProLeuIleHisThrAlaAlaTr 1056  
Db 3186 AGAACTCTGGAACTAGAAAGGCTTTTGGACACTTCAATCATCAACAGCTGTCTAC 3245  
Qy 1056 rProMetSerHisProLyseSerSerSerThrGlyAlaGlyAlaLeuGlySerLyse 1076  
Db 3246 ACCGATGTCACTGCCAAGAGCTCCAGCACAGGTGTGGGGAAAGCACTGGGCTGTGCTC 3305  
Qy 1076 rArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetCyse 1096  
Db 3306 TCGCCGACCAAGTAAAGT 3365  
Qy 1096 sProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpHisSe 1116  
Db 3366 ACCGCAAGTCCCGAAGCTCCCGCACAGTCTCTGAGGAGGAGCAAGCAAGCTGTGACAG 3425



QY 1116 rARgArSerSerARgAenSerLeuGIYAArgAlaProSerLeuLYsARgArSerProSe 1136  
DB 3426 CAGGGGCTCCAGCCGGAAGCGCTGGGCGGGCCCGCCAGCTGAAAGCGGAGCCAG 3485  
QY 1136 rGIYgluARgArSerSerLeuLeuSerGIYgluGIYngInuSerGIuAspGIuGIuSe 1156  
DB 3486 CGGGAGCGGAGGCTCCCTGCTGCTGGAAGGGGTCAAGAGACCAAGATGAGAGAGAG 3545  
QY 1156 rSerGIuGIuAspARgAlaSerProAlaGIYSerAspHisARgHisARgGIYSerLeuGI 1176  
DB 3546 TTCAGAGAGGAGCCGGGCGAGCCAGAGGAGTATCATCCCAAGGGGTTCCTTGA 3605  
QY 1176 uARgGIuAlaLYsSerSerPheAspLeuProAspThrLeuGIuValIleProGIYLeuHisAR 1196  
DB 3606 AGTGAGGCCAGAGATTCCTTGACCTGCTGACACCTCGAGGTGCGCGGCTTCATCG 3665  
QY 1196 gThrAlaSerGIYAArgSerSerAlaSerGIuHisGIuAspCYsAsnGIYLYsSerAlaSe 1216  
DB 3666 AACAGCCAGCGGTCCGAGCTCGCTGCTGAAACCCAGACTGTAAATGGCAAGTCGGCTTC 3725  
QY 1216 rGIYARgLeuAlaARgThrLeuARgThrAspAspProGIuLeuAspGIYAspAspAs 1236  
DB 3726 AAGGGGTTGGCCCGCACCCCTCGGGCTGATGACCCCGCACTGATGGGATGATGGCA 3785  
QY 1236 nAspGIuGIYAsnLeuSerLYsGIYgluARgTllegInAlaTPValARgSerARgLeuPr 1256  
DB 3786 rTATAGAGGCAACTGAGCAAGGGGAGAGCTTACAGAGCTGGGTCCAGCCGGCTCCC 3845  
QY 1256 oAlaCYsCYsARgGIuARgAspSerTrpSerAlaTYrIlePheProProGIuInSerARgPh 1276  
DB 3846 TCCGTTGTCGAGAGCGAGATTCCCTGGCTGCTATATCTTCCTCCCGCAAGCTT 3905  
QY 1276 eARgLeuLeuCYsHisARgTllegIleThrHisLYsMetPheAspHisValValLeuValII 1296  
DB 3906 TCGTCTCCGTGTCCAGCCGATCATCCCAAGATGTTGACATGAGTGTCTGTAT 3965  
QY 1296 eIlePheLeuAsnCYsIleThrIleAlaMetGIuARgProLYsIleAspProHisSerAl 1316  
DB 3966 CATCTTCTCCAACTGATATACATGCTATGAGAGGCCCAAAATTGACCCCAACGCC 4025  
QY 1316 aGIuARgIlePheLeuThrLeuSerAsnTYrIlePheThrAlaValIlePheValIGluMe 1336  
DB 4026 TGAACGCATCTTCCTGACCCCTGCCAACTTACAGCGCAAGCTTCTGGCTGAAT 4085  
QY 1336 rThrValLYsValValAlaLeuGIYTrpCYsPheGIYgluInAlaTYrLeuAspSerSe 1356  
DB 4086 GACAGTGAAGGTGGTGGCACTGGGCTGTGTGGGAGCAGGCTTACCTGCGACAG 4145  
QY 1356 rTPAsnValIleuAspGIYLeuLeuValLeuIleSerValIleAspIleLeuValSerMe 1376  
DB 4146 CTGGAAACGTGCTGAGCGGCTTGTGTCATCTCTGTCATCGACATCTGTGTCAT 4205  
QY 1376 rValSerAspSerGIYThrLYsIleLeuGIYMeLeuARgValIleuARgLeuLeuARgTh 1396  
DB 4206 GGTCTCTGACACGGGACCAAGATTCTCGGCATGTGAGAGGTGCTGCGCTCTCGGAC 4265  
QY 1396 rLeuARgProLeuARgValIleSerARgAlaGIuGIYLeuLYsLeuValValIGluThre 1416  
DB 4266 CCTAGCTCAGTCAAGGTATATAGCCGGGCGCAGAGGCTGAAGCTGTGTGAGACCTT 4325  
QY 1416 uMetSerSerLeuLYsProIleGIYAsnIleValValIleCYsCYsAlaPhePheIleI 1436  
DB 4326 GATGTATCTCCCAAAACCATTTGGCAACATTTGTGTGATCTGTGCTTCTTATCAT 4385  
QY 1436 ePheGIYIleLeuGIYValIGluLeuPheLYsGIYLYsPhePheValCYsGIuGIYgluAs 1456  
DB 4386 TTTTGGAAATTTCTTGGGGTGCAGCTCTTCAAGAGAAATTCTTCGTGTGCAAGGTGAAGA 4445  
QY 1456 rPhrARgAsnIleThrAsnLYsSerAspCYsAlaGIuAlaSerTYrARgTPValARgHis 1476  
DB 4446 CACCGAGAACATCATCACTAACAGTGTGTCTGTGAGGCCAGTTACCGGTGGGTCCGCA 4505

QY 1476 sLYsTYrAsnPheAspAsnLeuGIYgluAlaLeuMetSerLeuPheValLeuAlaSerLY 1496  
DB 4506 CAAGTACAACTTTGACAAACCTGGGCGCAGCTCTGATGTCCCTGTTGTGTGGCTCCAA 4565  
QY 1496 sAspGIYTPValAspIleMetTYrAspGIYLeuAspAlaValIGluYValAspGIuInPr 1516  
DB 4566 GGATGCTGTGGTTACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4625  
QY 1516 oIleMetAsnHisAsnProTPMetLeuLeuTYrPheIleSerPheLeuLeuIleValAl 1536  
DB 4626 CATCATGAACCAACACCTTGAATGCTGCTTACTTCAATCTTCTTCTTCAATGATGAGC 4685  
QY 1536 aPhePheValIleuAsnMetPheValIGluValValIGluAsnPheHisLYsCYsARgI 1556  
DB 4686 CTTCCTGCTCTGAACATGTTGTGTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4745  
QY 1556 nHisGIuGIuGIuGIuAlaARgARgARgGIuGIuLYsARgLeuARgARgLeuGIuLY 1576  
DB 4746 GCACAGAGAGAGAGAGGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4805  
QY 1576 sLYsARgArSerSerLYsGIuLYsGIuMetAla----- 1586  
DB 4806 AAAGAGAGAGTAAAG 4865  
QY 1587 -----GluAlaGIuCYsLYsProTYrTYrSerAspTYrSe 1598  
DB 4866 CGGCACTCAGCAGCGGCTGCTGCTGCAAGAGCCAGTGAACCTTACTTCTGACTACTC 4925  
QY 1598 rARgPheARgLeuLeuValHisHisLeuCYsThSerHisTYrIleuAspLeuPheIleTh 1618  
DB 4926 GCGCTTCGGCTCTCGTCCACACCTGTGTACAGCCACTGAGCTTGCCTTCTATCAC 4985  
QY 1618 rGIYValIleGIYLeuAsnValValIleThrMetAlaMetGIuHisTYrGIuInGIuProGIuII 1638  
DB 4986 TGTGTCTATCGGCTGATGATGT 5045  
QY 1638 eLeuAspGIuAlaLeuLYsIleCYsAsnTYrIlePheThrValIlePheValIlePheIle 1658  
DB 5046 CTGGAGAGAGCTTGAAAGATCTGCAACTATCATCTTACCTTATCTTGTCTTGGAGTCC 5105  
QY 1658 rValIlePheLYsLeuValAlaPheAlaPheARgARgPhePheGIuAspArGTTPAsnGIuLe 1678  
DB 5106 AGTATTCAACTGTGGCTTGGCTTCCGCGGTCTTCTTCAGAGACAGTGTGAACCAAGCT 5165  
QY 1678 uAspLeuAlaIleValLeuLeuSerIleMetGIYIleThrLeuGIuIleGIuValAs 1698  
DB 5166 GAACTGTGATGTGTGTCTTGTCTTGTATGATGATGATGATGATGATGATGATGATGATG 5225  
QY 1698 nLeuSerLeuProIleAsnProThrIleIleARgIleMetARgValLeuARgIleAlaAr 1718  
DB 5226 TGCTTCACTGGCCATCAACCCCAACATCATCGTATCATGAGGGTGTCCGCAATTGCTCG 5285  
QY 1718 gValIleuLYsLeuLeuLYsMetAlaValAGLYMetARgAlaLeuLeuHisThrValIleMetGI 1738  
DB 5286 AGTTCTGAAGCTGTGAAGATGCTGTGGCATCGGCGCACTGTGCAACAGGTGATGCA 5345  
QY 1738 nAlaLeuProGIuValIGluAsnLeuGIYLeuLeuPheMetLeuLeuPheIlePheAl 1758  
DB 5346 GGCCTGCCCCAGGTGGGAAACCTGGACCTTCTTCAATGCTATATTATTTTCACTTTGCG 5405  
QY 1758 aAlaLeuGIYValIGluLeuPheGIYAspLeuGIYCYsAspGIuThrHisProCYsGIuGI 1778  
DB 5406 AGCTCTGGCGTGGAGCTCTTTGGAGACTGGAAGTGTATGAGACACCCCTTGGAGGG 5465  
QY 1778 rLYeugIYARgHisAlaArTPheARgAsnPheGIYMeAlaPheLeuThrLeuPheARgVa 1798  
DB 5466 CTGGGCGGAGATCCACCTTTAGAACTTGTGATGCTTGTGTGACCTTTCCTCCAGT 5525  
QY 1798 ISeTYrGIYAspAsnTPAsnGIYIleMetLYsAspProSerARgAspCYsAspGIuGI 1818  
DB 5526 CTCACTGTGTACAACTGGAATGTATATATGAGACACCTTCGGGACTGTGACAGGA 5585  
QY 1818 useTYrCYsTYrAsnThrValIleSerProIleTYrPheValSerPheValLeuThrAl 1838



Db	5586	GTCCACCTGGCTACAAACACCGTCATCTCAACCCATCTACTGTGTCTTCTGCTGTACGGC	5645
Qy	1838	AGLNPheValLeuValAsnValValIleAlaValIleMetIshHisLeuGluIuSerAs	1858
Db	5646	CCACTTTGTGTGTGTCAACGTCGTCTATACGCGCTGTCTATGAAGACCTGGAGAAGACAA	5705
Qy	1858	nLYsgLualAlaYsgLugLualAgLueGluLualAgLueGluIuLeuGluIuMetIshTle	1878
Db	5706	CAAGAAGGCCAAGAAGAGGAGCGGAGTTGGAGCGGAGCTGGAGCTGAAGATGAAGAACT	5765
Qy	1878	uSerProGluProHisIserProLeuGlyIserProPheLeuTrpProGlyValGluGlyVa	1898
Db	5766	CAGCCCGGAGGCCCACTCCCGCTGGGAGGCCCTTCTCTGGCTGGGCTGAAGAGTGT	5825
Qy	1898	lAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAl	1918
Db	5826	CAATATGCCCTTACAGCCCTTAAGCTGGGGGCTTCACACACAGCGGCCCACTATGAAGCAGC	5885
Qy	1918	a---SerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProVa	1937
Db	5886	CTCTTACAGGGCTTCTCCCTTGAGCAACCCAGATGGTACTCACACTGAGGAGGGGCGAGT	5945
Qy	1937	lProLeuGlyProAspLeuLeuThrValArgLysSerGlyValIserArgThrHisSserIe	1957
Db	5946	CCCCCTAGAGACAGACCTCTGACTGTGAGGAAGTCGTGTGTCAGCCGGAGCAACTCTCT	6005
Qy	1957	uProAsnAspSerIlyMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisAr	1977
Db	6006	GCCCAATATACACTATCATGTGCGCAATGGAGACATCGCCAGAGATCCCTAGACACAG	6065
Qy	1977	gGlyTrpLylLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAl	1997
Db	6066	GGGCTGGGGGGCTCCCAAGGCCAGTCAAGCTCATCTTGTCTGTACTCCCAACAGCG	6125
Qy	1997	aAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrIleuLeuGlnProHisGl	2017
Db	6126	AGACACCGAGCTGCATCTTACAGCTTCCCAAGATGACACATATGCTCCAGCTCAATGG	6185
Qy	2017	YAlaProThrTrpGlyValIleProLysLeuProProGluIlyArgSerProLeuAlaGl	2037
Db	6186	GAGCTCCACCTGGGGCGGCATCTCTTAACCTACCCCCACTGCGCGCTCCCTTGCGCTCA	6245
Qy	2037	nArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGl	2057
Db	6246	GAGGCTCTCAAGGGCGGCCCAAGGACAAATAAAGACTGATCCCTGAGCGTGGAGGGCGTGG	6305
Qy	2057	ySerArgGluAspLeuLeuSerGluValIserGlyProSerCysProLeuThrArgSerSe	2077
Db	6306	TAGCCGGGAAGACCTGTTGTCAAGAGTGAAGTGGGCTCTGCGCTCTGACGCCCTCTCTC	6365
Qy	2077	rSerThrTrpGlyGlyIserSerIleGlnValGlnGlnArgSerGlyIleGlnIserIlyVa	2097
Db	6366	ATCCTTCTGGGGCGGGGTGAGGATCAAGATGACGAGCGCTCCGCGACGCCAAGCAAGT	6425
Qy	2097	lSerIlyshIleArgLeuProAlaProCysPProGlyLeuGluInuProSerTrpAlaIysAs	2117
Db	6426	CTCCAGACATCCCTCGCGCCAGCCCTTGGCCACAGCTTGAAACCACTGGGCCAAGGA	6485
Qy	2117	pProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAs	2137
Db	6486	CCCTCAAGAGACCAAGAAGACAGCTTGAAGCTGGACACGAGCTGAGCTGAATTTCAGGAGA	6545
Qy	2137	pleuLeuProSerSerGlnGluGluProLeuPheProArgAspLeuIlyAsCysIlyrSe	2157
Db	6546	CTCTCTGGCCACACATCAGAAAGAACCCCTGTCTCCACAGGACTTGAATAAATGTCTACG	6605
Qy	2157	rValGlnThrGlnIserCysArgArgArgProGlyIlyThrPheLeuAspGluGlnArgArgH	2177
Db	6606	TGTTAAGGCCCAAGACTGCGCGGCGCAGGCTGGGTCTGGCTAAGACGAACAGAGAGACA	6665
Qy	2177	sSerIleAlaValIserCysLeuAspSerGlyIserGlnProArgLeuCysProSerProSe	2197

Db	6666	CTCCATCGCTGAGCTGCTGAGCAAGCGGCTCCAGACCCCGGCTATGTC	CAAGCCCTC	6722	
Qy	2197	rser1euglyvlyglp1nProleucl1ygl1Progl1yserArqProlyblylyseuSerPr		2217	
Db	6726	AAAGCTCGGGGGGCAACCTCTTGGGGGGCCTGGAGCGGGCTTAAGAAAAA	CAAGCC	6785	
Qy	2217	oProser1leSer1leasProProgl1uSerGing1ySerArqProProCySeSerProgl1		2237	
Db	6786	ACCCAGATCTCTATAGACCCCCCGAGAGCCAGGGCCCTCGGCCCCCA	GCAGTCTGG	6845	
Qy	2237	YValCyseuArqArqArq1a1aPro1a1aSerArqSerLyAspProSerValSerSerPr		2257	
Db	6846	CGTCTGCTCAGAGGAGGAGGGCGCGGCACTGACTGAAAGATCCCTCGGCT	CTCAGGCC	6905	
Qy	2257	OLEuAspSerThAla1a1aSerProSerProLyAspThLeuSerLeuSerLeuSerLyLe		2277	
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DEFINITION	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit, mRNA (cDNA clone MGC:62312 IMAGE:6410519), complete cds.				
ACCESSION	BC057399				
VERSION	BC057399.1	GI:34783700			
KEYWORDS	MGC.				
ORGANISM	Mus musculus (house mouse)				
SOURCE	Mus musculus				
REFERENCE	1 (bases 1 to 7527)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L.H., Schaefer, C.F., Bhat, N.K., Altschul, S.F., Zeeberg, B., Bluet, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.T., Wang, J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stadelton, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L., Scherz, T.E., Brownstein, M.J., Ustin, T.B., Tohyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwen, P.J., McEwan, K.J., Malek, U.A., Gunaratne, P.H., Richards, S., Weller, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyard, S.W., Vallal, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Rodriguez, S., Bonifard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, U., Myers, R.M., Buterfield, A.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marz, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	human and mouse cDNA sequences				
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	22388257				
REFERENCE	12477932				
AUTHORS	2 (bases 1 to 7527)				
TITLE	Strausberg, R.				
JOURNAL	Direct Submission				
REMARK	Submitted (03-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
COMMENT	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> Contact: MGC help desk Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a> Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library Preparation: M. Bento Soares, University of Iowa cDNA Library Arrayed by: The I.M.A.G.E. Consortium (IUMI) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305				

Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson Mark) mcdgaxil.stanford.edu  
Dickson, M., Schmitz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNU at: <http://image.llnl.gov>  
Series: IRAX Plate: 114 Row: P Column: 1  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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ORIGIN

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D	3927	GGCCCGCACCTCGCGGGCTGATGACCCCACTGATGAGGAGATGATGGCATGTAGAGG	3986
Q	1239	YAsnLeuSerLysGlyGluHisArgIleGlnAlaTrpValArgSerArgLeuProAlaCysC	1259
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TITLE		1 (bases 1 to 7274) Montell,A., Chemin,J., Bourinet,E., Mennesier,G., Lory,P. and Nargeot,J.	
JOURNAL		Molecular and functional properties of the human alpha(1G) subunit that forms T-type calcium channels	
MEDLINE		J. Biol. Chem. 275 (9), 6090-6100 (2000)	
PUBMED		10692398	
REFERENCE		2 (bases 1 to 7274) Montell,A., Mennesier,G., Bourinet,E., Lory,P. and Nargeot,J.	
AUTHORS		Direct Submission	
TITLE		Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R.	
JOURNAL		1142, C.N.R.S., 141 rue de la Cardonille, Montpelllier 34396, France	
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[illegible]



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 LOCUS Homo sapiens low voltage-activated T-type calcium channel alpha 1G  
 DEFINITION

ACCESSION AF190860 splice variant Cavt.1a (CACNA1G) mRNA, complete cds.  
VERSION AF190860.1 GI:7021332  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 7349)  
AUTHORS Cribb, L.U., Gomora, J.C., Daud, A.N., Lee, J.H. and Perez-Reyes, E.  
TITLE Molecular cloning and functional expression of Ca(v)3.1c, a T-type  
calcium channel from human brain  
JOURNAL FEBS Lett. 466 (1), 54-58 (2000)  
MEDLINE 2015462  
PUBMED 10648811  
REFERENCE 2 (bases 1 to 7349)  
AUTHORS Cribb, L.U., Gomora, J.C., Lee, J.-H., Daud, A.N. and Perez-Reyes, E.  
TITLE Direct Substitution  
JOURNAL Submitted (29-SEP-1999) Physiology, Loyola University Medical  
Center, 2160 South First Avenue, Maywood, IL 60153, USA  
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ACCESSION AR201015
VERSION AR201015.1 GI:20251903
KEYWORDS
SOURCE
ORGANISM
REFERENCE
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AUTHORS Dubin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Brlander,M.G.
TITLE DNA encoding human alpha1G-C-T-Type calcium channel
JOURNAL Patent: US 6358706-A 4 19-MAR-2002;
FEATURES
source
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Best Local Similarity: 92.38% Mismatches: 112
Query Match: 92.01% Indels: 31
DB: Gaps: 5

US-09-611-257a-24 (1-2287) x AR201015 (1-7741)
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Qy 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly 62  
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Db 4025 CCAAGAGTTCCTTTGACCTGCACAGACACACTGCAAGTCCAGGGCTGCATCCACTGCCA 4084  
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Db	5045	ACCACACACCCCTGGATGCTGCTGTACTTCACTTCGTTCTGCTCATTTGGGCTTTCTTG	5104
QY	1539	alLeuAsnMetPheValGIyValValIaGIuAsnPheHisIuIysCyAspArgInHisGln	1559
Db	5105	TCCTGAACATGTTTGTGGGTGTGGTGGTGGAGAACTTCCACAAAGTGTGGGACGACG	5164
QY	1559	IuGIuGIuGIuAlaArgArgArgGIuGIuIyIyArgLeuArgArgLeuGIuIyIyIyArgA	1579
Db	5165	AGGAAGAGAGAGCCCGGGCGGGAGAGAAAGCGCTCGAAGATCGAGAGAAAGAGAA	5224
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QY	1599	rgPheArgLeuLeuValHisIleuIysCyTrpSerHisTyTrleuAspPheIleTrhg	1619
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QY	1619	IyValIleGIyLeuAsnValValThrMetAlaMetGlnHisTyArgInlProGlnIleI	1639
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QY	1639	euaSPGluAlaLeuIyIyIleCyAsnTyTrIlePheThrValIlePheValPheGluSerV	1659
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QY	1839	lnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGlnSerAsnL	1859
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QY	1859	ysGluValAsyGluGluValIleGluLeuGluAlaGluLeuGluValLeuGluMetLysTrpLeus	1879
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QY	1939	eugLyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProA	1959
Db	6298	--GGACCAAGCTTACGTACCTGTGCGGAAGCTGTGGGTGACCGGAACGACACTCTCGCCA	6355
QY	1959	snAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyT	1979
Db	6356	ATGCACACTCAAGTGTGCGGCATGAGGAGACATGCCAGGGGGCCCTGGGACACAGGGCT	6415
QY	1979	trpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspT	1999
Db	6416	GGGGGCTCTCCCAAGCTCAGTCAAGGCTCCGCTGTGCTGCTTCACTCCACCGACAGATA	6475
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Db	6596	CATCTCAGGCCCCAGGACGACATTAAGACGTGACTCTTGACGCTTACAGGCTCTGGGACGC	6655
QY	2059	rgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerP	2079
Db	6656	GGAGAGACTGCTGCGCAGAGGTAGTGGGCCCTTCCCGGCCCTTGCCCGGCGCTACTT	6715
QY	2079	heTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerL	2099
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Db	6896	TGCCCCCTGGCGGGCAGAGAGAGCCCCCAATCCCAAGGGACCTGAAGAAAGTCTACAGG	6955
QY	2158	alGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHis	2178
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Qy	2198	erleuglyglpProleuglyglpProglyserArgProlysylyslleuSerProp	2218		
Db	7076	ACCTGGGGGGCCAGCTCTTGGGGGGGCCGGGAGCCGGCCCAAGAAAACCTCAGGCCGC	7135		
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Db	7196	TCGCTCCGAGAGAGGGCTCCGCTCAGGACCTCCAGAGATCCCTTGGCCTCGGCCCCC	7255		
Qy	2258	euaAspSerThralalaserProserProlylysaAspThrleuSerleuSerSerProL	2278		
Db	7256	CTGACGACGATGCTGCTGCTGCTCCCAAGAGATGTGCTGAGTCTCTCGGTTTAT	7315		
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DEFINITION	Homo sapiens voltage-dependent calcium channel alpha 1G subunit b isoform (CACNA1G) mRNA, complete cds.				
ACCESSION	AF126965				
VERSION	AF126965.1	GI:4761538			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Monteill, A., Chemin, J., Bourinet, E., Mennessier, G., Lory, P. and Nargeot, J.				
TITLE	Molecular and functional properties of the human alpha 1G subunit that forms T-type calcium channels				
JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)				
MEDLINE	20158909				
PUBMED	10692398				
REFERENCE	2 (bases 1 to 7253)				
AUTHORS	Monteill, A., Mennessier, G., Bourinet, E., Lory, P. and Nargeot, J.				
TITLE	Direct Submision				
JOURNAL	Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R. 1142, C.N.R.S., 141 rue de la Cardonille, Montpellier 34396, France				
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Db	144	CCGATCGCCCGGGGGCCCCGGCTGGCCAGAGATGACAGAGAGAGATGAGCGGGG	203
Qy	43	ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProglyProgly	62
Db	204	CCGAGAGTCGGGACAGCCCGGAGCTTCATGCGGCTCAACACCTGTGCGGGGGCGGGG	263
Qy	63	Ala-AlaGlyAla-GlySerThrGluLysAspProglyserAlaAspSerGluAlaGluG	82
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Qy	82	yluendProThraAlaAlaAlaProValAlaPhePheThrleuSerSerInAspSerArgP	102
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Dd 1224 TCATCAGCTGGAGGGGTGGTGCAGATCATGTATCTTGTGATGGATCTCATTTCTTCT 1283  
Qy 402 TyrAsnPheIleTyrPheIleleuLeuIleIleValGlySerPhePheMetIleAsnLeu 422  
Dd 1284 ACAATTTATCTACTTCATCTCTCTCATCTATCTGTGGCTCTCTTTCATGATCAACCTGT 1343  
Qy 422 ySLeuValValIleAlaThrgInPheSerGIYnThIleGIYnArgIYleuSerGIYleuMetA 442  
Dd 1344 GCTGTGTGTATTCACAGCGAGTCTCAGAGACCAAGCAGGGGAAAGCCAGCTGATGC 1403  
Qy 442 rGIYGIYnArgValArgPheLeuSerAsnAlaSerThlleuAlaSerPheSerGIYProG 462  
Dd 1404 GGGACAGAGGTGTGGGTCTCTGCAAGCGCAGACCTTGCTGAGCTTCTTGTAGCCCG 1463  
Qy 462 lYSerCysTyrGIYnIleuLeuLeuYTYrTleuValTYrTlleuArgIYAsnAlaArgA 482  
Dd 1464 GCAAGTGTATGAGAGCTGTCAAGTACCTGTGTACATCTTGTAAAGGAGGCCCA 1523  
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Dd 1524 GCGTGGCTCAGGTCTCTCGGGAGCAGAGGTGTGGGTGTGGCTGTCCAGCAGCCAGCAG 1583  
Qy 502 lAArgSerGIYGIYnIYProGIYProSerGIYSerCysThrArgSerHisArgArgleuS 522  
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Dd 1644 CCGTCCACCACTGTGTGACCAACCAACCACTACCAACCACTACCACTGAGCAATG 1703  
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Qy 562 rGArgleuMetleuProProProSerThrProThrProSerGIYGIYProProArgGIY 582  
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Dd 1824 CAGAGCTGTGACAGCTTCTTACCATGCCAGTCCCACTTnAGACAGTCCGCTGCCAG 1883  
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Qy 622 YrProThrValHisThSerProProProGIYIleleuYAspIYAlaIleuValGIY 642  
Dd 1944 ATCCACCGTGCACACAGCGCTTCACCGAGACGCTGAAGAGAGAGCACTACTAGAG 2003  
Qy 642 AlAlaProSerProGIYProProThrleuThSerPheAsnIleProProGIYProPheS 662  
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Dd 2124 TCTCAGGCCCTTGCTTGAAGACAGACAGTGAAGCTGTGGTCCAGACGCTGCCCTACT 2183  
Qy 702 ySAlaArgThrGIYAlaGIYnIYProGIYAspIleAspHisValMetProAspSerAspS 722  
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Dd 2361 GAGAGCTnATGTGACACCTCCGAAAGATTGTGACAGAGATCTTnOGCCGGGGA 2420  
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Db 5337 TGGAGCTCTTTGGAGACCTGGAGTGTGAGAGACACACCCCTGTAGAGGCGCTGGCCGCG 5396  
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QY 1942 sPLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerT 1962  
Db 5868 ACTTACTGACTGTGGGAAAGTCTGGGGTCAAGCAAGCACTCTGCCCAATGACAGCT 5927  
QY 1962 yTrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTTrpGlyLeuP 1982  
Db 5928 ACATGTGTGCGATGGAGCACTGCGGAGGGGCCCTTGGGACACAGGGGCTGGGGGCTCC 5987

QY 1982 roLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysI 2002  
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QY 2002 |LeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyValaProThrTrpG 2022  
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QY 2022 |LValaIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgA 2042  
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QY 2042 rGglnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlyAspL 2062  
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QY 2082 |LysSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleA 2102  
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QY 2141 eSerGlnGlnGluProLeuPheProArgAspLeuLysLysCysTyrSerValGluThrG 2161  
Db 6468 GCGGCCAGAGAGAACCCCATCCCAAGAGACCTGAAGAAAGTGTACAGCTGAGAGGCC 6527  
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QY 2181 aLserCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyG 2201  
Db 6588 TCACTGCTGGAAGAGGGCTCCCAACCCCACTGGGCAAGACCCCTTAACTTGGGG 6647  
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QY 2221 eTrLeuAspProProGluSerGlnGlySerArgProProCysSerProGlyValaCysLeuA 2241  
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QY 2261 hrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAsp 2281  
Db 6828 TGGCTGCTCGCTCCCTCCCAAGAAAGATGTGTGATCTCTCGGTTATCTCTGAC 6887  
QY 2281 roThrAspMetAspPro 2286  
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RESULT 13  
AR201014 6822 bp DNA linear PAT 20-APR-2002  
LOCUS AR201014  
DEFINITION Sequence 3 from patent US 6358706.  
ACCESSION AR201014  
VERSION AR201014.1 GI:20251902  
KEYWORDS  
SOURCE unknown.



QY	653	erPheAsn11eProProGlyProPheSerSerMetHisLysLeuLeuGlnThrGlnSerT	673
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QY	673	hrg1VALCYHisSerSerCysLysL11SerSerProCysSerLysL1aAspSerGlyA	693
Db	1922	CAGGCGCTGCCAAGCTCTTGCAAGACTCCAGCCCTTGCTTGAAAGACAGACTGGAG	1981
QY	693	1aCYeGlyProAspSerCysProTyrCYsa1aargThrglyValaglyGlnProGlnSerA	713
Db	1982	CCTGGGTCCAGACAGCTGCCCTACTGTGCCGGGGCCGGGGAGGGAGGTGAGCTCG	2041
QY	713	1aAspHisValMetCProAspSerLAspSerGlyValaValTyrGlnPheThrGlnAsp1aG	733
Db	2042	CCGACCGTGAAATGTCTACTCAGACACGAGGCGAGTTATGATTCACACAGAGATGGCC	2101
QY	733	1nHisSerAspLeuArgAspProHisSerAArgArgGlnArgSerLeuGlyProAspA	753
Db	2102	AGCACAGGAGACTCCGGAGACCCCAACAC---CGCGGCGMAAGAGCTGGGGCCCAATG	2158
QY	753	1ag1uProSerSerValLeu1aPheTyrArgLeu11eCYaspThrPheArgLys11ev	773
Db	2159	CAGAGCCAGCTCTGTGCTGGGCTTCTGAGAGGCTATCTGTGAGACACTTCCGAAAGATTG	2218
QY	773	1aAspSerLysTyrPheGlyArgGlyL11eMet11eVal11eLeuVal1aThrLysSerM	793
Db	2219	TGGACAGCAAGTACTTTGGCCGGGGAAACAAGATGCCATCTGTGTCAACACCTCAGCA	2278
QY	793	etG111aG1uTyrHisG1uGlnProG1uG1uLeuThrAsn1aLeuG1uL11SerAsn1	813
Db	2279	TGGCGATGAAATACACAGACAGCCCGAGAGCTTACAGCCCTAGAAATCAGACACA	2338
QY	813	1eValPheThrSerLeuPhe1aLeuGlnMetLeuLeuLysLeuLeuValTyrGlyProp	833
Db	2339	TGCTCTTCACCAAGCTCTTTGGCCCTGGAGATGCTGCTGAGCTGTTGTATGGTCTCT	2398
QY	833	heGlyTyr11eLysAsnProTyrAsn11ePheAspGlyVal11eValVal11eSerValT	853
Db	2399	TTGGTATCATCAAGATCCCTACACACATCTTCAGAGGTGATGTGTATGATCAGCCGT	2458
QY	853	TPG111eValG1YG1nG1nG1uG1Yg1YLeuSerValLeuArgThrPheArgLeuMetA	873
Db	2459	GGGAGATCTGGGCGACAGAGGGGGGGCGGCTGTGCTGCTGCGAGCTTCCGCTGTATGC	2518
QY	873	1gVal1eLysLeuVal1ArgPheLeuPro1aLeuGlnArgG1nLeuVal1aLeuMetL	893
Db	2519	GATGCTGCAAGCTGGTGGCGTTCTCGCGGGCGCTGCAGCGGAGCTGGTGGTGCATGAG	2578
QY	893	YerThrMetAspAsnVal1aThrPheCYsMetLeuLeuMetLeuPhe11ePhe11ePheS	913
Db	2579	AGACCATGAGCAACCTGGCCACCTTCTGCATAGCTGCTTATGCTCTTCAATCTTCA	2638
QY	913	er11eLeuG1MetHisLeuPheGlyCYsLysPhe1aSerG1nArgAspGlyAspThrL	933
Db	2639	GCATCTTGAGCATGCATCTTCCGCTGCAGTTTGCCTCTGAGCGGAGTGGAGACACC	2698
QY	933	eupProAspArgLysAsnPheAspSerLeuLeuTyrP1a11eVal1ThrValPheGln11eL	953
Db	2699	TGCCAGACCGGAGAAGATTGTGACTCTTGCTGTGGCCATGCTACTCTTTCAAGATCC	2758
QY	953	euthrGlnGluAspTyrAsnLysVal1eLysTyrAsnGlyMetAlaSerThrsSerSerTyrA	973
Db	2759	TGACCCAGAGAGACTGGAACAAAGCTCTCTCAATGATGAGCCCTCCACGTCGTCGGG	2818
QY	973	1a1a1aLeuTyrPhe11e1a1aLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV	993
Db	2819	CGGCGCTTATTTACTTTCCTCTCAAGACTTTCGGCACTAGCTGTCTTCAATTTGCTGG	2878
QY	993	al1a1a1eLeuValG1uG1uPheGln1aG1u-----1003	
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QY	1004	-----GlyAsp1aThrLysSerG	1010

Db	2939	GACAGTTAAGCTGATTTCAGCTGCTCCATCTCCACGGGGGAGATGCCAACAGTCTCG					2998
QY	1010	lUsErGluPrOaspPheSeSerProSeRValaSpGlyaSPaRgLySlaRgLy					1030
Db	2999	AAATCAGAGCCCGAATTTCTTCTTCACCCAGCCCTGGATGTGTATGGGACAGGAGAAAGTCT					3058
QY	1030	euaIaLeuValAlaLeuGlyGluHlSaIaGluLeuAglYbSerLeuLeuProProLeuI					1050
Db	3059	TGGCTTGTGTGTCTCCTGGAGAGACCCCGAGCTGCGGAAGAGCTGTCTCCGCTTCTCA					3118
QY	1050	leIleHlSthRaIaIaIaThProWeSerHlSPoLySSaSerSeTThGlYValGlyG					1070
Db	3119	TCATTCACAGCGCCGACCACTATGTCTGCTGCCAAGAGACACAGACCGGCTGGGGC					3178
QY	1070	lualaLeuGlySerGlySerArgrThrSerSerSerGlySerAlaGluProGlyAla					1090
Db	3179	AGGGCGCTGGGCGCGGTGGCGGCGCACACAGACACGGGGTGGCAGAGCTGGGGCGG					3238
QY	1090	lAhIshIaGluMeTlyeCySProProSeRaIaArGSeSerProHlaSeTProTTrSeRa					1110
Db	3239	CC---CACGAGATGAATGCACCCGCCAGCGCCCGCACCTCTCCGACAGCCCTCGAGCG					3295
QY	1110	lAaIaSerSeTTrPThSerArgrgrSeSerArgrAnSeSerLeuGlyArAlaProSeRl					1130
Db	3296	CTGCAGAGAGCTGGACCAAGCGGGCTTCACGCGGAACAGCTTGCGCGTGCACCCAGCC					3355
QY	1130	eulYsArGArSeSerProSeRGlYgluaRgrArSeSerLeuSeuSerGlygluGlyngLus					1150
Db	3356	TGAAGCGGAGAGGCCAAGTGAAGAGGGGGGTCTCGTTGTGGGAGAAAGGCCAGGAGA					3415
QY	1150	erGlnaSPgluGluIuSeSerGluGluIuSPaRgAlaSeRProAlaGlySeRAspHlSa					1170
Db	3416	GCCAGGATGGAAGAGAGACTCAGAAAGAGAGCGGCGCACCCCTGCGGGAGATGACCATC					3475
QY	1170	rgHlSaRgGlySeTLeuGluIuRgGluAlaLySeSeSerPheAspLeuProAspThrLeuG					1190
Db	3476	GCCACAGGGGGTCCCTGAGCGGGAGGCCAAGATCTCTTTGACTTCGACAGACACTGC					3535
QY	1190	lInValProGlyLeuHlSaRgThRaIaSeRgLyArGSeSerAlaSeRGlUhlSaGlnaSPC					1210
Db	3536	AGGTCGCAAGGCTGCATTCGACTTCGCACTGGCGAGGGGTCTGCTTTCGACACACAGACT					3595
QY	1210	YsaAnGlyLySeSaIaSeRGlYArGLeuAlaArgrThrLeuAgrThRaSPaSPProGlnL					1230
Db	3596	GCAATGGCAAGTCCGCTTCAGAGGGCGCTGGCGCCGCGCGCTGAGTACAGACCCCCAC					3655
QY	1230	euaSPGlYaaSPaSPaSPaSPaSPgluGluIuAnuSeuSerLySGlyngLnaRgLeGlnaIaT					1250
Db	3656	TGGATGGGGAGTGAAGCCGATGAACAAGGGCAACTGACAAAGGGGAACGGGGTCCGCGGT					3715
QY	1250	rpValArGSeArGrLeuProAlaCySaRgGluArGSPaSPeTTrPSeRaITyrlleP					1270
Db	3716	GGATCCGAGCCGCACTCCCTGCTGCTGCTCGACGACAGACTCTGTGTACAGCTCAACTCT					3775
QY	1270	heProProGlnSeSaRgPheArgrLeuLeuCyShlSaRgIlleIleThHlSaLyWeRPha					1290
Db	3776	TCCCTCCTCAAGTCCAGGTCGCGCTCTGTGTACCGGATCATCAACCAACAAGATGTTCCG					3835
QY	1290	SPHlSaValLeuValIlleIlePheLeuAnCySlleThHlSaMeGluArgrProL					1310
Db	3836	ACCAAGTGGTCTTGTATATCTTCTTAACTGCATCACACATCCGATGAGAGGCCCA					3895
QY	1310	YSlleAsPProHlaSeSaIaGluRgIllePheLeuThrLeuSeSaRnTyrllePheThRa					1330
Db	3896	AAATTTAGACCCCAAGCGCTGAAGCAATCTTCTTCGACCTCTCCAAATTAATCTTCCACG					3955
QY	1330	lAValPheLeuAlaGluMeTThRaValLySaValAlaAlaLeuGlyTyTSPaSPheGlYgluG					1350
Db	3956	CAGCTTTTCTTGCTGAATGACAGTGAAGGTGGGACATGGGCTGTGCTTCGGGGAGC					4015
QY	1350	lInAlaTyTLeuAnGSeSerTrPAsnValLeuAspGlyLeuLeuValleuIleSeRaIT					1370



4016 AGCGCTACCTCGGAGCACTGGAACTGCTGAGCGGCTGTTGGTCTCATCTCCGTCA 4075  
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VERSION	AF227744.1	GI:7159260			
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SOURCE	Homo sapiens				
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AUTHORS	Montell,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.				
TITLE	Molecular and functional properties of the human alpha(1G) subunit that forms T-type calcium channels				
JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)				
MEDLINE	20158909				
PUBMED	10692398				
REFERENCE	2 (bases 1 to 6822)				
AUTHORS	Montell,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)				
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Qy	973	IaAlaIeuTYrPheIleAlaIeuMetThrPheGIyAsnTYrValIleuPheAsnIleuY	993
Db	2819	CGGCCCTTATTTCTATTCCTCATGACTTCGGCACTACGTGCTCTTCAATTGCTGG	2878
Qy	993	AlaIaIleIeuValGIuGIyPheGInIaGIu-----	1003
Db	2879	TGCGCATCTGTGGAGGGCTTCCAGCGGAGAAATCAGCAAACGGGAATGCGAGTG	2938
Qy	1004	-----GIYAspAlaThrIySerg	1010
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Qy	1010	IuSerGIuProAspPhePheSerProSerValAspGIYAspArgIySValSArgI	1030
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Qy	1030	euaIaIeuValaIaIeuGIyGIuHisAlaGIuIleuArgIySerIleuIleuProIleuI	1050
Db	3059	TGGCCTTGTCCTCGTGGAGAGCACCGGAGCTGCGGAAGAGCTGTGCGCCTCTCA	3118
Qy	1050	IeIleHisThralAlaIaThrProMetSerHisProIySergSerThrGIyValGIyG	1070
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Qy	1070	IuAlaIeuGIYSerGIYSerArGIuThrSergThrSerSerSerGIYSerAlaGIuProGIyAla	1090
Db	3179	AGGGCGTGGGCCCTGCGCTGCGCGCCAGCACAGCAGCGGCTGGCAGACCTGGGGCGG	3238
Qy	1090	IaHisIleGIuMetIyCyAspProIleSerAlaArgSerSerProHisSerProTrpSera	1110
Db	3239	CC---CACGAGATGAATGCACCGCCCAAGCGCCGCACTCTCCGACAGCCCTGTGACG	3295
Qy	1110	IaAlaIeSerSerTrpThrSeraArgSeraIySeraIyArgAlaIleuGIYArgAlaProSerI	1130
Db	3296	CTGACAAGCAGGTGACCAAGCGGCTTCACCGGAAACAGCTCGGCGGTGCACCCACAC	3355
Qy	1130	eulYsArgArgSerProSergIyGIuArgArgSerIleuIleuSerGIYGIuGIyGIuGIuS	1150
Db	3356	TGAAGCGAGAAAGCCCAAGTGAAGCGGCGGTCCCTTGTTCGGAGAAAGCCACAGAGA	3415
Qy	1150	erGIuAspGIuGIuIleuSergIuGIuAspArgAlaSerProAlaGIYSerAspHisA	1170
Db	3416	GCCAGATGAAGAGAGAGCTCAGAAAGAGAGCGGGCCAGCCCTTCGGGGCAGTGCATTC	3475

QY	1170	IGH1SARG1YSERLEUGLUAHGLUALYSSERSERPHEAPLEUPROAPRTHLEUG	1190
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QY	1190	INVAL1PROG1YLEUHN1AARGTHRALASERGLYTRPSERSERALASERGLHN1SGLNAPRC	1210
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QY	1210	YSAENG1LYSSER1ASERGLYARLEUUA1AARGTHLEUA1GTHRA1SPASBP1ROG1NL	1230
DB	3596	GCAATGGCAAGTGGCTTCAAGGGGCGCTGGCGCCGGGCGCTTGCGGCGCATGACCCGCCAC	3655
QY	1230	EUAAPRG1YAERPA1SPASBP1UGLYVSNLEUSERYLGLYGLUAHGL1EGLNAP1AT	1250
DB	3656	TGGATGGGGATGAGCCGACATGACCAAGGGCAACCTGACCAAAAGGGGAACGGGATCGCGCGT	3715
QY	1250	RPVAL1ARGSER1ARGLLEUPROL1ACYSYASARG1UA1GSA1PSER1TRP1SER1TYR1LEP	1270
DB	3716	GGATGCCAGGCCGCTCCCTGCTGCTGCTGCCGAGCCAGACTCTTGATCAGCTTACATCT	3775
QY	1270	HEPR1ROG1NSE1AR1PHE1AR1GLEU1EUCYVH1SARG1LE1ETHN1SLYSE1PHE1A	1290
DB	3776	TCCCTCTCAAGTCCAGGATTCGGCTCTGTGTGACCGGAGCATCACACCAACAAGTGTTCG	3835
QY	1290	SPH1SVAL1ALLEUVAL1LE1PHE1LEU1ANCYS1LETH1LE1ALAME1GLUAH1PROL	1310
DB	3836	ACCAACG1G1GCTCTGTATCATCTTCCCTTAAC1TGCA1CACCA1TCGCGCATCGATGAGCGCCCA	3895
QY	1310	YSL1LEAP1ROH1ASER1AGLUAH1RGL1PHE1LEUTH1LEUS1EAS1ANTY1LE1PHE1THRA	1330
DB	3896	AAATTTGACCCCAAGCGCTGAAAGCAATCTTCTGACCCCTTCCAA1TTAC1TTCA1CCG	3955
QY	1330	1AVAL1PHE1UUA1AG1MET1THRALY1SVAL1A1ALAE1UG1YTR1CYA1PHE1GLY1UG	1350
DB	3956	CAGCTTTCTGGCTCGA1AATGAC1AGTGA1AGGTGG1GGCA1TCGGGTGGTCTTGCGGGAGC	4015
QY	1350	1NAL1ATY1RLEUA1RSER1SE1TR1PASN1VAL1LEU1ASPG1YLEU1LEU1LEU1ESER1AL1	1370
DB	4016	AGGGTACCTGCGGAGCAGTTGGAA1CCTGTGAC1CGGGCTGTGTGCTCATCTCCCTCA	4075
QY	1370	1EAP1R1LEU1VAL1SE1MET1VAL1SER1SPER1GY1THR1LS1LE1UG11MET1LEUAH1RGV	1390
DB	4076	TCGACATTTCTGGTGTCCATGGTCTCTCA1ACGGCAGCCACCA1AGATCTCGGGATGCTGAGGG	4135
QY	1390	ALL1EAS1RGL1LEUA1R1GTH1R1LEUA1R1PRO1EUA1R1VAL11LE1SER1AR1AG1GLY1LEU1	1410
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QY	1410	YSL1EUA1VAL1GL1UTH1R1LEU1SE1SER1LEU1YSP1ROL1EG1YASN1LE1VAL11LEC	1430
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QY	1430	YSCY1SAL1APHE1PH1LE1LEPHE1LY1LE1EUG1YVAL1GL1NLEU1PHE1GLY1YU1SHPER	1450
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DB	4316	TCGTGTGCCAAGGGGAGGAT1R1CCA1GGA1KAT1CACCA1TAAT1GCA1CTGTG1CGCAGGCCA	4375
QY	1470	ERTY1RARG1TR1VAL1ARG1ISLY1SY1RASN1PHE1AP1EUA1NLEU1GLY1NAL1LEU1MES1ER1	1490
DB	4376	GTTACCGGTGGGTCCGGACA1AAGT1TTCG1CA1CCTTGGCCAGGCGCTGATGTCGCC	4435
QY	1490	EUPHE1VAL1EUA1ASER1LY1EAS1PG1Y1TR1VAL1SP1LEME1CTY1TR1APRG1YLEU1AS1PALAY	1510
DB	4436	TGTTTCG1TTTGGCTCCAA1GAGTGTGG1TG1GAC1CA1CAT1GT1GAG1AG1GGCTGATGCTG	4495
QY	1510	ALGLY1VAL1AS1PGL1NGL1PRO1LEME1ASN11SASN1POT1RPM1E1LEU1E1Y1TH1PHE1LES	1530
DB	4496	TGGCGGTGGACCAAGCCAT1CAT1GACCA1CAH1CCCTTGAT1GCTCTG1ACTTCA1CTCT	4555
QY	1530	ERPHE1LEU1LE1VAL1AL1APHE1PHE1VAL1EUA1N1MET1PHE1VAL1GLY1VAL1VAL1GLUA	1550

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Db	4616	ACTTCCAAAGATGTGGGAGACACAGAGAGAGAGAGCCCCGGCGGGAGAGAGAGC	4675
Qy	1570	rgLeuARgARgLeuGlulYelYvARgARgserLyvsgLulYvsgImetA1aGlua1aGlnc	1590
Db	4676	GCCTACGAAGACTGGAGAAAAGAGAGAGATAGAGAGAGATGGCTGGAAGCCAGT	4735
Qy	1590	yAlvsvProTyrTySerARpTySerARpHeARgLeuLeuValhihi1vLeuCyethrs	1610
Db	4736	GCAAACTTACTACTCCGACTACTCCGCTTCCGCTTCCTGTCCACACTGTGGACCA	4795
Qy	1610	erhi1sTyrieARpLeuPhe1LeThrgLyv11eGlYLeuAsnVal1ThxMetA1am	1630
Db	4796	GCCACTACCTGGACCTTCAATCAAGAGTGCATCGGGCTGMAAGCTGTCAACATGGCCA	4855
Qy	1630	etGhi1sTyrgLnGlnProGln1LeuARpGlu1aLeuYv1eCyAsnTyrl1ep	1650
Db	4856	TGGAGCACTACACAGCCCAAGTTCTGATGAGAGGCTGGAAGATCGCAACTACATCT	4915
Qy	1650	heThrvAl1ePheValPheG1uSerValPheLyvLeuValAlaPheAlaPheARgArp	1670
Db	4916	TCACGTGCATCTTGTCTTGGAGTCAGTTTCAACTTGGCCCTTGGTTTCCGTGGGT	4975
Qy	1670	hePheGlnARpARgTTPARngLn1eupARp1a11eValLeuLeuSer1LeMetG1Y1	1690
Db	4976	TCTTCCAGAGACAGGTGGAAACAGCTGGACCTGGCCATGTGCTGTCCATCATCGGCA	5035
Qy	1690	1eThrvLeuGlnG1u11eGlYValAsnLeuSerLeuPro1eAsnProThrv11e1Arg1	1710
Db	5036	TCACGCTCGAGGAATCGAGGTCAACGCTCGCTGCCATCAACCCACCATCATTCGCA	5095
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Db	5156	GGGGCTGTCTGGAACCGGTGATGACGGCCCTGGCCCCAGTGGAGAACTTGGAACTTCTCT	5215
Qy	1750	heMetLeuLeuPhePhe1LePheAlaAlaLeuG1YValG1LeuPheG1YAspLeuG1uc	1770
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Db	5456	ACTTGTGTCTCTGTGCTGACGGCCCAAGTTCTGTCTAATCAAGTGTGTATCGCGGTG	5515
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Db	5516	TGATTAAGACCTCGAGGAGAGCAACAAGAGGCCCAAGAGAGGCCAGACTTGAAGCTG	5575
Qy	1870	1uLeuG1uLeuG1uMetYvThrvLeuSerProGlnProhi1sErProLeuG1YserProP	1890
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Oy	1950	1yValSerArgThrHisSerLeuProAlaAspSerTrpMetCysArgAsnGlySerThra	1970
Db	5807	GGGTCACGCCCAAGCACACTCTCTGCGCAATAGACGTCATAGTGTCCGACATGGAGGACTG	5866
Oy	1970	1aGluArgSerLeuGlyHisArgGlyTrpGlyLeuPheProIlysAlaGlnSerGlySerIleL	1990
Db	5867	CCGAGGGGGCCCTTGAGCACAGGGGGCTGGGGGCTCCCAAGGCTCACTGAGGCTCCGCTG	5926
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Oy	2010	1sTrpLeuLeuGlnProHisGlyValaProThrTrpGlyAlaIleProIlyLeuProPro	2030
Db	5987	CTCATCTGCTCCAGCCCCCAGAGGCCCCCAACTGGGGACACATCCCAAACTGGCCCCAC	6046
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Db	6047	CAGAGCGCTCCCTTTGGCTCAGAGGCCACTCAGAGGCCAGGCGAGCAATAGAGACTGACT	6106
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Db	6107	CCTTGAGAGTTCAGAGGCTCTGGAGCCGGGAGAACCTGTGAGAGGTGATGGGCTCT	6166
Oy	2070	erCysProLeuThrArgSerSerSerPheTrpGlyGlySerSerIleGlnAlaGlnAla	2090
Db	6167	CCCCGCCCTGGCCCGGGCCCTACTCTTTCTGGGGCCAGTCAAGTACCAGGCAAGAGCAGC	6226
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Db	6227	ACTCCCGAGGCAAGAGATCTCCAAGCAGATGACCCCGCCAGCCCTTGCCACAGGC	6286
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Oy	2149	roArgAspLeuIlySerCysTrpSerValGluThrGlnSerCysArgArgArgProGlyP	2165
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DEFINITION	6897 bp mRNA linear PRI 06-MAR-2000		
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DEFINITION	Home sapiens voltage-dependent calcium channel alpha 1g subunit		
ACCESSION	AF227746		
VERSION	AF227746.1	GI:7159264	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
REFERENCE	1 (bases 1 to 6897)		
AUTHORS	Monteill, A., Cheman, J., Bourinnet, E., Mennessier, G., Lory, P. and Nargeot, J.		
TITLE	Molecular and functional properties of the human alpha (1g) subunit that forms T-type calcium channels		
JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)		
MEDLINE	10692398		
PUBMED	20158909		
REFERENCE	2 (bases 1 to 6897)		
AUTHORS	Monteill, A., Mennessier, G., Bourinnet, E., Lory, P. and Nargeot, J.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.) U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France		
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ORIGIN

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Best Local Similarity:	91.62%	Mismatches:	105
Query Match:	90.92%	Indels:	56
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US-09-611-257A-24 (1-2287) x AF227746 (1-6897)

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Qy	233	alThrluLeuLeuAspThrluProMetleuGlyAenValleuLeuLeuCySphheV	253
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Qy	253	alPhePheIlePheGlyTlleValGlyValGlnleuTTPAlaGlyLeuLeuArgAsnArgC	273
Db	662	TCTTCTTCACTTCTTGGCATGCTCGGCGTCACTGCTGAGGCGGCTCTTCCGAAACGAT	721



QY	273	YpPheLeuProGluuAnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT	293
Db	722	GCTTCCTACCTGAGAAATTTACAGCTCCCTCCGTGAGCGGTGACCTGAGGCGCTAATTCACAGA	781
QY	233	hngLuanGluAspGluSerProPheIleCysSerGlnProArgGluuAnGlyMetAgs	313
Db	782	CAGAAACGAGGATAGAGAGCCCTTCATCTGCTCCAGCCAGCGAGAAAGGACATGCCGT	841
QY	313	erCyArgSerValProThrLeuArgGlyGlyGlyGlyGlyProProCysSerLeuA	333
Db	842	CCTGAGAAAGCCTGCCCAACGCTGCCGGGGAGCGGGGGCGTGGCCACCTTCGGGTCTGG	901
QY	333	spTyrGluThrTyrAnSerSerSerSerAenThrThrCysValAsnTrpAnGlnTyrT	353
Db	902	ACTATGAGGCGCTACAAAGCTCCACCAACACCACTGTGTCAACTGAAACCAAGTCTACA	961
QY	353	hPheAnCysSerValaGlyGlnHisAnProPheGlyGlyAlaIleAnPheAspAnIleG	373
Db	962	CCAACTGCTCACCGGGGGAGACAAACCCCTTCAAAGGGCGCCATCACTTGACCAATGG	1021
QY	373	lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrPValAspIleMet	393
Db	1022	GCTATGCTGGATCGCCCATCTTCCAGGTATACCGCTGGAGGGCTGGGTCCACATCATGT	1081
QY	393	yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIev	413
Db	1082	ACTTGTGATGGATGCTCATCTTCCTTCACAAATTCATCATCTTCACTTCCTCATCATCG	1141
QY	413	alGlySerPhePheMetIleAnLeuCybLeuValValIleAlaThrGlnPheSerGluT	433
Db	1142	TGGGCTCTCTTCAATGATCAACCTGTGCTGGTGGTATGTCACGACGATTCAGAGA	1201
QY	433	hrrLyGIaArgGluSerGlnLeuMetAArgGluGlnArgValaArgPheLeuSerAenAlaS	453
Db	1202	CCAAAGCAGCGGAAAGCCAGCTGATGCGGAGACAGCGTGGCGTTCTGTCCAAACGCCA	1261
QY	453	erThrLeuAlaSerPheSerGluProGlySerCysTyrGlyGluLeuLeuLeuTyrLeuV	473
Db	1262	GCACCTGGCTAGCTTCTCTGAGCCCGGACGCTGATAGGAGGCTCAAGTACCTGG	1321
QY	473	alTyrIleLeuAlaGlyValAlaAlaArgGluLeuAlaGlnValSerArgAlaIleGlyValA	493
Db	1322	TGTATATCTTCCTGTAAAGCAGCGCCGACGGCTGCTCAGGCTCTCGGAGACAGGATGAGC	1381
QY	493	rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS	513
Db	1382	GGGTGGGGTGTCTACAGACCCACGACCCCTTGGGGGCCAGGAGACCCAGCCACAGCA	1441
QY	513	erCysThrArgSerHisArgArgLeuSerValHisHisbLeuValHisHisHisHisH	533
Db	1442	GCTGTCTCTGCTCCACCGCGCCCTATCGTCCACACCTGGTGCACCAACCAACCAACCC	1501
QY	533	HisHisHisbTyrHisbLeuGlyAnGlyThrLeuArgValProArgAlaSerProGluI	553
Db	1502	ATCACCAACCACTAACACCTGGGCAATGGGACCTCAGGCGCCCCCGGGCGACCCGAGA	1561
QY	553	leGlnAspArgAspAlaAnGlySerArgArgLeuMetLeuProProPheSerThrProT	573
Db	1562	TTCAGAGACGGGATGCAATGGGATCCCGCGGCTCATGCTGCACACCACTTCAGAGCCTG	1621
QY	573	hrProSerGlyGlyProProArgGlyAlaGlySerValHisSerPheTyrHisAlaAspC	593
Db	1622	CCCTCTCCGGGGCCCCCTCGATGGGCGAGATCTGTGCACAGCTTTCATCATGCGCACT	1681
QY	593	YHisbLeuGluProValAlaArgCybGlnAlaProProProArgCybProSerGluAlaSerG	613
Db	1682	GCCACTTAAGCCAGATCCGCTCCAGGCGCGCCCTCCAGGTGCCCATCTGAGGATCG	1741
QY	613	lyArgThrAlaGlySerGlyValValTyrProThrValHisHisSerProProGluI	633
Db	1742	GCAAGCATGTGGCAGCGGGAAGGTATATCCACCGTGACACCAAGCTTCACCGAGAA	1801
QY	633	leLeuLyAspLyValaLeuValaGluValaProSerProGlyProProThrLeuThS	653

Db	1802	CGCTGAAGAAAGCACTAGTAAAGGTGGCTGCCAGCTCTGGAGCCCCCAACCTTCAACA	1861
Qy	653	erPheAsn11eProProG1yProPheSerSerMetH1slyLeuLeuGluThrGlnSert	673
Db	1862	GCCTCAACATCCCAACCCGGGCGCTTACAGCTCATGACAAAGCTCTGGAGACAAGAGTA	1921
Qy	673	hrg1yAlaCyAnH1sSerSerCysAls11eSerSerProCysSerLeuAlaAspSerG1yA	693
Db	1922	CAGGTGCTCGTCCAAAGCTCTTGCAAGATCTCCACGCCCTTGTTGAAGCAACAAGTGAAG	1981
Qy	693	1aCysG1yProAspSerCysProG1yCysAlaAaGThrg1yAlaG1yGluProG1uSera	713
Db	1982	CCTGGTGTCCAGACAGCTGCCCCCTTACGTGTGCCCCGGGCGAGGGAGGTGAAGCTCG	2041
Qy	713	1aAspH1eValMetProAspSerAspSerG1uAlaValYrG1uPheThrGlnAsp1aG	733
Db	2042	CCGACCGTGAATGCTGTACCTACACAGCGAGGAGTTTATGAGTTTCAACAAGATGCC	2101
Qy	733	1nh1sSerAspLeuAArgAspProH1sSerAArgAArgG1nArgSerLeuG1yProAspA	753
Db	2102	AGCACAGAGCACTCCGGAGCCCCCAACAGC---CGGCGGCAACGAGCTCGGCGCCAGATG	2158
Qy	753	1aGluProSerSerValLeuAlaPheThrArgLeu11eCysAspThrPheArg1ys11eY	773
Db	2159	CAGAGCCCAAGCTCTGTGTGCGCTTGTGAAGGCTTATCTGTACACCTTCGAAAGATTG	2218
Qy	773	1aAspSerLeuYrPheG1yArgG1y11eMet11eAla11eLeuValAsnThrLeuSerm	793
Db	2219	TGACACAGAAAGTACTTTGGCCGGGAATCATGATCGCATCTGTGTCAACACATCGACA	2278
Qy	793	etG1y11eG1uYrH1sG1uGlnProG1uG1uLeuThrAsnAla1euglu11eSeraH1	813
Db	2279	TGGGCAATCGAATACCAAGACAGCCCGAGAGGCTTACCAAGCCCTTGAAATTCAGCAACA	2338
Qy	813	1eValPheThrSerLeuPheAla1euglu11eMetLeuLeuLeuLeuValYrG1yProp	833
Db	2339	TGCTTTTACACAGCTCTTGTCCCTGGAGATGCTGTGAACCTGCTGTGTATGATGCTCT	2398
Qy	833	hrg1YrT11eLysAsnProTyrAsn11ePheAspG1yVal11eValVal11eSerValT	853
Db	2399	TTGGCTTACATCAAGATCCCTTCAACAACATTCGATGCTGATCTGTGTCATCAAGCGT	2458
Qy	853	1rGlu11eValG1yGlnGlnG1yG1yG1yLeuSerValLeuArgThrPheArgLeuMetA	873
Db	2459	GGGAATCTGTGGGCAAGAGGGGGGGCGCTGTGCGTGTCTCGGACCTTCGCGCTGAATGC	2518
Qy	873	1rGValLeuLysLeuValArgPheLeuProAla1eugluArgG1nLeuValValLeuMetL	893
Db	2519	G1TG1GCTCAACCTGGTGGCTTCTCGCGGCGCTGACAGCGGACGTGTGTGTCATGA	2578
Qy	893	1ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPhe11ePhe11ePheS	913
Db	2579	AGACCATGACACAGTGGCAACCTTCTGCAAGCTGCTTATGCTCTTCACTTCACTTCA	2638
Qy	913	er11eLeuG1yMetH1sLeuPheG1yCysLysPheAlaSerG1uArgAspG1yAspThrL	933
Db	2639	GCATCTCTGGCATGATCTCTTCTGGCTGCAAGTTTGCTCTGAAGGGGATGGGAGACCC	2698
Qy	933	euProAspArgLysAsnPheAspSerLeuLeuTPAla11eVal1ThrValPheGln11eL	953
Db	2699	TGCCAGACCGGAAGATTTTGACTCTTGCCTGTGGCGCATGTCATCTCTTTCAGATCC	2758
Qy	953	euThrGlnG1uAspTrpAsnLysValLeuYrAsnG1yMetAlaSerThrSerSerTrpA	973
Db	2759	TGACCCAAGAGAGCTGGAACAAAGTCTTCAACATGGATGGATCCACAGTGTCTTGGG	2818
Qy	973	1aAlaLeuYrPhe11eAlaLeuMetThrPheG1yAsnYrValLeuPheAsnLeuLeuY	993
Db	2819	CGGCCCTTATTTACTTTCCTCATGACCTTCGGGACCTAGTGTCTTCAATTGCTGG	2878
Qy	993	alAla11eLeuValG1uG1yPheGlnAlaG1uG1yAspAlaThrLysSerLeuSertG1uP	1013



Dd 2879 TCGCATTCTGATGGAGGCTTCCAGGCGGAGGAGATGCCAAACATGCCAATCCAGAGC 2938  
Qy 1013 roaappphpheserproserValaapgiyaapgiyaapgiyalyaargyeuualaleuV 1033  
Dd 2939 CCGATTTCTTCTCAACCCAGCCTCGATGGTGTGGAGCAGAGAAAGATGGGCTTGG 2998  
Qy 1033 aAlaaleuGlygluhisAlaIleuArglyLysSerLeuLeuProbleuileiIshist 1053  
Dd 2999 TGTCTCTGGAGAGACCCGAGCTGCGAAGAGCTCTCTCGCTTCATTCACCA 3058  
Qy 1053 hralaalaThrProMetSerHisProLysSerSerSerThrGlyValGlylualaleuG 1073  
Dd 3059 CGGCGCCACACCCCATGTCGCTGCCAAGACACGAGCGGCTTGCGGAGGCGCTGG 3118  
Qy 1073 LysSerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyValAlaHisShiSG 1093  
Dd 3119 GCCCTGCTCGGCGGACACAGCAGCAGCGGCTCGCAGAGCTGGGGCGGCC---CACG 3175  
Qy 1093 lMetLysCysProProSerAlaArgSerSerProHisSerProThrSerAlaIasers 1113  
Dd 3176 AGATGAAGTCACGCCCCAGCCCGCAGCTTCTCCGACAGCCCTCGAGCGCTGCAGCA 3235  
Qy 1113 eTrrpThrSerArgArgSerSerArgAasnSerLeuGlyArgAlaProSerLeuLysArgA 1133  
Dd 3236 GCTGGACACGACGCGCTCCAGCCGGAACAGCTCGGCGGTGCACCCAGCCTGAAGCGGA 3295  
Qy 1133 rgsSerProSerGlygluArgArgSerLeuLeuSerGlygluGlygluLysSerGlnaapG 1153  
Dd 3296 GAAGCCCAAGTGGAGAGCGCGCTCCCTGTGTCTGGAGAAAGGCCAGAGCCAGAGATG 3355  
Qy 1153 luguGluLysSerSerGlygluAapArgAlaSerProAlaGlySerAspHisArgHisArgG 1173  
Dd 3356 AAGAGAGAGGCTCAAGAAAGAGGCGGCGCAGCCTTCGCGGAGTACATGCCACAGAGG 3415  
Qy 1173 lYserLeuGlyuaArglylualySserSerPheAspLeuProAspThrLeuGlnValProg 1193  
Dd 3416 GGTCTCTGAGAGGGAGGCAAGAGTTCCTTTGACTCTGCCAGACACACTGCAGGCGCAG 3475  
Qy 1193 lYleuHisArgThrAlaSerGlyArgSerSerAlaSerGlylunHisGlnaapCysaasnGlyL 1213  
Dd 3476 GGTCTCATTCGCACTGCCAGTGGCCGAGGGGTCTGCTTCAGACACAGACATGTCATGCA 3535  
Qy 1213 YSserAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA 1233  
Dd 3536 AGTCGGCTTCAGGGGCGCTGGCCCGGCGCTGCGCTGATGACCCCCACCTGATGGAGG 3595  
Qy 1233 sPAspAspAsnAspGlylualyasnLeuSerLysGlylualArglIleGlnAlaTrpValArgS 1253  
Dd 3596 ATGACGCCGATGACGAGGGCAACCTGAGCAAAAGGGAAAGGGTCCGCCGTGGATCCGAG 3655  
Qy 1253 eArgLeuProAlaCysCysArgGlyuaArgspSerTrpSerAlaTyrlIlePheProProG 1273  
Dd 3656 CCGCATCCCTGCTGCTGCTCGAGCAGACTCTCGGTCAAGCTTCACTTCTCTCTCTC 3715  
Qy 1273 lnsErArgPheArgLeuLeuLeuCysHisArgGlyIleIleThHisLysMetPheAspHisValV 1293  
Dd 3716 AGTCCAGGTTCGCTCTCTGTCTACCCGATCATACCCACAAAGATGTTCCAGCAGCGAG 3775  
Qy 1293 alLeuValIleIlePheLeuasnCysIleThrIleAlaMetGlyuaArgProLysIleAspP 1313  
Dd 3776 TCTCTGTCTATCTCTCTTAACCTGCATCACATCCATGAGGAGGCCCAAAATTTAGCC 3835  
Qy 1313 roHisSerAlaGlyuaArglIlePheLeuThrLeuSerAsnTyrlIlePheThrAlaValPheL 1333  
Dd 3836 CCCACAGCGCTGAAGACATCTTCTGACCTCTCCAAATTAATCTTTCACCCGAGAGCTTTC 3895  
Qy 1333 euAlaGluMetThrAlaLysValValAlaIleuGlyTrpCysPheGlygluGlnAlaTyrl 1353  
Dd 3896 TGGCTGAATATGACATGAAAGGAGTGGGCACTGGGCTGGGTGGGAGGAGCGGATACC 3955  
Qy 1353 euArgSerSerTrpAsnValIleuAspGlyLeuLeuValLeuIleSerValIleAspIleL 1373  
Dd 3956 TCGGAGACAGTTGGAAACGTGCTGGAAGGGCTGTGTCTCATCTCCGTCAATCCGATTC 4015

Qy 1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL 1393  
Dd 4016 TGTGTCTCAATGTTCTTGCAGACGGGACCAAGATCTCGGGCATGCTGAGGTGCTGGCGC 4075  
Qy 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValV 1413  
Dd 4076 TGTCTGCCGACCTTGCGCCGCTGAGGTGATACCGCGGCGCAGGGGCTGAAGCTGGTGG 4135  
Qy 1413 alGluThrLeuMetSerSerLeuLysProIleGlyasnIleValValIleCysGlyValaP 1433  
Dd 4136 TGGAGACGCTGATGTCCTCACTGAACCATCGGCAACATTGAATGATCTGCTGTGCT 4195  
Qy 1433 hePheIleIlePheGlylIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG 1453  
Dd 4196 TCTTCATCATTTTTCGGCATCTTGAGGAGTGCAGCTCTTCMAAGGAAATTTTTCGTGCC 4255  
Qy 1453 lnglylualasPThrArgAsnIleThrAsnLysSerAspCysAlaGlylualasErTyraRgt 1473  
Dd 4256 AGGCGAGAGATACGAGGAATCATCAACATTAATCGACTGTGGCGGAGCCGTTAACCGGT 4315  
Qy 1473 rpValaArgHisLysTyraSnPheAspAsnLeuGlyGlnAlaIleuMetSerLeuPheValL 1493  
Dd 4316 GGGTCCGGCAACAGTACAACTTTGACAACTTGGCCAGGCCCTGATGTCTCTGTTCGTT 4375  
Qy 1493 euAlaSerLysAspGlyTrpValaAspIleMetTyraSpGlyLeuAspAlaValGlyValA 1513  
Dd 4376 TGGCTCTCAAGAGATGGTGGTGGATCATGTAAGAGGCTGGATGCTGTGGGCGCTGG 4435  
Qy 1513 spGlnGlnProIleMetAsnHisasnProTrpMetLeuLeuTyraPheIleSerPheLeuL 1533  
Dd 4436 ACCAGCAGCCCATATATACACACAACCCCTGGAGCTGCTGTAATTCATCTCGTTCCTGC 4495  
Qy 1533 euIleValAlaPhePheValIleuasnMetPheValGlyValValValGluasnPheHisBL 1553  
Dd 4496 TCATTTGTGGCTTTCTTTGTCTGTAACATGTTTGGGGTGGTGGTGGAGAACTTCCACA 4555  
Qy 1553 ysCysArgGlnHisGlnGlnGlnGlylualaArgArgArgGlylualyLeuArgLeuArgA 1573  
Dd 4556 AGTGTGGACACACAGAGAGAGAGAGAGGCGCGCGGAGAGAGAAAGCGCTTACGAA 4615  
Qy 1573 rgleuGlyLysLysArgArgSerLysGlyLysGlnMetAlaGlylualGlnCysLysaProT 1593  
Dd 4616 GACTCGAAGAAAAAAGAAAGAGTAAAGAGAAAGAGATGGCTGAAGCCCAAGTCAAACTT 4675  
Qy 1593 yTyTySerAspTyraSerArgPheArgLeuLeuValHisShiLeuCysThrSerHisTyrl 1613  
Dd 4676 ACTACTCCGACTACTCCCGCTTCCGGCTCTCTGTCACCACTTGTGACACAGCCACTAAC 4735  
Qy 1613 euAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlylunIst 1633  
Dd 4736 TGAACCTTCTTATACAGGTGTCAATCGGCTGAACGAGTCCATCCATGAGCAAGCACT 4795  
Qy 1633 YrGlnGlnProGlnIleLeuAspGlylualaleuLysIleCysAsnTyrlIlePheThrValI 1653  
Dd 4796 ACCAGCAGCCCAATTTCTGATGAGGCTCGAAGATCTGAATCTGAATCTTCACTGTCA 4855  
Qy 1653 lePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPheGlna 1673  
Dd 4856 TCTTTGCTTGGAGTCTAGTTTCAAACTTGGGCTTGGGCTTGGTTCGCGGTCTTTCACAG 4915  
Qy 1673 sPArgTrpAsnGlnLeuAspLeuAlaIleValIleuLeuSerIleMetGlylIleThrLeuG 1693  
Dd 4916 ACAAGTGAACCACTGAAGCTGGCAATGTGTGCTGTCTCATATGAGGACATCCGCTGG 4975  
Qy 1693 lngluIleGlyValaAsnLeuSerLeuProIleasnProThrIleIleArgIleMetArgV 1713  
Dd 4976 AGGAATGAGGTCAAGCCTCGCTGCCATCAACCCACATATATCGCATATGAGGG 5035  
Qy 1713 alLeuArgIleAlaArgValIleuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuL 1733  
Dd 5036 TGTGTGGCATTTGCCGAGTGTGAAGCTGTGAAGATGGCTGTGTGGCATGGCGGCGCTGC 5095



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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 18, 2005, 16:26:56 / Search time 2326.68 Seconds  
(without alignments)  
5818.779 Million cell updates/sec

Title: US-09-611-257A-24  
Sequence: 1 MLPHRPRCVRRPPLRGSR.....KKDTLSLGLSDPTMDPZ 2287

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-DB=/cgn2.1/USPFO.spool/US09611257/runat.15092005.134300.25163/app.query.fasta.1.4878  
-LOOPEXT=0 -UNITS=bits -QFMT=fastap -SUFFIX=eng -MINMATCH=0.1 -DOOFC=0  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_MAP -LANG=EBLERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: N Geneseg.16dec04:\*

- 1: genesegn1980s:\*
- 2: genesegn1990s:\*
- 3: genesegn2000s:\*
- 4: genesegn2001as:\*
- 5: genesegn2001bs:\*
- 6: genesegn2002as:\*
- 7: genesegn2002bs:\*
- 8: genesegn2003as:\*
- 9: genesegn2003bs:\*
- 10: genesegn2003cs:\*
- 11: genesegn2003ds:\*
- 12: genesegn2004as:\*
- 13: genesegn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12024	100.0	7540	5	AAF31677 Rat alpha
2	11980	99.6	6942	13	ADSI6295 Rat volca
3	11829	98.3	7286	3	AAZ52309 Rat pancr
4	11798	98.1	6762	2	AAK83485 Rat T-ty
5	11767	97.8	6816	2	AAK83487 Rat T-ty

6	11751.5	97.7	6795	2	AAK83486
7	11747.5	97.7	6741	2	AAK83488
8	11066.5	92.0	7741	4	AAAD04756
9	10970.0	91.2	6750	2	AAK83481
10	10946.0	91.0	6804	2	AAK83483
11	10923.5	90.8	6783	2	AAK83482
12	10919.5	90.8	6729	2	AAK83484
13	10916.0	90.8	6892	5	AAF31684
14	10845.5	90.2	7648	13	ADQ85063
15	10845.5	90.2	7648	13	ADSI6298
16	10843.5	90.2	8002	4	AAH98402
17	6248.5	51.9	8447	5	AAF31678
18	6243.5	51.9	7898	8	AAK59081
19	6242.5	51.9	7898	8	AAZ58365
20	6241.5	51.9	7898	4	AAK59080
21	6103.5	50.7	3993	2	AAK501624
22	5895.5	49.0	6132	2	AAK83489
23	5886.5	48.9	6114	2	AAK83490
24	5738.5	47.7	6941	2	AAK59082
25	5432.5	45.2	6890	13	ADSI6296
26	5420.5	45.1	6816	6	AAK516826
27	5420.5	45.1	6816	8	ABX93560
28	5420.5	45.1	6816	12	ADH69264
29	5420.5	45.1	6855	6	AAK516827
30	5420.5	45.1	6855	8	ABX93561
31	5420.5	45.1	6855	12	ADH69266
32	5407.5	44.5	6503	12	ADH69275
33	5346.5	44.5	5469	2	AAK83491
34	5345.5	44.4	5505	2	AAK83492
35	5200.5	43.2	5735	5	AAK31679
36	3950.5	32.8	5562	2	AAV57542
37	3937.5	32.7	7969	4	ABU07263
38	3861.5	32.1	6073	13	ADSI6299
39	3861.5	32.1	6933	5	AAK51681
40	3399.5	28.3	6933	5	AAK51681
41	3336.5	27.9	2212	5	AAK31679
42	2091.5	17.4	3464	4	AAK94358
43	2091.5	17.4	3464	12	ADL31040
44	1974.5	16.4	1669	2	AAK59083
45	1751.5	14.6	7362	2	AAQ37817

ALIGNMENTS

RESULT 1  
ID AAF31677 standard; cDNA; 7540 BP.  
XX AAF31677;  
AC AAF31677;  
DT 09-APR-2001 (first entry)  
XX  
DE Rat alpha-IG calcium channel cDNA.  
XX  
XX Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;  
XX hypotensive; cardiant; nootropic; T-type calcium channel subunit;  
XX cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;  
XX epilepsy; alpha-IG calcium channel; ss.  
XX  
OS Rattus sp.  
XX  
XX WO200102561-A2.  
XX  
XX 11-JAN-2001.  
XX  
XX 04-JUL-2000; 2000MO-CA000794.  
XX  
XX 02-JUL-1999; 99US-00346794.  
XX  
XX (NEUR-) NEUROMED TECHNOLOGIES INC.  
XX  
XX Snutch TP, Baillie DL;  
XX  
XX

AAK83486 Rat T-ty  
AAK83488 Rat T-ty  
AAK04756 Human T-t  
AAK83481 Human T-t  
AAK83483 Human T-t  
AAK83482 Human T-t  
AAK83484 Human T-t  
AAF31684 Human alp  
AAQ89063 Human uro  
ADSI6298 Human vol  
AAH98402 Human EST  
AAF31678 Rat alpha  
AAK59081 Human act  
ABX58365 Human act  
AAK59080 Human act  
AAK01624 Human T-t  
AAK83489 Human T-t  
AAK83490 Human T-t  
AAK59082 Human act  
ADSI6296 Human vol  
AAK16826 Human T-t  
ABX93560 Human cDN  
ADH69264 Human T-t  
AAK16827 Human T-t  
ABX93561 Human cDN  
ADH69266 Human TCC  
ADH69275 Rat TCCV  
AAK83492 Rat T-ty  
AAK31679 Rat brain  
AAV57542 Human cal  
AAK31674 Human alp  
ADL07263 Drosophili  
ADSI6299 C. elegans  
AAK51681 DNA encod  
AAK31681 Human alp  
AAK94358 Human ful  
ADL31040 Full leng  
AAK59083 Human act  
AAQ37817 Sequence

DR WPI: 2001-123111/13.  
DR P-PSDB: AAB66475.  
XX Novel T-type calcium channel alpha-1 subunit gene useful for treating  
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and  
PT epilepsy.  
XX  
XX  
PS Example 2; Page 61-63; 103pp; English.  
CC The present sequence is given in a specification providing sequences and  
CC partial sequences for three types of mammalian (human and rat) T-type  
CC calcium channel subunits. An expression cassette has been generated which  
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha\_1  
CC subunit operably linked to control sequences to effect its expression.  
CC The novel calcium channel nucleic acids and proteins are useful for  
CC treating conditions characterised by undesirable levels of T-type calcium  
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,  
CC hypertension, sleep disorder and epilepsy

Sequence 7540 BP; 1502 A; 2313 C; 2161 G; 1564 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 0 Length: 7540  
Score: 12024.00 Matches: 2286  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.97% Indels: 0  
DB: 5 Gaps: 0

US-09-611-257A-24 (1-2287) x AAF31677 (1-7540)

QY 1 MetLeuProHieAArgValProArgCysValAArgThrProProLeuAArgGlySera1AaArg 20  
DB 365 ATGCTCCCCACCGGATCCCCCGTTGGTGAAGACACCTCTCTAGAGGGCTCCGCTGCG 444  
QY 21 ProSerSerAspProProGlyProArgLeuA1AArgGlyTTPThrAArgAArgMetGlu 40  
DB 445 CCCTCTTGAGACCCCGCGGGCCCGGGCTGCGCAGAGATGAGCAGAGAGAGATGAG 504  
QY 41 ArgAlaProArgSerAArgAspSerProValA1AAseraArgSerSerThrThyCysProGly 60  
DB 505 CGGGGCGGAGAGTGGGAGCAGCCCGTAGCTTACAGCAGCTCAACGACCTGTCGGGG 564  
QY 61 ProGlyAlaAlaGlyAlaGlySerThrglyuysAspProGlySera1AAspSerGluA 80  
DB 565 CCGGGGCGGCGAGGGGCGGGTGAACGGAAGACCCGGGAGCGCGGACTCCAGAGCG 624  
QY 81 GluGlyLeuProTyProAlaLeuA1AProValA1PhePheTyLeuSerGlnAspSer 100  
DB 625 GAGGGGCGCGGTACCCGGCGGTACCCCGGTGTTTCTTACTTGAAGCCAGACAGC 684  
QY 101 ArgProArgSerTTPCysLeuAArgThyValCysAanProTTPPhGluAArgValSerMet 120  
DB 685 CGCCCGCGAGCTGTGTCTCCGACAGCTGTAAACCGTGTGTGAGCGAGTCAGTATG 744  
QY 121 LeuVal11eLeuLeuAAsnCysValA1ThrLeuGlyMetPheArgProCysGluAsp11eA1 140  
DB 745 CTGGTCATTTCTTCTAAGCTGTGACTCTGGGTATGTTTCAGGCCCTGTGAGGACATTGCC 804  
QY 141 CysAspSerGlnAArgCysAArg11eLeuGlnA1AAspAspAspPhe11ePheA1AAspPhe 160  
DB 805 TGTGACTCCGACGCGTGCAGATCTCGAGCGCTTCGATGACTTCATCTTTCCTTCTTT 864  
QY 161 AlaVal11GluMetVal1Val1yMetValA1A1eLeuGly11ePheGly11yAlaCysArgTyLeu 180  
DB 865 GCTGTGAAGTGTGTGTGAAGTGTGTGGCTTGGGACATTTTGGAGAGAAAGTTACTCG 924  
QY 181 GlyAspTTPTrpAsnAArgLeuAspPhePhe11eVal11eA1A1yMetLeuGluTySer 200  
DB 925 GGAGCACTTGAACCGGCTTACTTTTTCATTGTCATTGTCAGGAGATGCTGAGATTCG 984  
QY 201 LeuAspLeuGlnAanVal1SerPheSerA1AValAArgThyValAArgVal1LeuArgProLeu 220

DB 985 CTGAGACTGAGAAAGTACGTTCTCCGACGTCAAGACAGTCCGTGTGTCGACCGCTC 1044  
QY 221 ArgAla11eAanAArgValProSerMetAArg11eLeuVal11ThrLeuLeuAAspThrLeu 240  
DB 1045 AGGGCATTAACCGGGTGCCAGATGGAGCATTTCTGTCAATTAACGTGGAGACCTTG 1104  
QY 241 PrometLeuGlyAanVal1LeuLeuLeuCysPhePheVal1PhePhe11ePheGly11eVal 260  
DB 1105 CTTATGCTGGGCAACGTCCTGCTCTGTTTCTTTCGCTTTTTCATCTTTGGCATCGTG 1164  
QY 261 GlyValGlnLeuTTPAlaGly1LeuLeuAArgAanAArgCysPheLeuProGluAanPheSer 280  
DB 1165 GCGCTGCAGCTGTGGGAGAGACTCTTTCGCAACCGGTGCTTCTCCCGAGAACTTCAGC 1224  
QY 281 LeuProLeuSerValA1AAspLeuGluProTyTTPThrGluAanGluAanGluSerPro 300  
DB 1225 CTCCCCGAGACCGTGACCTGTGACCTTATTAACAGACAGAAATGAGAGAGAGAGCCCC 1284  
QY 301 Phe11eCysSerGlnProArgGluAanGlyMetAArgSerCysAArgSerValProThrLeu 320  
DB 1285 TTCACTGCTCTCAGCCTCGGGAGAAATGATGATCTTCAGAGAGTGTGCCACACTG 1344  
QY 321 ArgGlyGlnGlyGlyGlyProProCysSerLeuAspTyArgTyThrTrpAsnSerSer 340  
DB 1345 CGTGGGGAAGCGGTGTGGGCCACCTGCAGTCTGAGACTATGAGACCTATTAACAGTTCC 1404  
QY 341 SerAanThrTrpCysValAanTTPAanGlyTTPThrTrpAanCysSera1A1GluHis 360  
DB 1405 AGCAACACACCTGTGTCACTGGAACCAAGTCAATCAACACTCTTCGCGGAGAGCAC 1464  
QY 361 AAnProPheTyGlyAla11eAanPheAAspAan11eGlyTyA1ATP11eAla11ePhe 380  
DB 1465 AACCCTTCAAAAGGCGCATCACTTGAACAACATTGGCTATGCTGGATGCCATCTTC 1524  
QY 381 GlnVal11eThrLeuGluGlyTTPValA1Asp11eMetTyPheVal1MetAspAlaHisSer 400  
DB 1525 CAGGTCAATCAACATCGAGGGCTGGGTGACATCATGATCTTGTAAATGAGAGCTCACCTCC 1584  
QY 401 PheTyAanPhe11eTyPhePhe11eLeuLeu11e11eValGlySerPhePheMet11eAan 420  
DB 1585 TTTCACACTTCATCTTCTTATTTCTTCATCATCGTGGCTCTCTTCTCATATCAAC 1644  
QY 421 LeuCysLeuVal11eAla11eThrGlnPheSerGluThrxlysglnAArgGluSerGlnLeu 440  
DB 1645 CTGTGCTGTGTGTGATTTGCCACGCAATTCGAGACCAACAGCGGAGAGTCAAGTGG 1704  
QY 441 MetAArgGlnAArgValAArgPheLeuSerAanA1AAserThrLeuA1AAserPheSerGlu 460  
DB 1705 ATGGGGGAGCAGCTGTACGATTCCTGTCCAAATCTAGACCCCTGGCAAGCTTCTGTAG 1764  
QY 461 ProGlySerCysTyrglnGluLeuLeuTyThrLeuVal1TyT11eLeuAArgValA1A1A 480  
DB 1765 CGAGCAGCTGTATAGAGACTCACTCAATGACTGTGGTATCATCTCCGAAAGAGAGCC 1824  
QY 481 ArgAArgLeuA1A 500  
DB 1825 CGAAGGCTGGCCAGAGTCTTAGGGCTATAGCGGTGGGGCTGGGCTGTCAAGAGCCCA 1884  
QY 501 ValA1AArgSerGlyGlnGluProGlnProSerGlySerCysThraArgSerHisAArgArg 520  
DB 1885 GTGGCCCTAGTGGGAGAGAGCCAGCCAGTGGAGCTGACATCTGCTCACACCGTCTGT 1944  
QY 521 LeuSerVal1His11eLeuVal1His11eHis11eHis11eHis11eHis11eHis11eHis 540  
DB 1945 CTGTCTGCACCACTGTGTCAACCAATCAATCAACCAATCAATCAATCAATCAATCAATCA 2004  
QY 541 AasnGlyThrLeuAArgVal1ProAArgA1AserProGlu11eGlnAAspAArgAAspA1AasnGly 560  
DB 2005 AATGGAGGCTCAAGATTTCCCGGGCCAGGCCCAAGATCAAGAGATGCAAGATGCAAGG 2064  
QY 561 SerAArgAArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArg 580  
DB 2065 TCTCGCGGCTCATGTACCAACCACTTACCAACCACTTCTGTGGGGGCGCTCCGAGG 2124

QY 581 G1A1AG1uSerValH1seSerPheThyRhiSa1aAspCyH1seLeuGluProValArgCys 600  
Db 2125 GGTGGGAGTCTGTACAGAGCTTTACATGCTGACTGCACCTTGAGGACAGTCCGTTGC 2184  
QY 601 G1A1APROProProArgCysProSerG1uA1aSerG1yArGThValG1ySerG1yLys 620  
Db 2185 CAGGACACCCCTCCAGAGTCCCATCGGAGCATCTGTAGGACCTGTGGGTGTGGGAAG 2244  
QY 621 ValTYrProThValH1seThSerProProGlu1leLeuLysAspLysAlaLeuVal 640  
Db 2245 GGTACCCACAGTGTGATACAGAGCTTCCACAGAGATCTGAAGATTAAGACTAGAG 2304  
QY 641 G1uValA1aProSerProG1yProProThLeuThSerPheAsn1leProProG1yPro 660  
Db 2305 GAGGTGGCCCAAGCCCTGGGCCCCCACTTCACAGCTTCAACATCCCACTGGGCCC 2364  
QY 661 PheSerSerMetH1b1yLeuLeuG1uThrG1nSerThG1yValaCyH1seSerCys 680  
Db 2365 TTACAGCTCATGACACAGCTCCTGGAGACACAGAGTACGAGAGCCCTGCATAGCTTCG 2424  
QY 681 LysH1seSerProCySerSerLysA1aAspSerG1yA1aCyG1yProAspSerCyPro 700  
Db 2425 AAAATCTCCAGCCCTGTCTCCAAAGCAGACAGTGGAGCTCGGGCCGAGACAGTTGCC 2484  
QY 701 TYrCyBa1aArgThrG1yA1aG1yGluProG1uSerA1aAspH1sValMetProAspSer 720  
Db 2485 TACTGTGCCGAGACAGAGACAGAGAGCCAGAGTCCGCTGACATGTATGCTGACTCA 2544  
QY 721 AspSerG1uA1aValTYrGluPheThrG1nAspA1aG1nH1seSerAspLeuArgAspPro 740  
Db 2545 GACAGGAGGCTGTGTATGATTCACACAGAGCGCTCAGACACAGTACCTCGGGAGTCCC 2604  
QY 741 H1seSerArgArgArg1nArgSerLeuG1yProAspA1aG1uProSerSerValLeuA1a 760  
Db 2605 CACAGCCGGCGGAGACAGGAGGCTGGGCCAGATGCAAGCTTGTGTGCTGGCT 2664  
QY 761 PheTrpArgLeu1leCyAspThrPheArgLys1leValAspSerLysTYrPheG1yArg 780  
Db 2665 TTCTGGAGGCTATCTGTACACATTCGGAAGATGTAGATGCAAAATATCTTGGCCG 2724  
QY 781 G1y1leMet1leAla1leLeuValAsnThrLeuSerMetG1y1leGluTYrH1seGluG1n 800  
Db 2725 GGAATCATGATGCGCATCTGTCATACATCAGCATGCGGCATCGAGATCCAGGAG 2784  
QY 801 ProGluGluLeuThzAsnA1aLeuG1u1leSerAsn1leValPheThzSerLeuPheA1a 820  
Db 2785 CCCGAGAGCTCCACCAAGCCCTGGAAATCAGCAACATGCTTTCACAGCTCTTCGCC 2844  
QY 821 LeuG1uMetLeuLeuThzAsnLeuValTYrG1yProPheG1yTYr1leLysAsnProTYr 840  
Db 2845 TTGGAGATGCTGCTGAACTGCTTGTCTACGCTCCTTTGGCTACATTAAGAAATCCCTAC 2904  
QY 841 Asn1lePheAspG1yVal1leVal1leSerValTYrG1u1leValG1yG1nG1y 860  
Db 2905 AACATCTTGATGTGTCTCATTTGTGCATCAGTGTGGAGATGTGGGCCGACAGGAG 2964  
QY 861 G1yG1yLeuSerValLeuArgThzPheArgLeuMetArgValLeuLysLeuValaGpHe 880  
Db 2965 GGTGGCTGTGGTGTGGGACCTTCGCTCATGTGGGTGGGTGAGAGCTGGTGGCTTC 3024  
QY 881 LeuProA1aLeuG1nArg1nLeuVala1leLeuMetLysThzMetAspAsnVala1aTh 900  
Db 3025 CTGCCGCCCTTGAGGCGCAGCTCGTGTGCTCATAGACATGGACAACTGGGCCACC 3084  
QY 901 PheCyMetLeuLeuMetLeuPhe1lePhe1lePheSer1leLeuG1yMetH1seLeuPhe 920  
Db 3085 TTCTGCATGCTCTCATGCTGTTCATCTTCATCTTCAGCATCTCGGACATCTCTTT 3144  
QY 921 G1yCyb1yPheH1aSerG1uArgAspG1yAspThzLeuProAspArgLysAsnPheAsp 940  
Db 3145 GGTTCGAAAGTTCCATCTGAACGGAGTGGGACAGTTGCCAAGCCGAGAAATTTTCGAC 3204

QY 941 SerLeuLeuTrpA1a1leValThzValPheG1n1leLeuThrG1nG1uAspTrpAsnLys 960  
Db 3205 TCCCTGCTGTGGCCATGCTACTGTCTTTCAAGATTCGACTCGAGAACTGGAATTA 3264  
QY 961 ValLeuTYrAaG1yMetAlaSerThzSerSerTrpA1a1aLeuTYrPhe1leAlaLeu 980  
Db 3265 GTCCCTACAAAGGATGGCTCCACATCGTCTTGGGTGCTCTTTACTTCATCGCCCTC 3324  
QY 981 MetThzPheG1yAsnTYrValLeuPheAsnLeuVala1leLeuVala1leGluTYrHe 1000  
Db 3325 ATGACTTTTGGCAACTAGTCTCTTTAACCTGTGGTGGCCATCTTGTGAAGGATTC 3384  
QY 1001 G1nA1aG1uG1yAspA1aThzLysSerG1uSerG1uProAspPhePheSerProSerA1 1020  
Db 3385 CAGGACAGGAGAGACCAACAGTGTAGTCAAGCTGATTTCTTTCCGCCAGTGTG 3444  
QY 1021 AspG1yAspG1yAspArgLysLeArgLeuA1aLeuG1yG1uH1seA1aG1u 1040  
Db 3445 GATGTGATGGGGACAGAAAGAGCGCTTGGCCCTGTGGCTTTGGAGAACAGCGGAA 3504  
QY 1041 LeuArgLysSerLeuLeuProProLeu1le1leH1stHra1a1aThzProMetSerH1s 1060  
Db 3505 CTACGAAAGAGCTTTTGCACCCCTCATCATCTCATGCGTGGACACCAATGTCAAC 3564  
QY 1061 ProLysSerSerSerThzG1yValG1yGluA1aLeuG1ySerG1ySerArgArgThzSer 1080  
Db 3565 CCCAAGACTCCAGACAGGTGTGGGAGAGACTGGGCTGTGGCTTCGACATCCAGT 3624  
QY 1081 SerSerG1ySerA1aG1uProG1yA1aA1aH1sH1sG1uMetLysCybProProSerA1a 1100  
Db 3625 AGCAGTGGTCCGCTGAGACCTGAGCTCCACCATGAGATGAATGTCCGCAAGTGC 3684  
QY 1101 ArgSerSerProH1seSerProTrpSerA1aA1aSerSerTrpThzSerArgArgSer 1120  
Db 3685 CGCAGCTCCCGCAGATCCCTGAGTGGCGGACAGACTGGACCAAGAGGCGCTCCAGC 3744  
QY 1121 ArgAsnSerLeuG1yArgA1aProSerLeuLysArgArgSerProSerG1yG1uArgArg 1140  
Db 3745 AGGAACAGCTGGGGCGGGCCCCAGCTTAAGCCGAGAGAGCCGAGGGGAGCGGAG 3804  
QY 1141 SerLeuLeuSerG1yG1uG1yG1nG1uSerG1nAspG1uG1uG1uSerSerG1uLys 1160  
Db 3805 TCCCTGCTGTCTGGAGAGGCGCAGAGAGTCAAGATGAGAGAAATGTCAGAAAGGAG 3864  
QY 1161 ArgA1aSerProA1aG1ySerAspH1sArgH1sArgLysSerLeuG1uArgG1uAlys 1180  
Db 3865 CGGGCAGGCCAGGACGAGTACCATCGCCACAGGGGTTCTTGGAACTGTAGGCCAAG 3924  
QY 1181 SerSerPheAspLeuProAspThzLeuG1nVala1leProG1yLeuH1sArgThzA1aSerG1y 1200  
Db 3925 AGTTCTTTGACCTGCTGACACTGTGACAGTGTGGGGCTGCACCGCACAGCCAGGGC 3984  
QY 1201 ArgSerSerA1aSerG1uH1sG1nAspCybAsnG1yLysSerA1aSerG1yArgLeuA1a 1220  
Db 3985 CGAGGCTTGCTCTGAGACCAAGACTGTAAATGCAAGTCCGCTTCAGGGGCTTTGGCC 4044  
QY 1221 ArgThzLeuArgThzAspAspProG1uLeuAspG1yAspAspAspAsnAspGluG1yAsn 1240  
Db 4045 CGCACCTGAGACATGATGATCCCCCACTGATGGGAGTGAAGAACATATATAGGGAAT 4104  
QY 1241 LeuSerLysG1yG1uArg1leG1nA1aThzPValaArgSerArgLeuProA1aCybCybArg 1260  
Db 4105 CTGAGCAAGGGGAAAGCATACAGCTGTGGTCAATCCCGGCTTCGCTGTGGCCGA 4164  
QY 1261 G1uArgAspSerTrpSerA1aTYr1lePheProProG1nSerArgPheArgLeuCyb 1280  
Db 4165 GAGCGAGATTCCTGTGGCTTAATCTTCTCTCTCAAGTTCAGAGTTCTGTCTGTGT 4224  
QY 1281 H1sArg1le1leThzH1sLysMetPheAspH1sVala1leLeuVala1le1lePheLeuAsn 1300  
Db 4225 CACCGGATCATACCCACAAAGATGTTGACATGTGTGCTCTGTATCATCTTCTCAAC 4284  
QY 1301 Cyb1leThz1leA1aMetG1uArgProLys1leAspProH1seSerA1aG1uArg1lePhe 1320

Db 4285 TGTATCACCATGCTATGAGGCGCCCAAAATGACCCCAAGCGCTGAGGCATCTTC 4344  
Qy 1321 LeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValIlyVal 1340  
Db 4345 CTGACCTCTTCCACATCACTCTTCAACGGCAGCTCTTCTAGCTGAATGACAGTGAAGGTG 4404  
Qy 1341 ValAlaLeuGlyTProCysPheGlyGluGlnAlaTyrLeuArgSerSerTProAsnValLeu 1360  
Db 4405 GTGGCACTGGGCTGGTCTTTGGGAGAGGCGCTTCCGCGACAGAGCTGGAAATGTCTG 4464  
Qy 1361 AspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSer 1380  
Db 4465 GACGGCTTGCTGTGTCTATCTCCGTCATCGACATCTGTGCTCCATGGTCTCCAGACGC 4524  
Qy 1381 GlyThrIlyIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeu 1400  
Db 4525 GGCACCAAGATCTCTGGCATGTGTGAGGGGTGTGCGGCTGTGCGGACCCCTGGCTCACCTC 4584  
Qy 1401 ArgValIleSerArgAlaGlnGlyLeuIlyLeuValValGluThrLeuMetSerSerLeu 1420  
Db 4585 AGGGCTATCAGCCGGGCCCAAGGACTGAGACTGGTGGTAGAGACTCTGATGTCAATCCCTC 4644  
Qy 1421 LysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeu 1440  
Db 4645 AAACCATTTGGCAACATTGTGGTCAATTGTGCTGTGCTTTCATCATTTTGGAAATCTTC 4704  
Qy 1441 GlyValGlnLeuPheIlyGlyIlySphPheValCysGlnGlyGluAspThrArgAsnIle 1460  
Db 4705 GGGGTGCAGCTCTTCAAAGGAGGTTCTTCGTGTCAAGGTGAGACCCAGGAACATC 4764  
Qy 1461 ThrAsnIlySerAspCysAlaGluIleAspTyrArgTProValArgHisIlySerTyrAsnHe 1480  
Db 4765 ACTTAACAAATCCGACTGCGCTAGGCGCACTACCAATGGGTCCGCAACAAGTCAACTTT 4824  
Qy 1481 AspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerIlyAspGlyTProVal 1500  
Db 4825 GACAACTGGGCGACAGCTCTGATGTCCCTGTTGTGTGCTGCGCTCCAAAGATGTGGGTT 4884  
Qy 1501 AspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetSerHis 1520  
Db 4885 GACATCATGTATGATGAGGTGTGATGCTGTGGGTGTGATCAGCACCCCATCATGTGAACAC 4944  
Qy 1521 AsnProTProMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeu 1540  
Db 4945 AACCCCTGGATCTGTATATCTTCATCTCTCTCTCATGTGTGGCTTCTTTGTCTG 5004  
Qy 1541 AsnMetPheValGlyValValValGluAsnPheHisIlyCysArgGlnHisGlnGlnGlu 1560  
Db 5005 AACATGTTTGTGGCGTGGTGGTGGAGAACTTCATTAAGTGCAGACAGACAGAGAGAG 5064  
Qy 1561 GlnGluAlaArgArgArgGlnGluIlySargLeuArgGluGluIlySargArgArgSer 1580  
Db 5065 GAGGAGGCGAGCGCGCTGAGAGAGAGCATACGAGAGCTGGAGAAAAAGAGAGAGT 5124  
Qy 1581 LysGlnIlySglMetAlaGluAlaGlnCysIlySProTyrTyrSerAspTyrSerArgPhe 1600  
Db 5125 AAGGAGAAAGCATGTGCGGAAGCCCAAGTGCAGAGCCCTACTACTCTGACTCTCGAGATTTC 5184  
Qy 1601 ArgLeuLeuValHisIleLeuCysThrSerHisIlyTyrLeuAspLeuPheIleThrIlyVal 1620  
Db 5185 CGGCTCTTGTCCACACCTGTGTACAGCCACTACCTGAGCCTTCTATCATCTGTGTGTC 5244  
Qy 1621 IleGlyLeuAsnValValIleThrMetAlaMetGluHisIlyTyrGlnGlnProGlnIleLeuAsp 1640  
Db 5245 ATCGGGCTGAAAGTGTGTCTATGGCCATGGAACATTAACCAAGACCCCAAGTCTTGAC 5304  
Qy 1641 GluAlaLeuValHisCysAsnTyrIlePheThrValIlePheValPheGluSerValPhe 1660  
Db 5305 GAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCATCTTTGCTTTGAGTCAAGTTTTC 5364  
Qy 1661 LysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTProAsnGlnLeuAspLeu 1680

Db 5365 AACCTTGCGCTTGGCTTCCGCCGTTTCTTCCAGACAGGTGAAACAAGCTGAGCTG 5424  
Qy 1681 AlaIleValLeuLeuSerIleMetGlyIlePheThrLeuGluGlnIleGluValAsnLeuSer 1700  
Db 5425 GCTATTTGCTTCTGTCCATCATGAGGACATCACTGAGAGAGATGAGTGAATCTGTGCG 5484  
Qy 1701 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu 1720  
Db 5485 CTGCCCAACAACCCCAACATCATCCGTATCATGAGGGGTGCTCCGCAATGCTCGAGTTCTG 5544  
Qy 1721 LysLeuLeuIlyMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeu 1740  
Db 5545 AAGCTGTGAAGATGGCTGTGGCATGGGCGACCTGCTGCACAGGTGATGCAGGCCCTG 5604  
Qy 1741 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu 1760  
Db 5605 CCCAGGTGGGAAACCTGGAGCTTCTCTCACTGATATGTTTTCATCTTTGCAAGCTCTG 5664  
Qy 1761 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1780  
Db 5665 GCGGTGAGAGCTCTTTGAGAGACTGGAGTGTATGAGACACACCTTGTGAGGGCTTGGGT 5724  
Qy 1781 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1800  
Db 5725 CGGATGCGCACCTTGAAGACTTGTGATGGCTTTTCTGACCCCTTCCGAGTCTCACT 5784  
Qy 1801 GlyAspAsnTProAsnGlyIleMetIlyAspProSerArgAspCysAspGlnGluSerThr 1820  
Db 5785 GGTACCAACTGAATGGATATATAGAGAACCTTTCGGGAGCTGTGACCAAGATCCACC 5844  
Qy 1821 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1840  
Db 5845 TGCTAACAACTGTCACTCTCCCTATCTACTTGTGTCTTCGATGTCGAGCGCCAGTTT 5904  
Qy 1841 ValLeuValAsnValValIleAlaValLeuMetIlyHisIleuGluGluSerAsnIlyGlu 1860  
Db 5905 GTGCTGTGCMAAGTGTGCATGTGTGTGTGATGAGACCTCGGAAGAAAGCAACAAAGAG 5964  
Qy 1861 AlaIlySglGluAlaGluLeuGluAlaGluLeuGluIleuLeuMetIlySThrLeuSerPro 1880  
Db 5965 GCAAGAGAGAGGCGCACTGAGGCGGAGCTGAGACTGAGATGAAGACCTCAGCCCG 6024  
Qy 1881 GlnProHisSerProLeuGlySerProPheLeuTProGlyValGluGlyValAsnSer 1900  
Db 6025 CAGCCCACTCCCGCGTGGCAGCCCTTCTCTGCGCCGGGGGTGAGGGTGTCAACAGT 6084  
Qy 1901 ThrAspSerProIlySProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerGly 1920  
Db 6085 ACTGACAGCCCTTAAGCCTGGGGCTCCACACCACTGCCCATTTGAGAGAGCTCGGGC 6144  
Qy 1921 PheSerLeuGlnHisProThrMetValProHisProGluGluValProValProLeuGly 1940  
Db 6145 TTCTCTCTTGACACCCACATGTATACCCACCCCAAGAGGTGCCAGTCCCTTAGA 6204  
Qy 1941 ProAspLeuLeuThrValArgIlySerGlyValSerArgThrHisSerLeuProAsnAsp 1960  
Db 6205 CCAAGCTCGTGAATGTGAGGAAGTGTGTGTACGCGGAAGCACTCTCTGCCCAATGAC 6264  
Qy 1961 SerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisIlyGlyTProGly 1980  
Db 6265 AGCTAACATGTGCCCAATGGAGAGCACTGTGAGAGATCCCTAGAGACACAGGGGCTGGGG 6324  
Qy 1981 LeuProIlySglAsnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSer 2000  
Db 6325 CTCCCAAGGCCAGTCAAGGCTCATCTTGTCCCTTCACTCCCAACAGCAGACACAGC 6384  
Qy 2001 CysIleLeuGlnLeuProIlyAspValHisIlyTyrLeuLeuGlnProHisIlyAlaProThr 2020  
Db 6385 TGCAATCTCAAGCTTCCCAAGATGTGCATATGTGTCCAGCTCANTGGGCTCCACAC 6444  
Qy 2021 TProGlyAlaIleProIlySLeuProProGlyIlyArgSerProLeuAlaGlnArgProLeu 2040  
Db 6445 TGGGGCGGCATCCTTAACATCAACCCCACTGGCGGCTCCCTCTGGCTCAGAGGCTCTTC 6504



QY 2041 ArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlu 2060  
 XX AGCCGCGAGGAGCAATAAGACTGACTCCCTGATGTCAGAGGCTGGGTAGCCGGAGA 6564  
 DB 6505 AGCCGCGAGGAGCAATAAGACTGACTCCCTGATGTCAGAGGCTGGGTAGCCGGAGA 6564  
 QY 2061 AppleLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerPheTrp 2080  
 DB 6565 GACCTGTTGTCAAGAGTGAGTGAGGCTCTGCTCCCTCAACCCGGCTTCATCTTCTGG 6624  
 QY 2081 GlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerValSerIleHis 2100  
 DB 6625 GCGGGGTCAGCATCCAGGTGACGACGACCTTCCGACATCAGAGCAATCTCCAAAGC 6684  
 QY 2101 IleArgLeuProAlaProCysArgProGlyLeuGluProSerTrpAlaValAspProGlu 2120  
 DB 6685 ATCCGCTCCAGCCCTTGGCCAGGCTCGAACCAGCTGGGCCAAGAGACCTCCAGAG 6744  
 QY 2121 ThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuPro 2140  
 DB 6745 ACCAGAGCAGCTTAGAGCTGACAGCAGAGCTGAGCTGATTTCAAGAGACCTCTTCCC 6804  
 QY 2141 SerSerGlnGluGluProLeuPheProArgAspLeuValLeuSerValGluThr 2160  
 DB 6805 AGCAGCCAGAGAGAACCTCTGTTCCACGAGACTTAAGAGAGTGTACGTAGAGACC 6864  
 QY 2161 GlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgIleAla 2180  
 DB 6865 CAGAGCTGACAGGCGCAGGCTGGGTTCTGGCTAGATGAAACAGCGAGACACTTCATTGCT 6924  
 QY 2181 ValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuGly 2200  
 DB 6925 GTACAGCTGTGGACAGCGGCTCCCAACCCCGCTATGTCCAAGCCCTCAAGCCCTCGGG 6984  
 QY 2201 GlyGlnProLeuGlyGlyProGlySerArgProGlyValLeuSerProProSerIle 2220  
 DB 6985 GGCCAACCTCTTGGGGGCTCTGGAGCGGCTTAAGAAAATCAAGCCCAACCAATATC 7044  
 QY 2221 SerIleAspProProGluLeuSerGlnGlySerArgProCysSerProGlyValCysLeu 2240  
 DB 7045 TCTATAGACCCCCCGAGAGCCAGGCTCTCGGCCCAATGACGTCTGTGTCTCTCCTC 7104  
 QY 2241 ArgArgArgAlaProAlaSerAspSerValAspProSerValSerSerProLeuAspSer 2260  
 DB 7105 AGGAGGAGGCGCGCGGCACTGACTTAAGATCCCTCGGCTCCAGCCCTTGAACGC 7164  
 QY 2261 ThrAlaIleSerProSerProGlyValAspThrLeuSerLeuSerGlyLeuSerSerAsp 2280  
 DB 7165 AGCGCTGCTCACCCTCCCAAGAAAGACACGCTAGTCTCTGTGTTGTCTTGAC 7224  
 QY 2281 ProThrAspMetAspPro 2286  
 DB 7225 CCAACAGACATGACCCC 7242  
 RESULT 2  
 ADS16295  
 ID ADS16295 standard; DNA; 6942 BP.  
 XX ADS16295;  
 AC  
 XX 02-DEC-2004 (first entry)  
 DT  
 XX Rat voltage-dependent T type alpha 1g subunit calcium channel DNA.  
 DE  
 XX Voltage-dependent ion channel; drug candidate;  
 XX aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;  
 KM anti-convulsant; antiarrhythmic; rat; alpha 1g subunit; ds.  
 XX  
 OS Rattus norvegicus.  
 XX  
 PN US2004175761-A1.  
 PD 09-SEP-2004.  
 XX

PF 01-MAR-2003; 2003US-00377139.  
 XX  
 XX 01-MAR-2003; 2003US-00377139.  
 PR  
 XX  
 PA (MACK/) MACKINNON R.  
 PA (MACK/) MACKINNON A L.  
 PA (JIAN/) JIANG Y.  
 PA (RUTA/) RUTA V.  
 XX  
 PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;  
 XX  
 DR MPI: 2004-642122/62.  
 DR REFSQ; NM\_031601.  
 XX  
 PT Screening drug candidates that target voltage dependent ion channel  
 PT protein, involves contacting screening protein with chemical compound,  
 PT which is drug candidate and determining whether chemical compound binds  
 PT to screening protein.  
 XX  
 PS Disclosure; SEQ ID NO 7; 61pp; English.  
 XX  
 CC The invention relates to the composition of matter suitable for use in  
 CC identifying chemical compounds that bind to voltage-dependent ion channel  
 CC proteins. The composition comprises a screening protein that consists of  
 CC an ion channel voltage sensor domain of the ion channel protein  
 CC immobilised on a solid support. The invention is useful for identifying  
 CC chemical compounds (drug candidate) that bind to voltage-dependent ion  
 CC channel proteins. The drug candidate of the invention is utilised for  
 CC treating a condition mediated by aberrant electrical activity that  
 CC initiates uptake or release of neurotransmitters and contraction of  
 CC muscles. The drug candidate of the invention is also utilised for  
 CC treating epilepsy and arrhythmia. The present sequence is a voltage-  
 CC dependent calcium channel DNA.  
 XX  
 SQ Sequence 6942 BP; 1383 A; 2126 C; 1961 G; 1472 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 0 Length: 6942  
 Score: 11980.00 Matches: 2283  
 Percent Similarity: 99.78% Conservative: 0  
 Best Local Similarity: 99.78% Mismatches: 3  
 Query Match: 99.60% Indels: 2  
 DB: Gaps: 0  
 US-09-611-257a-24 (1-2287) x ADS16295 (1-6942)  
 QY 1 MetLeuProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArg 20  
 DB 16 ArgCTCCCAACCGGCTCCCGCTTGGCTGAGGACACTCTCTAGGGGCTCCGCTGC 75  
 QY 21 ProSerSerAspProProGlyProArgGluAlaArgGlyTyrThrArgArgMetGlu 40  
 DB 76 CCTCTTGGGACCCCGCGGCGCCCGGCTGGCCAGAGATGACAGAGAGAGATGAG 135  
 QY 41 ArgAlaProArgSerThrArgAspSerProValAlaSerArgSerThrThrCysProGly 60  
 DB 136 CGGGGCGCCAGAGAGTCCGGAGACGCCCGGTACCGAGCTCAACGACCTGTCCGGGG 195  
 QY 61 ProGlyVala-AlaGlyVala-GlySerThrGluValAspProGlySerAlaAspSerGlu 80  
 DB 196 CCGGGGGCGGAGGGGCGGGGTGACCGAAGAAAGACCCGGGACCGGAGCTCCGAGG 255  
 QY 80 IagGluGlyLeuProTyrProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAsp 100  
 DB 256 CGAGGGGCTGCCTGATCCCGGCGCTAGCCCGGTGGTTTCTTCACTTGAACCGAGACA 315  
 QY 100 eArgProArgSerTrpCysLeuArgThrValCysAspProTrpPheGluArgValSerM 120  
 DB 316 GCGGCGCGGAGAGCTGTCTCCGACGCTGTAAACCGGTTCGAGCGAGTCAGTA 375  
 QY 120 eLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIle 140  
 DB 376 TGCTGTCTATTCTTCAACTGTGTACCTGTGGTATGTTCAGGCGCGTGTAGACATTG 435

QY 140 laCyAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAlaPhe 160  
Db CCTGTGACCTCCAGAGCGCTGCCGATCTCTGCAGAGCCTTGATGATCACTTCTTGCTTCT 495  
QY 160 heaIvalaGluMeValIalIysMetValAlaLeuGlyIlePheGlyIysIysCysTyrL 180  
Db TTGCTGTGGAAATGGTGGTGAAGATGGTGGCTTGGGCATCTTTGGGAAGAAATGTACC 555  
QY 180 euGIyAspThrTTPAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrS 200  
Db TGGGAGACACTTGGAAACCGGCTTGACTTTTCATTTGATTCAGAGGATGCTGGAGTATT 615  
QY 200 erLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuAspProL 220  
Db GCTGTGACCTGCAGAAAGCTCACTTCTCCGACGTAGAGACAGTCCGTGTGCTGCACCGC 675  
QY 220 euArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAspThrL 240  
Db TCAGGGCCATTAAACGGGTGCCAGACATGCCGATTCCTGTCATTTACGTGCGACACT 735  
QY 240 euProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleV 260  
Db TGCCATAGCTGGGCAACGCTGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTG 795  
QY 260 aIGIyValGlnLeuTTPAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPhS 280  
Db TGGGCTCCAGCTGTGGGCAAGACCTGCTTCGACACCGGTCTTCTCCCGAGAACCTTCA 855  
QY 280 erLeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerP 300  
Db GGCTTCCCTCGAGCTGGACCTGGAGCCTTATTACAGACAGAGAAATAGAGACGAGAGCC 915  
QY 300 roPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrL 320  
Db CTTATCATGCTCTCAGCCTCGGAGAAATGCGATAGATCTCGACGAGGTGGCCACAC 975  
QY 320 euArgGlyGluGlyIleGlyIleGlyIleProCysSerLeuAspTyrGlnThrTyrAsnSerS 340  
Db TGGCGTGGGGAAGCGGTGGTGGCCACCTCGACAGTCTGGACATAGACCTATTAACATT 1035  
QY 340 erSerAsnThrThrCysValAsnTTPAsnGlnTyrTyrThrAsnCysSerAlaGlyGluH 360  
Db CGAGCAACACCCACTGTGTCACTGGAACCAAGTACTATACCAACTGCTCTGGCGGCGAGC 1095  
QY 360 leAsnProPheLeuGlyAlaIleAsnPheAspAsnIleGlyTyrTrpIleAlaIleAlaIleP 380  
Db ACAACCCCTTCNAAGCGCCATCAACTTTGACAACTGGCTATGCTGGATCGGCATCT 1155  
QY 380 heGlnValIleThrLeuGluGlyTTPValAspIleMetTyrPheValMetAspAlaHisS 400  
Db TCCAGTCAATCACTGAGAGGCTGGGTGCATGATGATCACTTCCTAATGACGCTCACT 1215  
QY 400 erPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleA 420  
Db CTTTCTACAACTTCACTTCACTTCTTCTCATCATCGTGGGCTCTTCTTCTCATGATCA 1275  
QY 420 snLeuCyLeuValValIleAlaThrGlnPheSerGluThrIlysnArgGluAsnArgL 440  
Db ACCCTGTGCTGGTGGTGGATGCGACAGTCTTCGAGACCAAAACAGCGGAGATCGAC 1335  
QY 440 euMeArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerG 460  
Db TGAATCGGGAGAGAGCTGTACATTCCTGTCCAAAGCTAGACACCTTGGCAAGCTTCTG 1395  
QY 460 luProGlySerCysTyrGluGluLeuLeuLysTyrIleuValTyrIleuArgIyAlaA 480  
Db AGCCAGGACGAGCTGATAGAGAGCTACTCAAGTACCTGGTGTACATCTCCCAAAAGAG 1455  
QY 480 laArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerP 500  
Db CCCGAGGCTGGCCAGGCTCTAGAGGCTATAGGCGGTGGGCTGGGCTGCTCAGACAGCC 1515

QY 500 roValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgA 520  
Db CAGTGGCCCGTATAGTGGGAGAGAGCCCGACGCCAGTGGACGTGCTACACCGCTC 1575  
QY 520 rGLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHis 540  
Db GTCGTGTGTCCACACCTGGTCCACACCAATCCACACCAACCAACCAACCAACCAACCTGG 1635  
QY 540 lYAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnG 560  
Db GTAATGGGACCTCAGAGTTCCTCCGGGCCACCCAGATTCAGAGACGGGATCCCAATG 1695  
QY 560 lYSerArgArgLeuMeLeuProProProSerThrProThrProSerGlyGlyProProA 580  
Db GGTCTCGCGGCTCATGTACACCAACCTCTTACCCACATCCTCTGGGGGCCCTCGA 1755  
QY 580 rGglYAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgC 600  
Db GGGGTGGGAGTCTGTACACAGCTTTCACATGCTGACTGCTGACCTTGAGCCAGTCCGTT 1815  
QY 600 ySglnAlaProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyL 620  
Db GCCAGGACCCCTTCAGATGCCATCGAGGATCGATGGATCTGTGGATGTGGGA 1875  
QY 620 ySValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuV 640  
Db AGGTATACCCCACTGTGATTCAGCCCTCCACAGAGATCTGAAGATTAAGACACTAG 1935  
QY 640 aIGIyValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyP 660  
Db TGGAGGTGGCCCCAGGCTGGGGCCCCCACCCTTCACAGCTTAACATCCACACTGGGC 1995  
QY 660 roPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerC 680  
Db CTTTCACTCCATGACAGTCTCTGAGACACAGATGCGGAGCTGCATAGCTCTCT 2055  
QY 680 ySlyIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysP 700  
Db GCAAAATCTCCAGCCCTTGTGCTCCAAAGCAGACAGATGGAGCTTGGGCGGAGCTTGT 2115  
QY 700 roTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspS 720  
Db CTTACTGTGCCCGACAGAGACAGAGACAGAGCTCGCTGACCAATGTCATGCTTCACT 2175  
QY 720 erAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspP 740  
Db CAGACAGGAGGCTGTATATAGTTTACACAGAGCTCAGACAGATGACCTCCGGGATC 2235  
QY 740 roHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuA 760  
Db CCAACAGCCGCGGCGACAGCGGAGCTGGGCCAGATGACAGACCTAGTTCTGTGCTGG 2295  
QY 760 laPheTTPArgLeuIleCysAspThrPheArgIyIleValAspSerLysTyrPheGlyA 780  
Db CTTTCTGGAGCTATCTGTACACATTCGGAAGATCGTAGAGCAAAATCACTTTGAGCC 2355  
QY 780 rGglYIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluG 800  
Db GGGGATCATATATGCCATCTCTGTCATATACCTCAGCATGGGATGAGATCCACAGAC 2415  
QY 800 luProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheA 820  
Db AGCCGAGAGACCTCACCAAGCCCTGGAATCAGACACATGCTTCCACAGCCTCTTGG 2475  
QY 820 laLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProT 840  
Db CTTTGGAGATGCTGTAAATGCTTGTCTTACAGGCTCTTGGCTTACATTAAGATCCCT 2535  
QY 840 lYAsnIlePheAspGlyValIleValValIleSerValTPProGluIleValGlyGlnGln 860  
Db ACAACATCTTTGATGAGGTCTATTGTGTCACTAGTGTGGAGATTTGTGGCCACAGAG 2595  
QY 860 lYgIyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgP 880

Db | 2596 GAGGTGGCTCTGCGGTGCGGACCTTCCGCTGATGGGGGTGCTGAAGCTGGTGGCT | 2655  
Qy | 880 hLeuProAlaLeuGlnAArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaT | 900  
Db | 2656 TCTTGCCGGCCCTTGACGGCCGACGCTGTGTGCTCATGAAGACATGACCAAGTGGCCA | 2715  
Qy | 900 hPheCysMetLeuMetLeuMetPheIlePheIlePheSerIleLeuGlyMetHisLeuP | 920  
Db | 2716 CTTTCGATGATGCTCCATGCTGCTTTCATCTTTCATCTTTCAGCATCTCGGACATGCACTCTCT | 2775  
Qy | 920 hGlyCysAlaLysPheAlaSerGluAArgPGLYAspThrLeuProAlaPGLYAspPheA | 940  
Db | 2776 TTGGTTGGCAAGTTCGATCTGAACGGGAATGGGACAGTTGCCAGACCGGAAGAAATTTGG | 2835  
Qy | 940 gSerLeuMetLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnL | 960  
Db | 2836 ACTCCCTGCTGTGGGCAATGTCATGTCCTTTTCAGATTCTGACTCAGGAAGACTGGAAAT | 2895  
Qy | 960 yValLeuTyraAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyPheIleAlaL | 980  
Db | 2896 AGTCTCTTAACAACGGCAATGGCTCCACATCGTCTTGCGGTGCTTTACTTCATCGCCC | 2955  
Qy | 980 eLueThrPheGlyAsnTyPValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyP | 1000  
Db | 2956 TCATGACTTTTGGCACTATGTGCTCTTAACTGCTGTGGCCATCTTGTGGAAGGAT | 3015  
Qy | 1000 hGlnIaGluGlyAspAlaThrLysSerGluSerGluProAlaPhePheSerProSerY | 1020  
Db | 3016 TCCAGGCAAGGGAGATGCCAACAAGTCTGATCAGACCTGATTTCTTTTGGCCCAAGTG | 3075  
Qy | 1020 aLaspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaG | 1040  
Db | 3076 TGGATGTGATGGGACAGAAAGAGGGCTTGGCCCTGGGTGGCTTTGGGAGAACAGCGG | 3135  
Qy | 1040 lLeuLysArgLysSerLeuLeuProLeuIleIleHisThrAlaAlaThrProMetSerH | 1060  
Db | 3136 AACTAGAAAGAGCCCTTTGGCCACCCCTCATCATCAATACGGCTGGGACACCAATGTGAC | 3195  
Qy | 1060 iProLysSerSerSerThrGlyValGlyGlnAlaLeuGlySerGlySerArgThS | 1080  
Db | 3196 ACCCAAGAGCTCAGACAGGTGTGGGAGAGACCTGGGCTTGGCTTCGACGTAACCA | 3255  
Qy | 1080 eSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerA | 1100  
Db | 3256 GTAGCAGTGGGTCCGCTGAGACCTCGAGCTGCCACCATGATGAAATGCCCCCAAGTG | 3315  
Qy | 1100 lAspSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgSers | 1120  
Db | 3316 CCGGCAAGCTCCCGCACAGTCCCTGGAGTCCGGCAGACAGCTGGACCAAGAGCGCTCCA | 3375  
Qy | 1120 eArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgA | 1140  
Db | 3376 GCAAGAAACAGCTCGGGCGGGGCCCCAGCCTTAAGCCGAGAGAGCCGAGCGGGAGCGGA | 3435  
Qy | 1140 rSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluGluA | 1160  
Db | 3436 GGTCCCTGCTGTGAGAGAGGCGCAAGAGATGACAGATGAGAGAAAGTTTCAGAAAGAG | 3495  
Qy | 1160 sPArgAlaSerProAlaGlySerAspHisAlaArgHisAlaArgGlySerLeuGluArgLAlaL | 1180  
Db | 3496 ACCGGGCAACCCAGCAGGAGATGACCATCGCCACAGAGGGTTCCTTGGAACTGTAGGCCA | 3555  
Qy | 1180 yAspSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisAlaArgThrAlaSerG | 1200  
Db | 3556 AGAGTTCTTTGACCTTCTGACACTTTCAGAGGTGGCGGGGCTGCACCGACAGCCAGCG | 3615  
Qy | 1200 lYArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuA | 1220  
Db | 3616 GCGGAGACTCTGCTCTGAGACCAAGACATGTAAATGCAAGTGGCTTACGGGGGTTTGG | 3675  
Qy | 1220 lAspThrLeuArgThrAspAspProGlnLeuAspGlyLysAspAspAspAsnAspGluGlyA | 1240

Db | 3676 CCGGCAACCTTGAGACATGATGACCCCAACTGGATGGGAGATGACATATGAGGAA | 3735  
Qy | 1240 sNLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysA | 1260  
Db | 3736 ATCTAGCAAAAGGGAGACGATACAGAGCTGGGTGAGATCCCGGCTTCTGCTGTGGC | 3795  
Qy | 1260 rGluArgAspSerTrpSerAlaTyPTrilePheProGlnSerArgPheArgLeuLeuC | 1280  
Db | 3796 GAGAGCGAGATTCCTGTGGCTGATATCTTCTCTTCAGTCAAGGTTTGGCTCTCTCT | 3855  
Qy | 1280 yHisAlaArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuA | 1300  
Db | 3856 GTACCGGATCATCAACCAAGATGTTTGAACATGTGGTCTCGTCAATCTTCTCTCA | 3915  
Qy | 1300 sNysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIleP | 1320  
Db | 3916 ACTGTATCACCATCCCTATGAGCGCCCAAAATGACCCCAAGCGGTGAGCCATCT | 3975  
Qy | 1320 hLeuThrLeuSerAsnTyPTrilePheThrAlaValPheLeuAlaGluMetThrValLysV | 1340  
Db | 3976 TCTTGACCTTCTCAACTACATCTTCAAGGAGTCTTCTTACCTGAATGACATGGAAG | 4035  
Qy | 1340 aValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyPLeuArgSerSerTrpAsnValL | 1360  
Db | 4036 TGGTGCACTGGGCTGTGCTTTGGGGAGCAGGCTACCTGGCAGAGCTGGAATGTGC | 4095  
Qy | 1360 eAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspS | 1380  
Db | 4096 TGGACGGCTTGGGTGCTCATCTCGTCATGACATCTGTGCTTCACATGCTCCGACA | 4155  
Qy | 1380 eGlyTyPThrLysIleLeuGlyMetLeuArgValLeuArgLeuMetArgThrLeuArgProL | 1400  
Db | 4156 GCGGCAACCAAGATCCTTGGCATGTAGGGTGTCTGGGTGCTGAGACCTTGGCTCCAC | 4215  
Qy | 1400 eArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerL | 1420  
Db | 4216 TCGGGTCAATCAACCGGCGCCAGGAGTGAACCTGGTGTAGAGTCTGATGTATCCC | 4275  
Qy | 1420 eLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleL | 1440  
Db | 4276 TCAAAACCATGGCAACATTTGTGTCATTTGCTGTCCTTTCATCATTTTGGAAATTC | 4335  
Qy | 1440 eGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspTrpArgAsnI | 1460  
Db | 4336 TCGGGGTGAGCTCTTCAAAAGGAGTCTTGTGTGTAGGGGTGAGACACAGGAACA | 4395  
Qy | 1460 lEthraAsnLysSerAspCysAlaGluAlaSerTyraGTrpValArgHisAlaLysTyraAsp | 1480  
Db | 4396 TCACTTAACAAATCCGACTCGCTGAGGCCAGCTACCGATGGGTCCGGCACAAATCAACT | 4455  
Qy | 1480 hAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTyP | 1500  
Db | 4456 TTGACAACCTGGGCGAGGCTCGATGTCTCTGTTTGTGCTGGCTCAAGATGTGTTGG | 4515  
Qy | 1500 aLAspIleMetTyraPGLYLeuAspAlaValGlyValAspGlnGlnProIleMetAsnH | 1520  
Db | 4516 TTGACATCATGATATGATGGCTGTGATGTGTGTGATGACAGCCCATCATATAACC | 4575  
Qy | 1520 iAsnProTrpMetLeuLeuTyPTrilePheLeuLeuIleValAlaPhePheValL | 1540  
Db | 4576 ACAACCTCGATGTCTGCTATCTTCACTTCTCTCATCGTGGCTTCTTTGTCC | 4635  
Qy | 1540 eLAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluG | 1560  
Db | 4636 TGAACATGTTTGGGCGTGTGTGAGAAACTTCCATTAAGTGCACAGCACAGCAAGAG | 4695  
Qy | 1560 lGluGlnGluAlaArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgS | 1580  
Db | 4696 AGGAGAGGCGAGGCGCGGTGAGAGAACGACTTACGAGGCTTGAGAAAGAAAGAGAG | 4755  
Qy | 1580 eLysGluTyPGLYMetAlaGluAlaGlnCysLysAspProTyPTrilePheAspTyPSerArgP | 1600  
Db | 4756 GTAAAGAGAAAGATGGCCGAAGCCCAAGTGCAGAGCCTAATCTATGACTATCGAGAT | 4815

Qy	1600	nearGleuLeuValHisHisLeuCySthrSerHisrYrLeuAspLeuPheIleThrGly	1620
Db	4816	TCCGGCTCTTGTCCACCACTGGTGACACCACTCACTGGACCTCTTCATCATCTGGTG	4875
Qy	1620	allIegILeuAsnValAlaThrMetAlaMetGluHisrYrGluGluProGlnIleLeuA	1640
Db	4876	TCATCGGGCTGAACGTGGTCACTATGGCCATGGAACATTACCAAGCCCAAGATCTCGG	4935
Qy	1640	spgIuaIaLeuLysIleCySaAsnYrIlePheThrValIlePheValPheGluSerValP	1660
Db	4936	ACGAGGCTCTGAAGATCTGCAATTACATCTTACCGTCATCTTGTGTCATGACATTT	4995
Qy	1660	helysLeuValAlaPheAlaPheArgArgPhePheGluAsnArgTrpAsnGluLeuAspL	1680
Db	4996	TCAAACTGTGGCTTGTGGCTTTCGGCCCTTCTTCACAGACAGGTGGAAACGATGGACC	5055
Qy	1680	euaIaIaIeValLeuLeuSerIleMetGcYrIleThrLeuGluGluIleGluValAsnLeuS	1700
Db	5056	TGGCTATTGTCTTCTGTGCCATCATATGGGCATCAACATGGAAGAAATTGAGTCAATCTGT	5115
Qy	1700	eIeUpProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValI	1720
Db	5116	CGCTGCCCATCAACCCCAACATCATCCGATCATAGAGGTGCTCCGCAATCTCGAATTC	5175
Qy	1720	eulyrLeuLeuLysMetCAlaValGlyMetArgAlaLeuLeuHisrThrValMetGlnAlaL	1740
Db	5176	TGAAGCTGTTAAAGATGGCTGTGGGCAGACGGGCATCTGTGCACACGATGATGAGGCC	5235
Qy	1740	eUPrGlnIValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaIal	1760
Db	5236	TGCCCAAGTGGGAACTGGGACTTCTCTTCATGTTATTTGTTTTCATCTTTGCAGCTC	5295
Qy	1760	eugIyValGlyLeuPheGlyAspLeuGluCySaAspGluThrHisrProCyAsnGluYLeuG	1780
Db	5296	TGGGGTGGAAGCTCTTTGGAGACCTGGAGTGATGAGACACACCTTGTGAGGGCTTGG	5355
Qy	1780	lyAArgHisAlaIaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerT	1800
Db	5356	GTCGGCAAGCCACTTATAGAACTTGGTATAGGCTTTCTACACCTCTTCGCAATCTTCCA	5415
Qy	1800	hrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCySaAspGlnGluSerT	1820
Db	5416	CTGGTGAACATCGAATAGTATTTATGAAGACACCTCCGGGACTGTGATCCAGAGATCCA	5475
Qy	1820	hrCySyrAsnThrValIleSerProIleYrPheValSerPheValIleuThrAlaGlnP	1840
Db	5476	CCCTGCTACAAACATGTCATCTCCCTCATCTCTTGTGTCCTTGCTGCTGACGGCCAGT	5535
Qy	1840	heValIleuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerMetLysG	1860
Db	5536	TTGTGCTGTGTAAACGTGTGTCAATAGCTGTGTGATGAAGCACTGTGAAGAAACAACAAAG	5595
Qy	1860	IuaIaLysGluGluAlaGluLeuGluIuaIaGluLeuGluLeuGluIleMetLysThrLeuSerP	1880
Db	5596	AGGCCAAGGAAGGACCGAAGCTCGAAGCCGAGCTGTGAAGTGAATGAAGACGCTCAGCC	5655
Qy	1880	roGlnProHisSerProLeuGluYrSerProPheLeuTrpProGlyValGluGlyValAsnS	1900
Db	5656	CGAGACCCCACTCCCGCTGGGACAGCCCTTCCTGTGGCCGGGAGTGAAGGTGTCAACA	5715
Qy	1900	eErThrAspSerProLysProGlyValAlaProHisrThrThrAlaHisrIleGlyValAlaSerG	1920
Db	5716	GTACTGACAGCCCTTAAGCTGTGGGTCCACACACCACTGCCCCAATGTGACACACCTCGG	5775
Qy	1920	lyPheSerLeuGluHisrProThrMetValProHisrProGluGluValAlaProValProLeuG	1940
Db	5776	GCTTCTCCCTTGAAGCAACCAACGATGTAACCCCAACCCGAAGAGGTGCAATCCCCCTAG	5835
Qy	1940	lyProAspLeuLeuThrValAlaArgLysSerGlyValSerArgThrHisSerLeuProAsnA	1960
Db	5836	GACACAGACCTGTGACTGTGAGAAAGTGTGTGTGTCAAGCCGAGACCACTCTGTGCCCAATG	5895

QY	1360	spserTYrmecY/batYasnGlySerThralaGlnaGserLeuGlyhiGarglyYTrpG	1980
Db	5896	ACACCTCACTAGTGGCCGAATGGGAGCACTCTGTGAGATCTCTTAAGACAAGGGGGCTGGG	5955
QY	1980	lyLeuProLySAIaGInSerGlySerllLeuSerValhIsSerGInProAlaAPhThrs	2000
Db	5956	GGCTTCCCCAAGCCCACTCAGGCTCCACTTGTTCCTGCTTCACTCCCAACAGACACACCA	6015
QY	2000	erCySllLeuGInLeuProLyAspValhIsTyrlLeuGInProhIeglyVALaProT	2020
Db	6016	GCTGCATCTCAACAGCTTCCCAAGATGTGACATATCTGCTCCAGCCCTCATGGGGCTCCCA	6075
QY	2020	hTrTPGlyAlaIlleProLyLeuProProProGlyAlaGserProLeuAlaGInArgProL	2040
Db	6076	CCTGGGGGGCCATCTCCCTMAACTACCCCACTGGCCCTCCCTGGCTTCAGAGGGCTTC	6135
QY	2040	eUAArgArgInAlaAlaIlleArgThrasPserLeuAPValGInGlyLeuGlySerArgG	2060
Db	6136	TCAGGCGCCAGGACAGCAATTAAAGACTACTTCCTGGATGTGACAGGAGCTGGGTACGGGG	6195
QY	2060	lUaPserLeuSerGluValSerGlyProSerCySProLeuThrArgSerSerPhet	2080
Db	6196	AAGACCTGTGTGTCAGAGGTGAGTGGGCGCTTCGGCCCTTGACCCGGTCTCATCTTCT	6255
QY	2080	rPglYglySerSerllleGInValGInGInArgSerGlyllleGInSerLyValSerLysh	2100
Db	6256	GGGGCGGGGTGAGAGATCCAGGTGAGAGAGGGTTCGGGCATCCAGAGCAAGAGTCTCCAGC	6315
QY	2100	IsllleArgLeuProAlaProCyAProGlyLeuGInuProSerTTPAlaLYaAPProProg	2120
Db	6316	ACATTCGGCTTGCCAGCCCTTGCCAGGAGCTTGGAACCAAGTGGGCCAAGGACCTTCAG	6375
QY	2120	lUThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIlleSerGlyAspLeuLeup	2140
Db	6376	AGACCAAGAGAGCTTTAGAGCTGACACAGGAGCTGAGACTGGATTTTCAGAGAGACCTCTTC	6435
QY	2140	roSerSerGInGluInProLeuPheProArgAspLeuLyblyCySfTySerValGluT	2160
Db	6436	CCACGACCCAGGAAGAACCCCTGTTCACAGGGGACCTGAAGAGAGTGTCAAGTGTAGAGA	6495
QY	2160	hrgInserCySArgArgArgProGlyPheThrLeuAspGluGInArgArgHIsSerllleA	2180
Db	6496	CCGAGACTGACGGCGCAGGCTGTGGGTTCTGGCTAGATGAACAGCGGAGACACTCCACTTG	6555
QY	2180	lAValSerCySLeuAspSerGlySerGInProArgLeuCySProSerPProSerSerLeuG	2200
Db	6556	CTGTCACTGTCTGTGACAGGGGCTCCCAACCCGGCTATGTCCAAAGCCCTCAAGCCTCG	6615
QY	2200	lyGlyGInProLeuGlyGlyProGlySerArgProLyblyblybLeuSerProProSerI	2220
Db	6616	GGGGCCCAACCTCTTTGGGGGTCCTGGGAGCCGGCTTAAGAAAAAACTCAGGCCACCCAGTA	6675
QY	2220	leSerllleAPProProGluSerGInlySerArgProProCySserProGlyValCySl	2240
Db	6676	TCTTATAAGACCCCCGAGAGCCAGGGGCTCTGGCCCCCATGACAGTCTGGGTGTCTGCC	6735
QY	2240	eUAArgArgArgAlaProAlaSerAspSerLyAspProSerValSerSerProLeuAspS	2260
Db	6736	TCAGAGAGAGGGCGCCCGCAGTACCTTAAGATTCCTGGGTCTCCAGGCCCTTGTACA	6795
QY	2260	erThralAlaAlaSerProSerProLyblyAspThrLeuSerLeuSerSerGlyLeuSerSerA	2280
Db	6796	GCAAGGCTGCTCACTCCCTCCCAAGAAACACAGCTGAGTGTCTGTGTTGTCTTCTG	6855
QY	2280	spProThrasPmetAspPro 2286	
Db	6856	ACCCAACAGACATGAGACCC 6875	
RESULT 3			
AAZ52309			
ID	AAZ52309	standard; cDNA; 7286 BP.	
AC	AAZ52309;		

XX 18-JUL-2000 (first entry)  
XX Rat pancreatic T-type calcium channel cDNA.  
XX Rat: pancreatic T-type calcium channel alpha subunit; insulin;  
XX pancreatic beta cell; alphaIG, low voltage activated Ca2+ channel family;  
XX antidiabetic; calcium influx; L type calcium channel; NIDDM;  
XX type II diabetes; non-insulin dependent diabetes mellitus; ss.  
XX Rattus sp.  
XX  
XX Key Location/Qualifiers  
XX misc\_feature 1..157  
XX /tag= b  
XX /note= "Region upstream to the coding region of  
XX pancreatic T-type calcium channel protein"  
XX 2..7285  
XX /tag= a  
XX /product= "Pancreatic T-type calcium channel alpha  
XX subunit"  
XX /transl\_except= (pos:11..13, aa:Xaa)  
XX /transl\_except= (pos:7022..7024, aa:Xaa)  
XX /transl\_except= (pos:7112..7114, aa:Xaa)  
XX /note= "Xaa corresponds to in-frame stop codon. This  
XX region includes sequence upstream to the coding region of  
XX pancreatic T-type calcium channel protein. Does not  
XX include stop codon"  
XX /partial  
XX 158..7285  
XX /tag= c  
XX /product= "Pancreatic T-type calcium channel alpha  
XX subunit"  
XX /note= "This region is claimed as SEQ ID NO: 1"  
XX  
XX WO200015845-A1.  
XX  
XX 23-MAR-2000.  
XX  
XX 26-AUG-1999; 99WO-US019675.  
XX  
XX 26-AUG-1998; 98US-0098004P.  
XX 27-JAN-1999; 99US-0117399P.  
XX  
XX (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.  
XX  
XX Li M;  
XX  
XX WPI; 2000-271475/23.  
XX P-PSDB; AAY70720.  
XX  
XX Novel nucleic acids encoding pancreatic T-type calcium channels used for  
XX regulation of T-type calcium channels and treatment of type II diabetes.  
XX  
XX Example 1; Page 114-119; 124pp; English.  
XX  
XX The present cDNA encodes a protein that includes pancreatic T-type  
XX calcium channel alpha subunit derived from rat insulin secreting beta  
XX cell line, INS-1. The protein shows 96.3 % identity to the neuronal T-  
XX type calcium channel alpha subunit (alphaIG). The T-type Ca2+ channel  
XX from INS-1 (alphaIG-INS) and neuronal alphaIG are alternative splice  
XX isoforms of the same gene. The INS-1 isoform is also expressed in brain,  
XX neonatal heart and kidney besides pancreatic beta cells. T-type Ca2+  
XX channel belongs to the family of low voltage activated Ca2+ channels. The  
XX present sequence is used for treating diseases associated with abnormal  
XX expression or function of T-type calcium channels. They are especially  
XX used for treating type II diabetes. Modulators of pancreatic T-type Ca2+  
XX channel e.g. antisense oligonucleotides, ribozymes and inhibitors are  
XX used in methods for modifying insulin secretion by pancreatic beta cells,  
XX basal calcium levels, potential L type calcium channel activity,  
XX pancreatic cell death, pancreatic beta cell proliferation and calcium  
XX influx through L type calcium channels in cells

Seq Sequence 7286 BP; 1467 A; 2224 C; 2064 G; 1531 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 0 Length: 7286  
Score: 11829.00 Matches: 2270  
Percent Similarity: 97.72% Conservative: 1  
Best Local Similarity: 97.68% Mismatches: 15  
Query Match: 98.35% Indels: 38  
DB: 3 Gaps: 2  
US-09-611-257A-24 (1-2287) x AA252309 (1-7286)  
QY 1 MetLeuProH1sArg-Val1ProArg-CysValArgThrProProLeuArgGlySerAlaA 20  
DB 58 ATGCTCCCAACCGGGGTCCTCCGTTGCTGAGGACCTCTCTGAGGGCTCCGCTC 117  
QY 20 rGProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetG 40  
DB 118 GCCCTCTTCGGACCCCGGGGGCCCGGCTGGCCAGATGAGCGAGAGAGATGG 177  
QY 40 lUaArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrCysProG 60  
DB 178 AGCGGGCCCGAGAGAGTGGGACAGCCCGTAGCTTCAAGAGCTCAACGACTGTCCGG 237  
QY 60 lYProGlyVala-AlaGlyVala-GlySerThrGluysAspProGlySerAlaAspSerg1 79  
DB 228 GCGCGGGGCGGCGGGGGCGGGGTCCAGGAAAGAACCCGGCAGCGGAGCTCCGA 297  
QY 79 uAlaGluGlyLeuProTyProAlaLeuAlaProValValPhePheTyLeuSergLnas 99  
DB 298 GCGGAGGGGCGTCCGTCACCGGCGCTAGCCCGGTGTTTCTTCTTCTTCTTCTTCTTCTT 357  
QY 99 pSerArgProArgSertTPCySLeuArgThrValCysAsnProTTPPheGluArgValaSe 119  
DB 358 CAGCGCGCGCGAGACTGTGTCTCCGACCGCTGTAAACCGTGTTCAGCCGAGTCA 417  
QY 119 rMetLeuVal11LeuLeuAsnCyVal1ThrLeuGlyMetPheArgProCySGLuAsp11 139  
DB 418 TATGCTGTGATCTTCTTCACTGTGATCTGTGGATTTGTTCAAGCCGTGTGAGACAT 477  
QY 139 eAlaCysAspSergLnaArgCySArg11LeuGlnAlaPheAspAspPhe11ePheAla1a 159  
DB 478 TGCTGTGATCTCCACGCGCTGCGGATCTGTGAGCCCTTTCATGTATCTTGTCCCT 537  
QY 159 ePheAlaValGluMetVal1Val1yMetVal1AlaLeuGly11ePheGly1ySArg1 179  
DB 538 CTTGCTGTGAAATGTGTGTGAAATGTGTGCTTGGGCTATCTTGGGAAATGTTA 597  
QY 179 rLeuGlyAspThrTrpAsnArgLeuAspPhePhe11eVal11eAlaGlyMetLeuGluTy 199  
DB 598 CTTGGAGACACTTGTGAACCGGCTTGACTTTTCAATTGTCAATTGACAGGATCTGGAGTA 657  
QY 199 rSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgVal1LeuArgPr 219  
DB 658 TTTCGCTGACCTGCGAAGACTGACCTTCCGCACTGAGGACAGTCCGTCTGTGGAGC 717  
QY 219 oLeuArgAla11eAsnArgVal1ProSerMetArg11eLeuVal11ThrLeuLeuAspTh 239  
DB 718 GCTCAGGGGCATTAAACCGGCTGCCAGATGCGCATTCGTCAATTACTCTGAGCAC 777  
QY 239 rLeuProMetLeuGlyAsnVal1LeuLeuLeuCySAspPheVal1PhePhe11aPheGly1 259  
DB 778 CTTGCTTAAGCTGGCAAGCTCTGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 837  
QY 259 eValGlyValGlnLeuTPAlaGlyLeuLeuArgAsnArgCySAspLeuProGluAsnPh 279  
DB 838 CTTGGCGCTGACCTGTGTGGCAGAGCTGTTGCAACGATCTTCTTCTTCTTCTTCTTCTT 897  
QY 279 eSerLeuProLeuSerValAspLeuGluProTyTyTyGlnThrGluAsnGluAspGluSe 299  
DB 898 CAGCTTCCCTCGAGAGGTGACCTGAGCTTATTAACAGACAGAAAGAGAGAGAG 957  
QY 299 rProPhe11eCySserGlnProArgGluAsnGlyMetArgSerCySArgSerValProTh 319

Db	958	CCCCCTTCATCGCTCTCAGCCTCCGGAGAAATGGCATAGAACTTCGACAGAGTGGCCAC	101.7
Qy	319	rLeuArgG1VGIuGIyGIyGIyGPProCySeSerLeuAspYrGIuThrYTrAAsE	339
Db	1018	ACTCGTGGGGAGGCGGTGGTGGCCACCTCGACGTCTGGACTATGAGACTTAAACAG	107.7
Qy	339	rSeSerAsnThrThrCysValaEntPAsnGlnTYrThrAsnCysSeraIaGIyGI	359
Db	1078	TTCCAGCAACAACCACTGTGTCAACTGGAAACCACTACTATACCAACTGTCTGGGGGGA	113.7
Qy	379	ePhGIGVal1leThrLeuGIuGIyTPPValAsp1ImecTYrPheValMetAspAlaH1	399
Db	1198	CTTCAGGTCAACACTGAGGGCTGGGTGACATCACTGTACTTGTAATGAGCGCTCA	125.7
Qy	399	sSeSerPheTYrAsnPhelIeTYrPhe1leLeu1le1eValGIySePhePheMet1	419
Db	1258	CTCCTTCACAACTTCATCACTTCACTTCCTCATCATGTGGGCTCCTTCATGAT	131.7
Qy	419	eAenLeuCysLeuValVal1lealathrGlnPheSerGIuThrYsGIuArgIuSerGI	439
Db	1318	CAACCTGTGCTGGTGTGATGGACAGCACTTCGAGACCAAAACGCGGAGAGATCA	137.7
Qy	439	nLeuMeArGIuGIuArgValAcGPheLeuSerAsnAlaSerThrLeuAlaSerPheSe	459
Db	1378	GCTATAGGGAGACAGCGGTGACATTCCTCTCCAAATGCTAGCACTTCGACACTTC	143.7
Qy	459	rGIuProGIySeCYrTYrGIuGIuLeuLeuYsTYrLeuValTYr1leLeuArgYsAl	479
Db	1438	TGAGCCAGGACGCTGATAGAGAGCTACCACTGATGTAACATCCTCGAAAGC	149.7
Qy	479	aAlaArgArgLeuAlaGlnValSerArgAla1leGIyValArgAlaGIyLeuLeuSerSe	499
Db	1498	AGCCCGAAGGTGGCCAGAGTCTTAAAGGGCTAATAGGGGTGGGGCTGGGCTGCACAG	155.7
Qy	499	rProValAlaArgSerGIyGlnGIuProGlnProSerGIySeCYrThrArgSerH1sAr	519
Db	1558	CCAGTGACCCGTAATGTGGAGAGAGCCCAACCAAGTGGACGTCACTGGCTACACCG	161.7
Qy	519	gArgLeuSerValH1sh1sLeuValH1sh1sh1sh1sh1sh1sh1sh1sh1sTYrH1sLe	539
Db	1618	TGGTCTGTCTGTCCACCACTCGTGTCCACACACATCACCAACCATCACCACTACACT	167.7
Qy	539	uGIYAsnGIyThrLeuArgValProArgAlaSerProGIu1leGlnAspArgAspAlaAs	559
Db	1678	GCGTAATGTGGACGCTCAGAGTTCCCGGGGCGACGCCAGAGATCCAGGACAGGGATGCCAA	173.7
Qy	559	ngIySerArgArgLeuMetLeuProProProSerThrProThrProSerGIyGIyProPr	579
Db	1738	TGGGTCTGTGGCGGTCAATGCTAACCAACCTCTTACACCACTCTCTCTGGGGGCGCTCC	179.7
Qy	579	oArgGIyAlaGIuSerValH1sSerPheTYrH1sAlaAspCYsH1sLeuGIuProValAr	599
Db	1798	GAGGGGTGGAGTCTGTACACCACTTCTACAGCTGACGTGCCACTTTGGAGCCAGTCCG	185.7
Qy	599	gCYsGlnAlaProProProArgCYsProSerGIuAlaSerGIyArgThrValGIySerGI	619
Db	1858	TTTGCACAGCAACCCCTCCAGATCCCATCGGAGGACATCTGGTGTGAGACTGGGTGATGGG	191.7
Qy	619	YlYsValTYrProThrValH1sThrSerProProProGIu1leuYsAspYsAla1e	639
Db	1918	GAAGGTGTAACCACTGTGATACCAAGCCTTCAACAGAGTACTGAAAGATTAAGCACT	197.7
Qy	639	uValGIuValAlaProSerProGIyProProThrLeuThrSerPheAsn1leProProGI	659
Db	1978	AGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTACCAAGCTTCAACATCCACCTGG	203.7
Qy	659	YProPheSerSerWech1sYsLeuLeuGIuThrGlnSerThrGIyAlaCYsH1sSerSe	679

Db	2038	GCCCTTCAGCTCCATGCAACAGCTCTCTGGAGACACAGATGACGGAGACCTTCGCATACGCTC	2097
Qy	679	TCYSLVAILSSERSEPRocYssERlysaIAaSPserGIvAlaCYagIyProaSPserCY	699
Db	2098	CTGMAAAATCTCCAGCCCTTGCTTCACAGGACAGACATGGAGACCTCGCGGGCCGACAGTTG	2157
Qy	699	SPProTYCyaaIAaRgThrIyIaGIyIuPRoGluSerAlaSPHIsaIaIeCProaS	719
Db	2158	TCCCTACTGTGCCCGGACAGAGACAGAGACAGATCCGCTGACCATCTCATGCTCTGA	2217
Qy	719	PSERASPSERGIuAlaValTYrGIuPheThrGIuNaSPaIAaGHIIsERxSPleuArGaS	739
Db	2218	CTCAGACAGGAGGCTGTGTATGATGTCAACACAGAGAGCTTCAGACAGTAACTCCGGGA	2277
Qy	739	PCProHIsERArGaRgRgIuNaRgSERleuGIyProaSPaIaGIuPRoSERseValle	759
Db	2278	TCCCCACAGCCGGGGGACAGCGAGACCTTGCGGCCAGATGACAGAGCCTATGTGTGCT	2337
Qy	759	uAlaPheTYPaRgIeulIeCYaSPaThrPheaRgIyIsIeValaSPserIyTYrPheGI	779
Db	2338	GGCTTTCGAGAGGCTGATCTGTGACACATTCGGAGAGATGRTGATAGCAAAATACCTTGG	2397
Qy	779	YARgIyIIsMeCIIaIaIleIeuvAIsaNTThrIeSerMeCIIyIleGIuTYrHIsGI	799
Db	2398	CCGGGGAATATATATCCGACCTCGTGCAATATACCTGATGATGGGACATCGAATCACGA	2457
Qy	799	UGINPRoGIuGIuIeuvThzAsnaIaIeugGIuIsERAsnIIsEaIaPheThrSerIeupH	819
Db	2458	GCAGCCGAGAGAGGTCCACACGCCCTGGAAATACAGAACATGCTGTTCCACGAGCCTCTT	2517
Qy	819	EaIaIaIeugIuMeIeuleuIySleuIeuvAlIYrGIyProPheGIYTYrIleIySaSPR	839
Db	2518	CGCCTTGGAATATGCTGTCGAAACGTCTGTCTPAACGCGCTTGCTTGCTTACCTTAAGAATCC	2577
Qy	839	CTYrAsnIIsPheASpGIyValIIsEaValIIsERValITrGIuIIsEaIyGIyngI	859
Db	2578	CTACAAATCTTTGATGATGATGATCATGTGGATCATAGTGTGGAGATTTGGGCCACGA	2637
Qy	859	ngIyGIyGIyIeUsERseValIeuaRgThrPheaRgIeMeCArgValIeulIySleuValaC	879
Db	2638	GGAGAGTGGCTGTGGGTGCTGGGACCTTCCGCTCATGCGGGTGTGTGAAGCTGGTGGC	2697
Qy	879	gPheIeuproAlaIeugIuNaRgIuIeuvAlIaIleuMeClySThrMeCAsPaSaNaValaI	899
Db	2698	CTTCTCGCCGACCTGACGCGCAGAGCTCGTGGTGCTCATGAACATGACGAACAGTGGC	2757
Qy	899	aThrPheCYaMeIeuleuMeIeupHeIIsPheSeriIeIeugIyMeThIsIe	919
Db	2758	CACCTTGTGATGTCTCTCATGTCTGTTCATCTTCATCTTACAGATCTCTGGGCATGATCT	2817
Qy	919	uPheGIyCYaIyPheAlaSERGIuArGaSPGIyAsPThrIeupRoAsPRgIySaSaNH	939
Db	2818	CTTTGGTTCGAAGTTCGCATCTGAACGGAGATGGGGACAGCTTGCACAGCCGAAAGATTT	2877
Qy	939	eASPSERleuIeupTpaIaIIsEaIaIeValIThrValIePheGIIeIeuthrGIuIuAsPTrPaS	959
Db	2878	CGACTCCCTGCTCGGGCCATCGCACTGCTTTCAGATCTGACTCAGAGAAACGTGGAA	2937
Qy	959	uIySaValIeulTYrAsnIyMeCIIaIaSerThrSERsetTpaIaIaIeulIyRheIIsaI	979
Db	2938	TAAAGTCTCTTACAAACGGCATGGCTCCACATGCTGTGGGCTGCTCTTAACTTCATCGC	2997
Qy	979	aIeMeCThrPheGIyAsnTYrValIeupHeaSNleuIeValaIaIIsEaValaGIuGI	999
Db	2998	CCTCATACCTTTTGGCACTATGTGCTTTAACTGCTGTGTGGCCATCTTGTGGAAAG	3057
Qy	999	yPheGIIaIaGIu-----GIySaPaIaThrIySaSERGIuSerGIuProAsPhePh	1003
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Qy	1004	-----GIySaPaIaThrIySaSERGIuSerGIuProAsPhePh	1016
Db	3118	GCTGCTGTGCACTCTCAGGGGGGAGATGCGACCAAGTCTGAATGACAGGCTTAATTTCTT	3177

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Db 3228 ACCAATGTCACTACCAAGAGCTTCAGCACAAGTGTGGGGAAGCACTGGCTTGCTC 3357  
QY 1076 rArgArgThSerSerSerGlySerAlaGluProGlyAlaAlaHIsHIsGluMetIleCy 1096  
Db 3358 TCGAGCTACCACTAGAGAGTGGGTCCGCTGAGCTGGAGCTGCCACATGATGAATAAC 3417  
QY 1096 sProProSerAlaAqSerSerProHIsSerProTTPSerAlaAlaSerSerTTPThSe 1116  
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QY 1116 rArgArgSerSerArgAsnSerleuGlyArgAlaProSerleuLyArgArgSerProSe 1136  
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Db 3658 AGCTGAGCCCAAGATCTCTTGACCTGCTGACACTCTGACAGTCCCGGCGCTGACCG 3717  
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Db 3778 AGGGCTTTGGCCCGCAGCCTGAGACTATGACCCCAACTGGAGGGAGATGATCAAA 3837  
QY 1236 nAspGlyGlyAsnleuSerleuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 1256  
Db 3838 TGAATGAGGAATCTGAGCAAGAGGAGGACATCAAGCTGGGTCAATCCGCGCTTCC 3897  
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Db 3898 TGCCTGTTCCGAGAGCGAGATTCCGTGCGGCTATATCTTTCCTCAAGTCAAGGTT 3957  
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QY 1296 eIlePheLeuAsnCyAlaIleThrIleAlaMetGlyuArgProLyHIsAspProHIsSerAl 1316  
Db 4018 CATCTTCTCAACTGATCACTACCTGATGAGCGCCCAAAATTGACCCCAKAGCGC 4077  
QY 1316 agluArgIlePheLeuThrleuSerAsnTyrlIlePheThrAlaValaPheleuAlaGluMe 1336  
Db 4078 TGAAGGCATCTTCTCAACCTCTCAACATCACTTCAAGGAGTCTTCTAGTGAAT 4137  
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QY 1376 cValSerAspSerGlyThrIleLyHIsleuGlyMetleuArgValleuArgleuLeuArgTh 1396  
Db 4258 GATCTCCAGAGCGGACCAAGATCTTGGCATGTGAGGAGTGTGCGGCTGCTCGGAC 4317  
QY 1396 rleuArgProleuArgValIleSerArgAlaGlnGlyleuLySerValaValaGluThrLe 1416  
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Db 4378 GATGTCACTCCCTCAACCATTTGGCAATTTGGTCAATTTGTCTGTGTCTTTCATCAT 4437  
QY 1436 ePheGlyIlyleuGlyValaGlyleuPheLyGlyLyAspPheValaCyAsnGlyGlyuAs 1456  
Db 4438 TTTGGAAATCTCGGAGTGCAGCTCTTCAAGGAGAGTTCTTGTGTCTCAGGAGAGA 4497  
QY 1456 rThrArgAsnIleThrAsnLySerAspCyAlaGlyuAlaSerTyArgTrpValaArgHIs 1476  
Db 4498 CACCGAACAATCACTAACAATCCGACTGGCTGAGGCCAGCTACCGATGGGTCCGCA 4557  
QY 1476 sLyArgTrAsnAspAsnleuGlyGlnAlaMetSerleuPheValaIleValaSerLy 1496  
Db 4558 CAAGTCAAACTTTGACAACTGGGCGCAGGCTCTGATGTCCCTGTTGTGTGGCTCCAA 4617  
QY 1496 sAspGlyTrpValaIlePheMetTyArgGlyleuAspAlaValaGlyValaAspGlnGlnPr 1516  
Db 4618 GGATGTTGGTTGACATCATGATGATGAGGCTGATCTGTGATGTGTGATCAGCAGCC 4677  
QY 1516 oIleMetAsnHIsAsnProTTPMetleuLeuTyArgPheIleSerPheleuLeuIleVala 1536  
Db 4678 CATCATGAACAACAACCCCTGATGCTGTACTTACTTACTTCTCCCTCATCTGCTGAC 4737  
QY 1536 aPhePheValleuAsnMetPheValaGlyValaValaGlyuAsnPheHIsLyAspArgGly 1556  
Db 4738 CTTCTTTGCTTGAACATGTTGTGTGGCTGTGTGAGAACTTCCATTAATGAGACA 4797  
QY 1556 nHIsGlnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 1576  
Db 4798 GCACAGAGAGGAGAGGAGGCGAGCGGCTGAGAGAAAGCACTTACCGAGCTGAGAA 4857  
QY 1576 sLyAspArg-----SerLyGlyLySerGlnMe 1585  
Db 4858 AAGAGAGAGATCTAAATGTTGAGAGATGATTTGCTCCGCGACCTCAGCAGGCTCC 4917  
QY 1585 cAlaGlyuAlaGlnCyAspProTyTrpSerAspTySerArgPheArgleuLeuValaHIs 1605  
Db 4918 GTCAAGAGCCAGTCCAGCCTTACTACTGACTGAGATTCGCGCTCTGTGTCA 4977  
QY 1605 sHIsleuCyethrSerHIsGlyleuAspLeuPheIleThrGlyValaIleGlyleuAsnVa 1625  
Db 4978 CCACCTGTGTACACACCACTACCTGACCTTCACTGATGATGAGGCTGAGACCT 5037  
QY 1625 lValaThrMetAlaMetGlyHIsGlyGlnGlnProGlnIleleuAspGlyuAlaIleuLyHIs 1645  
Db 5038 GGTCACTATGCGCAAGCAATTAACAAGGCCAGATCCGAGAGGCTCTGAAGAT 5097  
QY 1645 eCyAsnTyrlIlePheThrValaIlePheValaPheGlySerValaPheLySerValaIle 1665  
Db 5098 CTGCAATTAATCACTTACCGTATCTGTGTGTGATGATGATTTCAAACTGTGTGCTT 5157  
QY 1665 eAlaPheAspArgPhePheGlnAspArgTrpAsnGlyleuAspLeuValaIleValaIleu 1685  
Db 5158 TGGCTTCCGCGCTTCTTCCAGAGAGGAGGAGCAAGCTGAGCCTGGCTATGTGCTTCT 5217  
QY 1685 uSerIleMetGlyIleThrleuGlyGlyIleGlyuValaAsnleuSerleuProIleAsnPr 1705  
Db 5218 GTCCATCAAGGCAATCACTGAGAGAGATTAAGGTCAATGCTTGGCTCCATCAACCC 5277  
QY 1705 oThrIleIleArgIleMetArgValleuArgIleAlaArgValaIleuLySerleuLyMe 1725  
Db 5278 CACCATCATCCGATCATAGAGGTGCTCCGCAATGCTCGAATTTCTGAAGCTGTGAAGAT 5337  
QY 1725 cAlaValaGlyMetArgAlaIleleuHIsIleThrValaMetGlnAlaIleuProGlnValaGlyuAs 1745



Db	5338	GGCGTGGGCAATGGGGCACTGGACAGCGTATCAAGGCTTCGCCAGAGGGGAA	5397
Qy	1745	nLeuGIvLeuLeuPheMetLeuLeuPhePheIlePheAlaIleuGIvAlaGIleuPh	1765
Db	5398	CTGGGACTTCTCTTCAATGTTATTTGTTTTCATCTTTTGCACTCTGGGCGTGAAGCTT	5457
Qy	1765	eGIvAspLeuGIvCysAspGIuThrhiAspCysGIuGIvLeuGIvAArghisAlaThrph	1785
Db	5458	TGGAGACTGGAGGTGATGATGAGACACCCTTGAGAGGCTTGAGGTGGGATGCCACTT	5517
Qy	1785	eArgAsnPhGIvMetAlaPheLeuThrLeuPheArgValSerThrGIvAspAsnTPas	1805
Db	5518	TAGGAACCTTGGATGAGCCCTTTCGACCCTTTCGAGTCTCCACTGATGCAACTGAA	5577
Qy	1805	ngLIvIleMetIvAspProSerArGAspCysAspGIvGIvSerThrCysTyraEntThv	1825
Db	5578	TGGATATATAGAGACACCCTCCGGGACTGTGACACAGAGTCCACTGTCTACAACTGT	5637
Qy	1825	IleSerProIleTyPheValSerPheValLeuThrAlaGlnPheValIleuValaEnva	1845
Db	5638	CATCTCCCTATCTACTTTGTGTCTTCGTGCTGACGGCCAGTTTGCTGTCAACGT	5697
Qy	1845	IValIleAlaValIleuMetIvshIleuGIvGIvSerAsnIvsgIvAlaIvGIvGIvAl	1865
Db	5698	GGTCATGCTGTGTGTGATGAAGCACTGGAGAAAGCAACMAAGGCCAAGAGGAGGC	5757
Qy	1865	AGIvLeuGIvAlaGIvLeuGIvGIvLeuGIvMetIvshIleuSerProGIvProhiSsaPr	1885
Db	5758	CGACTCGAGGCCGAGCTGAGCTGAGATGATGAACGCTCAGCCCGACCCCACTCCC	5817
Qy	1885	oLeuGIvSerProPheLeuTrpProGIvAlaGIvGIvAlaAsnSerThrAspSerProIy	1905
Db	5818	GGTGGCAGCCCTTCTCTGTGGCCCGGGGTGAGAGGTGTCAACAGTCCGTCAAGCCCTAA	5877
Qy	1905	sProGIvAlaProhiSthrThrAlaHisIleGIvAlaAlaSerGIvPheSerLeuGIvhi	1925
Db	5878	GCCGGGGCTCCACACACACTGCCCACTGGAGAGCCCTCGGGCTTCTCCCTTGAGCA	5937
Qy	1925	sProThrMetValProhiSproGIvGIvGIvAlaProvalProleuGIvProAspLeuLeuTh	1945
Db	5938	CCCCACATGTATCCCCACCCCGAGAGATGCCAGTCCCTTAGAGACCAAGCTGTGAC	5997
Qy	1945	rValArgIvSerGIvAlaSerArGThrhiSserLeuProAsnAspSerTyMetCysAr	1965
Db	5998	TGTGAGGAAGTCTGTGTGCAGCCGAGCACTCTCTGCCCAATAGACTACATGTCCG	6057
Qy	1965	gAsnGIvSerThrAlaGIvArgSerLeuGIvHisArgIvTYTrpGIvLeuProIvAlaGI	1985
Db	6058	CAATGGGAGCACTGCTAGAGATTCCTTAGAGCAACAGGGGCTGGGGGCTCCCAAGGCCA	6117
Qy	1985	nSerGIvSerIleuSerValHisSerGIvProAlaAspPheSerCysIleleuGIvle	2005
Db	6118	GTCAGGCTTCATCTTGTCTCGCTTCACTCCCAACAGCAACACAGCTGTACTACACT	6177
Qy	2005	uProIvAspValHisTyLeuLeuGIvProhiSgIvAlaProThrTrpGIvAlaIlePr	2025
Db	6178	TCCCAAGAGTGTGACTATCTGCTCCAGCCTCAAGGGGCCCCCACTGGGGCGCATCCC	6237
Qy	2025	oIvGIvLeuProProGIvArgSerProLeuAlaGlnArgProleuArgArgIvAlaI	2045
Db	6238	TAAACTACCCCACTGGCGGCTCCCTCTGGCTCAAGAGGCTCTCAGCGCCAGGAGC	6297
Qy	2045	aIleArgThrAspSerIleuAspValGlnGIvLeuGIvSerArgIvAspLeuLeuSergI	2065
Db	6298	AATTAAGCACTGACTCCTGTGATGTGCAGGGCTGTGGTGAACGGGAAACCTGTGTGAGA	6357
Qy	2065	vAlaSerGIvProSerCysProleuThrArgSerSerSerPheTrpGIvGIvSerSerI	2085
Db	6358	GGTGAAGTGGGCGCTCGGCCCTCGACCCGGTCTTACTTCTGGGGCGGGTGTGAACAT	6417
Qy	2085	eGlnValGlnGlnArgSerGIvIleGlnSerIvValSerIvshIleArgLeuProAl	2105

Db	6418	CCAGGTGCAGACAGCGTTCCGGCATCCAGAGCAAAGTCTCCAGACACATCCGGCTCCAGC	6477
Qy	2105	apProCySPProGlyLeuGluuProSerTriPalalyAspProProGluThraRgsSerLe	2125
Db	6478	CCCTTGCCCAAGGCGCTGGAAACCGAGCTGGGCGCAAGAACCTCCAGAGACCGAAGACGCTT	6537
Qy	2125	uGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu	2145
Db	6538	AGAGCTGTGAACCGAGAGCTGAGCTGAGATTTCAGAGAGACCTCTTCCAGCGACGAGAA	6597
Qy	2145	uProLeuPheProArgAspLeuLysLysCyTrsSerValGluThGlnSerCyAspArg	2165
Db	6598	ACCCCTGTCCCCACCGGAGCTTGAAAGAGTCTCAAGTGTAGAACCCAGAGCTGCAGGCG	6657
Qy	2165	gArgProGlyPheThrLeuAspGluGlnArgArgHisSerIleAlaValSerCyLeuAs	2185
Db	6658	CAGGCTCGGGTCTCGGTATATGAAAGCGGAGACACTCCATTGTGTGTCAGTGTCTGGA	6717
Qy	2185	pSerGlySerGlnProArgLeuCySPProSerProSerSerLeuGlyGlnProLeuG	2205
Db	6718	CAGCGGCTCCCAACCCCGCTTATGTCCAAAGCCCTCAAGCCTCGGGGCGCAACCTCTTG	6777
Qy	2205	YGLYProGlySerArgProLysLysLysLeuSerProProSerIleSerIleAspProPr	2225
Db	6778	GGGTCCTGGAGAGCGGGCTTAAGAAAAAACTCAGCGCACCCAGATCTCTATAGACCCCC	6837
Qy	2225	oGluSerGlnGlySerArgProProCySerProGlyValCyLeuArgArgArgAlaPr	2245
Db	6838	GGAGAGGCCAAGGCGCTCTCGGCCCCCATGCACTCTCGTGTGTGCTCAGAGAGAGGGGCC	6897
Qy	2245	oAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAspPr	2265
Db	6898	GGCGAGTGACTTAAGGATCCCTCGGCTTCCAGCCCCCTTGAGACAGACGCGCTCTCAC	6957
Qy	2265	oSerProLysLysAspThrIleuSerLeuSerGlyLeuSerSerAspProThrAspMetAs	2285
Db	6958	CTCCCCAAGAAAGAACACGCTGAGATCTCTGGTTGTCTTGTGACCAACCAAGCATTGA	7017
Qy	2285	pPro 2286	
Db	7018	CCCC 7021	
RESULT 4			
AAx83485	AAx83485 standard; cDNA; 6762 BP.		
XX	AAx83485;		
AC			
DT	07-DEC-1999	(first entry)	
XX			
DE	Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1a) cDNA.		
XX			
KM	Human; T-type voltage-gated calcium channel; membrane; pore; ion;		
XX	activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.		
OS	Rattus sp.		
XX			
PN	W09929847-A1.		
XX			
PD	17-JUN-1999.		
XX			
PF	30-OCT-1998; 98MO-US023161.		
XX			
PR	05-DEC-1997; 97US-00985809.		
XX			
PA	(LOYO ) UNIV LOYOLA CHICAGO.		
XX			
PI	Perez-Reyes E, Cribbs LL;		
XX			
DR	WPI: 1999-394972/33.		
XX	P-PSDB; AA114590.		
XX			
TT	New T-type voltage-gated calcium channels.		



Db 1682 GCGACTGGAGCAGTCCGTTGGCCAGGACCCCTCCAGATGCCATCGGAGGACATCTG 1741  
Qy 613 1YAAGThValG1ySerg1yLysVal1YrProThValH1SthSerProProG1u1 633  
Db 1742 GTAGACAGTGTGGTGTGGGAGGAGTACCCCACTGTGCATACCAAGCCCTCCACCAAGGA 1801  
Qy 633 1eLeuLysAspLysAlaLeuVal1GluVal1AlaProSerProG1yProThrThLeuThrs 653  
Db 1802 TACTGAAGATTAAGCACTAGTGGAGGTGGCCCAAGCCCTGGGCCCTCCACCTCACCA 1861  
Qy 653 ePheAsn11eProBroG1yProPheSerSerMetH1sLysLeuLeuG1uThrG1nSert 673  
Db 1862 GCTTCACATCCCACTGGGCCCTTCAGCTCATCACAAGCTCTCGAGACACAGAGTA 1921  
Qy 673 hrG1yAlaCyeh1sSerSerCyS1yS11eSerSerProCySerSer1yAlaAspSerG1yA 693  
Db 1922 CGGAGCCTGCCTATGCTCTCGCAAAATCTCCAGCCCTTGCTCCAAAGCACAAGTGGAG 1981  
Qy 693 1aCyG1yProAspSerCyProTyrcysAlaArgThG1yAlaG1yG1uProG1uSera 713  
Db 1982 CCTGGGGCCGGACAGTGTCTCCCTACTGTGCCCGGACAGAGCAGAGACAGAGTCCG 2041  
Qy 713 1aAspH1sValMePProAspSerAspSerG1uAlaVal1Tyrg1uPheThrG1nAspAlaG 733  
Db 2042 CTGACCATGTCTATGCTGACTCAGACAGAGGCTGTGATGAGTTCAACACAGAGCGCTC 2101  
Qy 733 1nH1sSerAspLeuArgAspProH1sSerArgArgArg1nArgSerLeuG1yProAspA 753  
Db 2102 AGCACAGTACCTCCGGGATCCCAACCCGCGGACAGCGAGCCTGGGCCCAAGTG 2161  
Qy 753 1aG1uProSerSerValLeuAlaPheTrpArgLeu1eCyAspThrPheArgLys11eV 773  
Db 2162 CAGAGCCTAGTTCGTGTGCTGCTTCTGAGGCTGATCTGACACATTCGGAAAGATCG 2221  
Qy 773 a1AspSerLysTyrcPheG1yArgG1y11eMet11eAla11eLeuVal1AsnThrLeuSerm 793  
Db 2222 TAGATAGCAAAATACTTTGGCGGGGAATCATGATGCCATCTGGTCAATACACTACGA 2281  
Qy 793 eG1y11eG1uTyrtH1eG1uG1nProG1uG1uLeuThrAsnAlaLeuG1u11eSera 813  
Db 2282 TGGGATGAGTACCAAGCAGCAGCCGAGGAGCTCACCAAGCCCTGGAAATCAGCAACA 2341  
Qy 813 1eValPheThSerLeuPheAlaLeuG1uMetLeuLeuLysLeuVal1Tyrg1yProp 833  
Db 2342 TCGTCTTACCAAGCTCTTCGCTTGGAGATGCTGTAAGTGGTTGTTCTTACGCTCCCT 2401  
Qy 833 heG1yTyrt11eLysAsnProTyrcAsn11ePheAspG1yVal11eVal11eSera1T 853  
Db 2402 TTGGCTTACATTAGAATCCCTTACAACTCTTGAATGATGTCATTGTGCTCATCACTGTGT 2461  
Qy 853 rpg1u11eValG1yG1nG1nG1yG1yG1yLeuSerValLeuArgThrPheArgLeuMetA 873  
Db 2462 GGGAAATTGTGGGCGAGAGGAGGTGGCTGTGCTGTGGAGACTTTCGCGCTGAATGC 2521  
Qy 873 rGValLeuLysLeuVal1ArgPheLeuProAlaLeuG1nArgG1nLeuVal1ValLeuMetL 893  
Db 2522 GGGTGTCTAAGTGTGTGGCTTTCCTGCGGCGCTTGCACCGCAAGTCTGTGTGCTCAAGA 2581  
Qy 893 ySTHMeCAspAsnVal1AlaThrPheCySmetLeuLeuMetLeuPhe11ePhe11ePheS 913  
Db 2582 AGACCATGAGACAACGTGGCCACCTTCATGATGCTCTCATGCTGTTCATTTCATCTTCA 2641  
Qy 913 eR11eLeuG1yMeH1sLeuPheG1yCyS1ySphAlaSerG1uArgAspG1yAspThrl 933  
Db 2642 GCATCTTGAGCATGATCTTTTGGTGTCAAGTTTGCATCTGAAGGGATGGGACAGCT 2701  
Qy 933 eUProAspArgLysAsnPheAspSerLeuLeuTrpAla11eValThrVal1PheG1n11eL 953  
Db 2702 TCGCAGACCGGAGAAATTCACATCCCTGCTGTGGCCATGCTACTGTCTTTTCAGATTC 2761  
Qy 953 eUTHrG1nG1uAspTrpAsnLysVal1LeuTyrcAsnG1yMetAlaSerThSerSertTPA 973

Db 2762 TGACTCAGGAAGACTGGAATTAAGTCTCTTACAAAGGCACTGCGCTCCACATCGTCTTGG 2821  
Qy 973 1aAlaLeuTyrcPhe11eAlaLeuMetThrPheG1yAsnTyrcVal1LeuPheAsnLeuV 993  
Db 2822 CTGCTCTTACTTATGCTCCCTCAATGACTTTTGGCAACTATG1CTCTTTTAACTGTGCG 2881  
Qy 993 a1Ala11eLeuVal1G1uG1yPheG1nAlaG1uG1yAspAlaThrLysSerG1uSerG1uP 1013  
Db 2882 TGGCCATTTCTTGTGAAGAGATCCAGGACAGGAGAGATGCCACCAAGTCTGAGTCAGAGC 2941  
Qy 1013 roAspPhePheSerProSera1AspG1yAspArgLysLysArgLeuAlaLeuV 1033  
Db 2942 CTGATTTCTTTTCCCGCAGTGTGATGTGTGGGACAGAAAMAACGCTTGCCCTCGG 3001  
Qy 1033 a1AlaLeuG1yG1nH1sAlaG1uLeuArgLysSerLeuLeuProProLeu11e11eS1T 1053  
Db 3002 TGGCTTTGGGAACAGCGGAACCTTACGAAGACCTTTTGCCACCCCTCATCTCACTA 3061  
Qy 1053 hrAlaAlaThrProMetSerH1sProLysSerSerSerThrG1yAlaG1yG1uAlaLeuG 1073  
Db 3062 CGGCTGGGACACCAATGTCAACCCCAAGCTTCACACAGAGTGTGGGGAAAGCACTGG 3121  
Qy 1073 1ySerG1ySeraArgArgThSerSerSerG1ySera1aG1uProG1yAlaAlaH1sH1SG 1093  
Db 3122 GCTCTGGCTCTCGACGTACCAAGTGAAGTGGGTCCGCTGAAGCTGGAGCTGGCCACCATG 3181  
Qy 1093 1uMetLysCySProProSera1aArgSerSerProH1sSerProTrpSera1aAlaSers 1113  
Db 3182 AGATGAATGTCCCGCAAGTCCCGCAGCTCCGCAAGTCTCTTGAGTGGCGCAAGCA 3241  
Qy 1113 eRTPrHrSerArgArgSerSerArgAsnSerLeuG1yArgAlaProSerLeuLysArgA 1133  
Db 3242 GCTGACACAGAGCGCTCCACAGAGAACGCTGGGCCCGGCCCAAGCTTAAGCGGA 3301  
Qy 1133 rGSerProSerG1yG1uArgArgSerLeuLeuSerG1yG1uG1yG1nG1uSerG1nAspG 1153  
Db 3302 GGAAGCCGAGGGGAGCGGAGGTCCCTGCTGTGAAGGGGACAGAGGTGAGATG 3361  
Qy 1153 1uG1uG1uSerSerG1uG1uAspArgAlaSerProAlaG1ySerAspH1sArgH1sArgG 1173  
Db 3362 AGGAGGAAGTTCCAGGAAGAGACCGGGCCAGCCACAGAGCAGTGCATGCGCACAGGG 3421  
Qy 1173 1ySerLeuG1uArgG1uAlaLysSerSerPheAspLeuProAspThrLeuG1nVal1ProG 1193  
Db 3422 GTTCTCTGGAACG1GAGGCCAAGATTCTTTGACCTGCTGACATCTGCAAGGTGCGCG 3481  
Qy 1193 1yLeuH1sArgThAlaSerG1yArgSerSera1aSerG1uH1eG1nAspCyAsnG1yL 1213  
Db 3482 GGCTGCACCGCACAGCGCGCGGAGCTCTGCTGTGAGCAACCAAGACTGTATGTGCA 3541  
Qy 1213 ySera1aSerG1yArgLeuAlaArgThrLeuArgTrpAspAspProG1nLeuAspG1yA 1233  
Db 3542 AGTGGCTTCAGGGCGTTTGGCCCGCACCTTGAGAGACTGATGACCCCAACTGATGGGG 3601  
Qy 1233 sPaAspAspAsnAspG1uG1yAsnLeuSerLysG1yG1uArg11eG1nAlaTrpValArgS 1253  
Db 3602 ATGATGACAATGATGAGGAATCTGAGCAAAAGGGAACGATACAGCTGGGCTGAGAT 3661  
Qy 1253 eArgLeuProAlaCyCyCyArgG1uArgAspSertTPSera1aTyrt11ePheProProG 1273  
Db 3662 CCCGCTTCCTGCTGTGGCGAGAGGAGATTCCTGTGGCTTAAATATCTTCTCTCTC 3721  
Qy 1273 1nSerArgPheArgLeuLeuCyH1sArg11e11eThrH1sLysMetPheAspH1sVal1V 1293  
Db 3722 AGTCAAGTTTCGTCTCTGTGTACCGGATCATCACCCACAGATGTTTGCACATGTGG 3781  
Qy 1293 a1LeuVal11e11ePheLeuAsnCyS11eThr11eAlaMetG1uArgProLys11eAsp 1313  
Db 3782 TCCGTGATCATCTTCTCAACTGTATCAACATCGTATGAGAGCGCCCAAAATTGACCC 3841  
Qy 1313 roH1sSera1aG1uArg11ePheLeuThrLeuSerAsnTyrt11ePheThrAlaVal1PheL 1333  
Db 3842 CCCACAGCGCTGAGCGCATCTTCTGACCTTCCAACTACATCTTCAACGCGCAAGTCTTTC 3901

QY 1333 euAlGluMetThrValIysValAlaLeuGlyTPCyAspHeGlyGluGlnAlaTyrl 1353  
DB TAGCTGAATGACAGTGAAGGTGGTGGCACTGGGGCTGTGGTGGGGAGGAGCCCTAC 3961  
QY 1353 euAArgSerSerThrPheValIleuAspGlyIleuLeuValIleuIleSerValIleAspIle 1373  
DB TGGCGAGCAGCTGGAAATGTGTGAGCGGCTGTGGTGTCTCCATCTCCATCGACATCC 4021  
QY 1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL 1393  
DB TGGTCTCCATGGTCTCCGACAGCGGACCAAGATCCTTGGCATGTGAGAGGTGTGGCG 4081  
QY 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuValIleVal 1413  
DB TGTGGGAGCCTCGCTCATCTCAGGGGTATCAGCGGGCCCAAGGAGTCAAGCTGGTGG 4141  
QY 1413 aIGluThrIleuMetSerSerIleuLysProIleGlyAsnIleValIleCybCybAlaP 1433  
DB TAGAGCTCTGATGTATCTCTCAACCCATTGGCAACATGTGTGATTTGTGTGCTTC 4201  
QY 1433 hePheIleIlePheGlyIleLeuGlyValGlnLeuPheIleGlyLysPhePheValCyeg 1453  
DB TCTTCATCTTTTGGAAATTTCTGGGGGTGAGCTCTTCAAGGAGATCTTCTGTGTTC 4261  
QY 1453 IngIyGluAspThrArgAsnIleThrAsnLysSerAspCybAlaGlnAlaSerTyArgT 1473  
DB AGGGTGAAGACACACAGAACATCATCAAAATCCAGTGCCTGAGGCGACGATACCGAT 4321  
QY 1473 rPValArgHisLysTyTrAsnPheAspAsnLeuGlyGlnAlaIleuMetSerIleuPheVal 1493  
DB GGGTCGGGACAAAGTCAACTTGTGACAACTGGGCGAGGCTGTGATGTCTCTGTGTTC 4381  
QY 1493 euAlaSerIysAspGlyTyTrPValAspIleMetTyArgAspGlyLeuAspAlaValAla 1513  
DB TGGCTCCCAAGATGGTGGGTGATCATCATGATATGAGGCTGTGATGTGTGGTGTGG 4441  
QY 1513 apGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyRheIleSerPheLeu 1533  
DB ATCAGACAGCCCATCATGAACCAACACCCCTGGATGTGCTATCTCATCTCTTCTCC 4501  
QY 1533 euIleValAlaPhePheValIleuAsnMetPheValGlyValValIleGluAsnPheHisL 1553  
DB TCATCTGGCTCTTCTTGTCTGTACATGTGTGTGGCGGTGTGTGGAGAACCTTCCATA 4561  
QY 1553 yecYbArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeuArgA 1573  
DB AGTGCAAGACGACCAAGAGAGAGAGAGAGGCGGCGCTGTGAGAGAACCACTACGGA 4621  
QY 1573 rglLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGlnAlaGlnCybLysProT 1593  
DB GGTGGAGAAAAAGAGAGAGATGAAGAGAGATGGCCGAAGCCAGTGCACGCCCT 4681  
QY 1593 yTyTrSerAspTyTrSerArgPheArgLeuLeuValHisHisLeuCybThrSerHisTyrl 1613  
DB ACTACTCTGACTACGAGATTCGGGCTCTTGTCTCAACCACTGTGTACAGGCACTAC 4741  
QY 1613 euAspLeuPheIleThrGlyValIleGlyLeuAsnValValIleThrMetAlaMetGlnHis 1633  
DB TGGACCTCTTCACTGCTGCTGTATGGGCTGTGAACCTGTGTCACTATGGCCATGGA 4801  
QY 1633 yGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCybAsnTyrlIlePheThrValI 1653  
DB ACCAGACAGCCCAAGATCCTGAGCAGAGCTGTGAAGATCTGCAATTCATTTACGTC 4861  
QY 1653 lePheValIlePheGluSerValIlePheLysLeuValAlaPheAlaPheArgArgPhePheGlnA 1673  
DB TCTTTGTCTTGTGAGTCAAGTTTCAAACTGTGGCTTGTGGCTTCCGCTTCTTCAG 4921  
QY 1673 spArgTrpAsnGlnLeuAspLeuAlaIleValIleuLeuSerIleMetGlyIleThrLeuG 1693  
DB ACAGGTGGAACCAAGCTGTGACTGTGTCTTGTCTGTCTCATCATGGGCACTACACTGG 4981

QY 1693 IngLuiIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgV 1713  
DB AGGAGATGGAGTCAATCTGTGCTGCCATCAACCCACATCATCTCCGTATCATGAGGG 5041  
QY 1713 aLeuArgIleAlaArgValIleuLysLeuLeuLysMetAlaValGlyMetArgAlaLeu 1733  
DB TGTCTCGCATGTCTGAGATTGTGAAGCTGTGAAGATGGCTGTGGGCACTGGCGCACTGC 5101  
QY 1733 euHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeu 1753  
DB TGCACACGGTATGAGGCGCCCTGCCAGGTGGGGAACCTGGAGCTTCTTCAATGTAT 5161  
QY 1753 euPhePheIlePheAlaIleuGlyValGluLeuPheGlyAspLeuGlyCybAspGlyT 1773  
DB TGTTTTTCATCTTGCAGCTCTGGGCGTGGAGCTTTTGGAGACCTTGAAGTGTATGAGA 5221  
QY 1773 hrHisProCybGluGlyLeuGlyArgHisAlaIleThrPheArgAsnPheGlyMetAlaPhe 1793  
DB CACACCTTTGTAGGGCTTGGGTGGCATGCCACTTTAGGAACCTTGGTATGGCTTTC 5281  
QY 1793 euThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerA 1813  
DB TGAACCTCTTCCGAGTCTCACTGGTGAACACTGAATGTATTTATGAAGACACCTTC 5341  
QY 1813 rGAspCybAspGlnGluSerThrCysTyTrAsnThrValIleSerProIleTyRheValS 1833  
DB GGGACTGTACCAAGAGATCACCTGTACACATGTCTATCTCCCTTATCTTCTTGTGT 5401  
QY 1833 ePheValIleuThrAlaGlnPheValIleuValAsnValValIleAlaValIleuMetLysH 1853  
DB CTTGTGTGTGAGGCGCCAGTTTGTGTGTGTCAAGTGGTGTATCTGTGTGTGTGTGAG 5461  
QY 1853 iLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGlu 1873  
DB ACCCTGAAGAAAGCAACAAAGAGGCGCAAGAGAGCGGAGCTTCAAGCGCGAGCTGAG 5521  
QY 1873 euGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrp 1893  
DB TGGAGATGAAGAGGCTCAGCGCCGAGCCCATCTCCCGTGGGAGAGCCCTTCTGTGG 5581  
QY 1893 rGluValIleGlyValIleAsnSerThrAspSerProLysAspProGlyAlaProHisThrA 1913  
DB CGGGGTGAGAGGTGTCAACATCATCAAGACCCCTTAAGCTTGGGGTCCACACACACTG 5641  
QY 1913 laHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProG 1933  
DB CCCACATTTGAGACAGCTCGGGCTTCTCCCTTGAAGACCCCAAGATGTATACCCCG 5701  
QY 1933 IngLuiValProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValIleSerA 1953  
DB AGGAGGTGCAGTCCCTTAAGACCAAGACTGTGTGAGAACTGTGTGTGAGCC 5761  
QY 1953 rGThrHisSerLeuProAsnAspSerTyRmetCybArgAsnGlySerThrAlaGluArgS 1973  
DB GGAAGCACTCTTGTCCCAATGACATGATGTGCGCAATGGAGCACTGTGAGAGAT 5821  
QY 1973 eTrLeuGlyHisArgGlyTyTrGlyLeuProLysAlaGlnSerGlySerIleLeuSerValH 1993  
DB CCTTAGGACACAGGGGCTGGGGCTTCCCAAGGCCAGTCAAGCTTCACTTGTCTGCTTC 5881  
QY 1993 iAsSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyTrLeu 2013  
DB ACTCCCAACCAACAGACACACACTGTATCTTAAGCTTCCAAAGATGTGACTATCTGC 5941  
QY 2013 euGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyArgS 2033  
DB TCCAGCTCATGGGGTCTCCACCTGGGGGCGCATCCCTTAATCATCCCACTGGGCGCT 6001  
QY 2033 eTrProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspV 2053  
DB CCCCTGTGCTCAGAGGCTTCAAGCGCGCAAGCAATTAAGACTGTCCCTGGAGT 6061  
QY 2053 aIGlnIlyLeuGlySerArgLysAspLeuSerGluValSerGlyProSerCybProL 2073

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Db      6062  TGCAGGGCTGGGTACGGGGAAGACCTGTTGTCAAGAGTGA GTGGGCGCTCTCCCTC 6121
Qy      2073  eUTThArGSeSerSeSerPheTTPgLyGlySeSerIleGlnValGlnGlnArGSeGlyI 2093
Db      6122  TGACCCGGCTCCATCTTCTGGGGCGGGTCCAGATCCAGGTGACAGACGCTTCCGGCA 6181
Qy      2093  leglSerIyValSerIyShIeArGleuProAlProCySPProGlyLeuGluProS 2113
Db      6182  TCCAGAGCAAAATCTCCAGACATCCGCTTCCAGCCCTTTGCCAGGCTGGAAACCA 6241
Qy      2113  eRTIPAlAlYsAsPProGluThrArGSeSerSeSerIleuAspThrGluLeuSeT 2133
Db      6242  GCTGGGCCAAGACCTCCAGACACAGACAGCTTAGAGCTGACACGAGGCTGAGCT 6301
Qy      2133  rPlISerGlyAsPleuLeuPProSeSerGlnGluGluProleuPheProArGAsPleuL 2153
Db      6302  GGATTTCAAGAAACCTCTTCCACAGCAGCAGAAAGAACCCCTGTTCACCGGACTGA 6361
Qy      2153  YbLYsCyEYSeSerValGluThrGlnSerCyArGArGArGProGlyPheTrPleuAspG 2173
Db      6362  AGAAGTCTACAGTGAAGACCCAGAGCTGCAAGCGCAGGCTTGAGTTCTGGCTAGATG 6421
Qy      2173  lUGlnArGArGhISerIleAlaValSerCySleuAsPserGlySeGlnProArGleuC 2193
Db      6422  AACAGCGGAGACATCCATTGCTGTCAAGCTGTGAGACAGCGGCTCCCAACCCGCTAT 6481
Qy      2193  YSPProSePProSeSerIleuGlyGlyGlnProleuGlyGlyProGlySeArGProLyBL 2213
Db      6482  GTCCAGAGCCCTCAAGCCCTCGGGGGCCAACTCTTGGGGGTCTCTGGAGCCCGCTAAGA 6541
Qy      2213  YbLYsLeuSeSerProProSeSerIleSerIleAsPProGluSerGlnGlySeArGProP 2233
Db      6542  AAAAATCTAGCCCAACCACTATCTCTATAGACCCCGGAGAGCCAGGGCTCTGGCCCC 6601
Qy      2233  rOCYSeSerProGlyValCySleuArGArGAlaProAlaSerAsPserIyAsPProS 2253
Db      6602  CATGCAAGTCTGCTGTGCTGCTCAGAGAGAGGGCGCGGCGAGTCACTTAAGATCCCT 6661
Qy      2253  eRValSeSerProleuAsPserThrAlaAlaSerProSeSerProLySlyAsPThrIleuS 2273
Db      6662  CGGTCTCCAGCCCTTGAACAGCAGCGGCTGCTCACTCCCAAGAAAGACAGCTGA 6721
Qy      2273  eRLeuSeSerGlyLeuSeSerAsPProThrAsPMeTAsPPro 2286
Db      6722  GTCTCTGAGTTTGTCTTCTGAACCAAGACATGGAACCC 6782

RESULT 5
AAx83487
ID      AAx83487 standard; cDNA; 6816 BP.
XX      AAx83487;
XX
DT      07-DEC-1999 (first entry)
XX
DE      Rat T-type voltage-gated Ca channel alpha-1-G (rCAvT1c) cDNA.
XX
KW      Human; T-type voltage-gated calcium channel; membrane; pore; ion;
XX      activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS      Rattus sp.
XX
PN      MO9929847-A1.
XX
PD      17-JUN-1999.
XX
PF      30-OCT-1998; 98WO-US023161.
XX
PR      05-DEC-1997; 97US-00985809.
XX
XX      (LOYO ) UNIV LOYOLA CHICAGO.
XX
XX      Perez-Reyes E, Cribbs LL;
XX
PI
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XX      MPI: 1999-394972/33.
DR      P-PSDB; AAY14592.
XX
XX      New T-type voltage-gated calcium channels.
XX
PS      Disclosure; Page 85-94; 138pp; English.
XX
CC      This sequence represents the coding region for a rat T-type voltage-gated
CC      calcium (ca) channel alpha-1-g designated rCAvT1c. Voltage gated channels
CC      are membrane bound glycosylated proteins formed of several subunits. The
CC      large alpha subunits form a pore in the membrane that is selective for a
CC      given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC      and IV) and each domain contains 6 putative transmembrane helical
CC      segments (SI-S6). T-type Ca channels are activated at a lower voltage
CC      than L- or N-type channels. Characteristics of T-type channels include
CC      short current time, slow activation kinetics near threshold, fast
CC      inactivation kinetics and slow tail current. The sequences AAx83481-
CC      X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC      and rats. Each of the novel Ca-channels contains a putative IV64 region
CC      comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC      voltage-gated calcium channel proteins can be used to screen for drugs
CC      which affect calcium channels. Methods are also disclosed for creating a
CC      disease or disorder associated with a deficiency in a native T-type
CC      calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ      Sequence 6816 BP; 1373 A; 2058 C; 1932 G; 1453 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 11767.00 Matches: 2248
Percent Similarity: 98.90% Conservative: 0
Best Local Similarity: 98.90% Mismatches: 5
Query Match: 97.83% Indels: 20
Db: 2 Gaps: 1

US-09-611-257A-24 (1-2287) x AAx83487 (1-6816)
Qy      34 TrpThArGArGArGMeTGlUArGAlProArGSeSerArGAsPserProValAlaSerArG 53
Db      2 TGAAGAGAGAGAGAGATGAGACGGAGCGCCGAGAGAGTGGAGACACCCCGTAGCTTACGC 61
Qy      54 SeSerThrThrCySPProGlyProGlyAla-AlaGlyAla-GlySeSerThrGluSAsP 73
Db      62 AGCTCAAGACACTGTCCGGGCGCGGGGCGCGAGGGCGGGGTCGACGGAAGAAAGACC 121
Qy      73 rOGlySeSerAlAsPserGluAlaGluGlyLeuProLyrrProAlaLeuAlaProValValP 93
Db      122 CGGGCAGCGCGGACTCCGAGCGGAGGGGCTGCCGTACCCCGGCTGACCCCGGTGGTTT 181
Qy      93 hePheYrLeuSeSerGlaSPserArGProArGSeSerTPCySleuArGThrValCySAsnP 113
Db      182 TCTTCTACTTGAAGCAGAGACAGCGCCCGCGAGCTGGTGTCTCCGACGGATCTGTAAAC 241
Qy      113 rOTrPheGluArGValSerMeTleuValIleLeuLeuAsnCyValThrIleuGlyMeT 133
Db      242 CGTGGTTGAGCGAGTACGTATGTGTCATTTCTTCAACTGTGATCTGGGTATGT 301
Qy      133 heArGProCyGluAsPleAlaCySAsPserGlnArGCyArGIlleuGlnAlaPheA 153
Db      302 TCAGGCGCTGTGAAGACATTCCTGTGATCCACGCGCTGCCGATCTTCAGAGCCTTTCG 361
Qy      153 sPAsPpHeIlePheAlaPhePheAlaValGluMeTValIleYsMeTValAlaIleuGlyI 173
Db      362 ATGACTTCATCTTGGCTTTCTTCTGTGTGAAGATGTGTAAAGATGTGGCTTGGGCA 421
Qy      173 lePheGlyLyLyCyEYrIleuGlyAsPThrTPAsArGleuAsPpHeIleValI 193
Db      422 TCTTGGGAAGAAATGTACTCGGAGACACTTGAACCCGCTTGACTTTTCATTGCA 481
Qy      193 leAlaGlyMeTleuGluTrYSerIleuAsPleuGlnArGlnValSerPheSerAlaValArG 213
Db      482 TTGCAAGGATGCTGAGATTCGCTGAGACCTGACAGAACTCACTTCTCCGACGTCAAGA 541
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213 hrValArgValIleuArgProIleuArgAlaIleAsnArgValIleProSerMetArgIleLeuV 233  
542 CAGTCGGTGTGGCGACCGCTCAGGGCCATTAAACGGGGTGGCCAGCATGCCATTCTCG 601  
233 aIThIleuLeuLeuAphThIleuProMetLeuGIYAsnValIleuLeuLeuCyPhePheV 253  
602 TCACATTACTGTGGACACCTTGCTATGCTGGGCAACGTCCTGCTGCTGTTCTTTG 661  
253 aIPhePheIlePheGIYIleValIGIYValIGIYLeuTrpAlaGIYLeuLeuArgAsnArgC 273  
662 TCTTTTTCATCTTTGGCATCTGAGGGCTCAGCTGTGGGCAAGACCTGCTCCGACCGGT 721  
273 yAPheLeuProGIYAsnPheSerIleuProLeuSerValIlePheLeuGIYProTYrGIYTr 293  
722 GCTTCTCCCGAGAACTTCAGCTCTCCCTGAGCGTGGACCTGGAGCTGATTACCA 781  
293 hrGIYAsnGIYAsnGIYUserProPheIleCyAsnGIYProArgIYUAsnGIYMetArgS 313  
782 CAGAGATGAGGACGAGAGCCCTTCATCTGCTCAGGCTCGGAGAAATGGCATGAGAT 841  
313 eCYAsnArgSerValIleProThIleuArgIGIYGIYGIYGIYGIYProProCySerIleuA 333  
842 CCTGCAGAGGTGTGCCACACTGCTGGGGAGGCGGTGTGGCCACCTCGACGTCTGG 901  
333 aPTYrGIYUThTYrAsnSerSerSerAsnThTYrCYValAsnTrpAsnGIYTYrTYrT 353  
902 ACTATGAGACTTATAACGTTCAGACAAACCACTGTGTCACTGGAACCACTGATCTATA 961  
353 hrAsnCySerAlaGIYGIYUAsnProPheIYAsnGIYValaIleAsnPheAsnIleGG 373  
962 CCAACTGCTCTGGGGCGAGCAACACCTTCMAAGCGCCATCAACTTGAACAACATTGG 1021  
373 IYTYrAlaTrpIleAlaIlePheGIYValaIleThIleuGIYUIGIYTrpValAspIleMet 393  
1022 GCATGCTGGATGCGCATCTTCAGGTCACTCACTGGAGGCTGGGTGCATCATGT 1081  
393 yCPheValMetAspAlaAsnSerPheTYrAsnPheIleTYrPheIleLeuIleIleY 413  
1082 ACTTCTTAAGACGCTCACTCTTCAACAACCTTCACTTCACTTCTTCATCATCG 1141  
413 aGIYSerPhePheMetIleAsnLeuCyLeuValValaIleAlaTrpGIYnPhSerGIYU 433  
1142 TGGGCTCTCTTCATGATCAACCTGTGCTGTGTGTGATTCACGCACTTCTCCAGA 1201  
433 hrIYLeuGIYUserGIYULeuMetArgGIYUIGIYUArgValaIArgPheLeuSerAsnAlaS 453  
1202 CCAAAAGCGGGAGAGTCACTGATGGGAGCAAGCTGTACATTCCTGTCCAAATGCTA 1261  
453 eThIleuAlaSerPheSerGIYUProGIYSerCYTYrGIYUIGIYULeuIYsTYrLeuV 473  
1262 GTACCCCTGGCAACTTCTGTGACCAAGGAGCTGTATGAGAGTACTCAATGACTCGG 1321  
473 aIYTrIleuAlaGIYValaIleArgArgLeuAlaGIYUAsnIleSerArgAlaIleGIYVala 493  
1322 TGTACATCTCCCAAAAAGCAGCCGGAAGGCTGGCCCAAGTCTCTAAGGGCTATAGGGCTGC 1381  
493 rGIYAGIYULeuUserSerProValaIleArgSerGIYUIGIYUProGIYnPhSerGIYs 513  
1382 GGGCTGGGCTGTCAAGAGCCCAAGTGGCCGTAAGTGGGCAAGAGCCCAAGCCCAAGTGGCA 1441  
513 eCYAsnTrpArgSerAlaArgArgLeuSerValaIleAsnIleuValaIleAsnIleAsn 533  
1442 GCTGCACTGCTCAACCGTGTGTGTCTGTCCACCACTGTGTCAACCACTCAACCAACC 1501  
533 IAsnIleAsnIleTYrAsnIleuGIYAsnGIYThIleuAlaGIYValaIleSerProGIYU 553  
1502 ACCATCACTCACTCAACCTGGGTATAGGAGCGCTCAAGATTCCCGGCGCAAGCCCAAGA 1561  
553 IeGIYnAspArgAlaAsnGIYSerArgArgLeuMetLeuProProProSerThTYrProT 573  
1562 TCCAGGACGAGGATGCCAAATGGGTCTGCGCGCTCATGCTACCAACCACTCTTACACCA 1621

573 hrProSerGIYGIYProProArgGIYAlaGIYUserValaIleSerPheTYrAsnIleAsnPC 593  
1622 CTCCCTCTGGGGGCCCCCTCGAGGGGTGGAGTCTGTACACAGCTTCTTACCATGTGACT 1681  
593 yAsnIleuGIYUProValaIArgCYAsnAlaIProProProArgCYAsnProSerGIYAlaSerG 613  
1682 GCCACTTGGAGGCAATCCGTTGGCCAGGCAACCCCTCCAGATGCCATCGAGGCGATCTG 1741  
613 IYArgThValaGIYSerGIYUValaIYProThValaIleThSerProProProGIYU 633  
1742 GTAGAGCTGTGGGTGTGGGAAGGTGTACCCCACTGTGCATACAGCCCTCCACAGAGA 1801  
633 IeLeuIYAsnTrpValaIleuValaIleIleProSerProGIYProProThIleuTrs 653  
1802 TACTAAGGATTAACACTAGTGAAGGTGGCCCCAGCCCTGGGCCCCCACTTACCA 1861  
653 eCPheAsnIleProProGIYProPheSerSerMetAlaIYUserLeuGIYUThTrGIYnSerT 673  
1862 GCTTCAACATCCCACTGGGCCCTTCAGTGCATCAACAAGCTCTGGAGACAGAGATTA 1921  
673 hrGIYAlaCyAsnIleSerSerCYUValaIleSerSerProCYSerIYUAlaAspSerGIY 693  
1922 CCGGAGCTGCGCATAGCTCTGCAAAATCTCAGGCCCTTGCTCCAAAGCGACAGTGGAG 1981  
693 IeCYGIYProAspSerCYsProTYrCYValaIArgThGIYAlaGIYUProGIYUserA 713  
1982 CCTGGGGCGGAGAGTGTCTCTACTGTGCCGAGAGAGAGAGAGAGAGAGAGTCCG 2041  
713 IAspIleValaIleCPheProAspSerAspSerGIYUAlaValaIYrGIYUThTrGIYnAspAlaG 733  
2042 CTGACCATGTACTGCTGACTGACTGACAGAGGAGGCTGTGTATGATTTCAACAAGAGCTC 2101  
733 IAsnIleSerAspLeuArgAspProIleSerArgArgArgIleArgSerIleuGIYProAspA 753  
2102 AGCACAAGTACTCGGGATCCCAACAGCGGGCGAGAGAGGAGCTCGGGCCCAAGATG 2161  
753 IeGIYUProSerSerValleuAlaPheTrpArgLeuIleCYAsnIlePheArgIYUValaY 773  
2162 CAGAGCTTACTGTGTGGCTTCTGAGGCTGATCTGTACACATTCGGAGATGG 2221  
773 aIAspSerIYsTYrPheGIYArgGIYIleMetIleAlaIleuValaAsnThIleuSerM 793  
2222 TAGATGCAAAATCTTTGGCCGGGATATGATGATGCCATCTGGTCATTAACATCAGCA 2281  
793 eGIYIleGIYUThIleGIYUIGIYUIGIYUProGIYULeuThAsnAlaIleuGIYUleSerAsnI 813  
2282 TGGGATGCGAGTACCAAGAGAGCCGAGAGAGCTCAACACCCCTGGAAATCAAGCAACA 2341  
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2342 TCGTCTTCAACAGCCTCTTGGCTTGGAGATGCTGTGAACCTGTGTACAGTCCCT 2401  
833 heGIYTrIleIYAsnProTYrAsnIlePheAspGIYValaIleValaIleSerValT 853  
2402 TTGGCTACATTAAAGATCTCTACACATTTTGTATGTCTCATTTGTGTGCATCAGTGTG 2461  
853 rGIYUleValaGIYUIGIYUIGIYUIGIYUIGIYUIGIYUIGIYUIGIYUIGIYUIGIYUIGIYU 873  
2462 GGGAGATTGTGGGCGAGAGGAGGTGGCTGTGGTGTGGGAGCCTTCCGCTGATGC 2521  
873 rGIYUleuIYUleuValaIArgPheLeuProAlaIleuGIYUArgIYUleuValaIleuMetI 893  
2522 GGGTGTGAAAGCTGGGCTCTTGGCCGAGCTGTGAGGCGCAAGCTCGAGTGTCTATGA 2581  
893 yThTrMetAspAsnValaIleThPheCYMetLeuLeuMetLeuPheIlePheS 913  
2582 AGACATGAGCAACGAGGCACTTGTGCATGTCTCATGTCTTCACTTCACTTCA 2641  
913 eITleuGIYUleuThIleuPheGIYCYAlaPheAlaSerGIYUArgAspGIYAspThI 933  
2642 GCATCTCGGGCATGCACTCTTGTGTGCAAGTTCCATCTGAACGGAGTGGGACACGT 2701  
933 eUProAspArgIYUAsnPheAspSerIleuTrpAlaIleValaIleThValaPheGIYUle 953

Db 2702 TGGCAGACCGAAGAAATTTCAGCTCCCTGCTCTGGGCCATGCTCATGCTTTTCAGATTCC 2761  
Qy 953 eutHrGlnuAspTTPaSnlySValleuYrAenGlyMeaIaSerThSerSerTTPA 973  
Db 2762 TGACTCAGAGAGACTGGAATAAAGTCTCTACAAAGCATGGCTCCACATCGTCTTGGG 2821  
Qy 973 lAaIaLeuTYrPheIIeAlaLeuMetThrPheGlyAAsnTYrValleuPheAsnLeuIuV 993  
Db 2822 CTGCTCTTACTTCAATCCCTCATGACTTTTGGCAACTATGTGCTTTTAACTGTCTGG 2881  
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Db 2882 TGGCCATTCTTGGAAGAGATTCCAGGCAAGAGAGATCCCAAGCTGATGATGAGC 2941  
Qy 1013 rOaSPhePheSerProSerValaAspGlyAspGlyAspArglySylsArgleuAlaLeuV 1033  
Db 2942 CTGATTTTCTTTCCGCCAGTGTGATGGTGAATGGGGAAGAAAGCGCTTGGCCCTGG 3001  
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Db 3002 TGGCTTTGGAGAACACGGGAACTACGAAGAAGCTTTTGCACCCCTCATCATCATA 3061  
Qy 1053 hrrAlaAlaThrProMetSerHisProlySesSerSerThrGlyValaGlyIuaIaLeuG 1073  
Db 3062 CGGCTGGCAACCAATGTCAACCCCAAGAGCTCCAGCACAGGTGGGGGAAGCACTGG 3121  
Qy 1073 lYSerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHsI 1093  
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Db 3962 TGGCAGACAGCTGAATGTCTGACCGGCTTGCTGAGTGTCTCATCTCCGTCAATCAATCC 4021  
Qy 1373 euValSerMetValSerAspSerGlyThrIySIIeLeuGlyMetLeuArgValleuArgL 1393  
Db 4022 TGGTCTCATGTGTTCCGACAGCGGACCAAGATCTTGGATGCTGAGGGTGTGGGCGC 4081  
Qy 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLYsLeuValV 1413  
Db 4082 TGCTGGGACCCCTCGTCCACTCAGGGTCAACCGGGCCCAAGGACTGAAGCTGTGG 4141  
Qy 1413 aGluThrLeuMetSerSerLeuLYsProIIeGlyAsnIleValIaIIeCyCySAlaP 1433  
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Qy 1493 euAlaSerLYsAsnGlyLTrpValaAspIleMetTYrAspGlyLeuAspAlaValaGlyVala 1513  
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Db 4562 AGTCDAACACACACAGGAGGAGGAGGAGGCGGCGGAGAGAGAGGACTTACGGA 4621  
Qy 1573 rGLEuGluLYsLYsArgArgSerLYsGluLYsGlnMeAlaIa----- 1586  
Db 4622 GGCTGGAGAAAGAGAGAGAGTAAAGAGAGAGAGTGGCCGATCTAATGTTGAGCATG 4681  
Qy 1587 -----GluuIaGlnCyLySProTYrYS 1595  
Db 4682 TAAATTGCTTCCGAGAGCTCAAGCAGCGCTGTCAGAAAGCCCAATGCAAGCCCTTAACT 4741  
Qy 1595 eRAspTYrSerArgPheArgLeuLeuValHsIeAsuCyThSerHisTrpLeuAspL 1615  
Db 4742 CTGACTACTGAGATTCGGGCTCTTGTGCCACACCTGTGTACAGGACCACTACCTGGAGC 4801  
Qy 1615 eupheIIeThrGlyValIleGlyLeuAsnValaIleThrMeAlaMetGluuHsIeTYrGlnG 1635  
Db 4802 TCTTCATCATCTGTGTCACTGGGCTGAACGTGTGCATCTAGTGGCATGGAAATTAACAGC 4861  
Qy 1635 lnsProGlnIleLeuAspGluAlaLeuLYsIleCySAsnTYrIlePheThrValIlePheV 1655  
Db 4862 AGCCCAAGATCTGAGAGAGGCTGTGAAGATCTGCAATTACATCTTAACTGATCTTTTG 4921



QY 1655 aPheGluSerValPheUlySerValaIaPheAlaPheArgPhePheGluInaPArgT 1675  
 Db 4922 TCTTTGAGTCACTTTTCAAACTTGTGGCTTGGCTTCCGCGTTCTTCCAGGACAGGT 4981  
 QY 1675 rPAsnGlnLeuAAspLeuAlaIleValLeuSerLleWetGlyIlePheLeuGluI 1695  
 Db 4982 GGAACCAAGCTGAGCTGGCTATGTGCTTCTGTCCATGAGGACATCACTGAGAGAA 5041  
 QY 1695 leGlyValaAsnLeuSerLeuProIleAsnProThrIleIleArgIleWetArgValLeuA 1715  
 Db 5042 TTGAGGTCAATGTGTGCTGCTGCCATCAACCCACCATCATCCGTATCAAGAGGTGCTCC 5101  
 QY 1715 rGlyIleAlaArgValLeuUlySerLeuUlyMetAlaValIleMetArgAlaLeuLeuHieT 1735  
 Db 5102 GCATTGCTCGAGTTCGAGCTGTGAAGATGGCTGTGGCATGCGGACATGCTGCACA 5161  
 QY 1735 hValaMetGlnAlaLeuPProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheP 1755  
 Db 5162 CGGTGATGCAAGCCCTCGCCCAAGTGGGAACTGGGACTTCTCTCATGTATATGTTTT 5221  
 QY 1755 heIlePheAlaAlaLeuGlyValaGlyLeuPheGlyAspLeuGlyCyAspGlyUthrHiAP 1775  
 Db 5222 TCACTCTTCAAGCTCTGGGCGTGAAGCTCTTGGAGACCTGAGTGTGATGAGACACACC 5281  
 QY 1775 rCyAspGlyUlyLeuGlyATGHiAlaIthrPheArgAsnPheGlyMetAlaPheLeuThrL 1795  
 Db 5282 CTGTGAGGGCTTGGGTGGCATGCCACTTGTAGAACTTGGTATGCGCTTGTGACCC 5341  
 QY 1795 euPheArgValSerThrGlyAspAsnTrpAsnGlyIleWetUlyAspProSerArgAspC 1815  
 Db 5342 TCTTCGAGACTCCACTGTGATCACTGATGAACTGATTAAGAGACACCTTCGGAGCT 5401  
 QY 1815 yAspGlnGluSerThrCyTyAsnThrValIleSerProIleTyPheValSerPheY 1835  
 Db 5402 GTGACCAAGATCTCACTGCTCAACACATGTCACTCCCTATCTATCTTGTCTTCG 5461  
 QY 1835 alLeuThrAlaGlnPheValLeuValAsnValaIleAlaValLeuMetUlyHisLeuG 1855  
 Db 5462 TGTGTACGGCCGCTTGTGTGCTGTGTCAACGTGTCTCATGCTGTGATGAACACCTGG 5521  
 QY 1855 lUglUserAsnUlyGlyAlaUlyGlyUglUAlaGlyUleuGlyUAlaGlyUleuGlyU 1875  
 Db 5522 AAGAAAGCAACAAAGAGGCGCAAGAGAGGCGAGCTCGAGCGCGAGCTGAGCTGAGA 5581  
 QY 1875 euTyThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGly 1895  
 Db 5582 TGAAGAGCTCAAGCCCGACGCCCATCTCCCGCTGGGACGCCCTTCTGTGCGCGGG 5641  
 QY 1895 alGlyUlyValaAsnSerThrAspSerProUlyAspProGlyAlaProHisSerThrAlaHis 1915  
 Db 5642 TGAAGGCTGTCAACAGTACTGACGCCCTTAAGCTGGGGCTCCACACACACATGCCACA 5701  
 QY 1915 leGlyAlaAlaSerGlyPheSerLeuGlyUhiAspOthrMetValProHisAspProGlyU 1935  
 Db 5702 TTGAGACAGCTCGGGCTTCTCTCTTGAAGCACCCCAAGATGATCCCAACCCGAGAGG 5761  
 QY 1935 alProValProLeuGlyProAspLeuLeuThrValArgUlySerGlyValaSerArgThr 1955  
 Db 5762 TGCAGAGTCCCTTGAAGCAAGACCTGTGACTGTGAAGAGTCTGTGTGACCGGAGCG 5821  
 QY 1955 lAspSerLeuProAsnAspSerTyMetCyAspArgAsnGlySerThrAlaGlyUlySerLeu 1975  
 Db 5822 ACTCTGTGCCCATGACAGTCACTGTGCGCATATGGACATCGTGAAGATATCCCTAG 5881  
 QY 1975 lYhiAspGlyTyTrpGlyLeuProUlyAlaGlnSerGlySerIleLeuSerValHisSerG 1995  
 Db 5882 GACACAGGGGCTGGGGCTCCCAAGCCCAAGCTCACTTGTTCGGTTCACCTCC 5941  
 QY 1995 lInProAlaAspThrSerCyAlleuGlnLeuProUlyAspValHisTyTrpLeuLeuGlnP 2015  
 Db 5942 AACACGACGACACAGCTGCACTCTACAGCTTCCCAAGATGTGCACTATCTGCTCAGC 6001

QY 2015 rOhisGlyAlaProThrTrpGlyAlaIleProUlyLeuProProGlyUlyArgSerProL 2035  
 Db 6002 CTCATGGAGCTCCCACTGGGGCGCCATCCTTAACCTACCCCACTGGCGCTCCCTC 6061  
 QY 2035 euAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnG 2055  
 Db 6062 TGGCTCAGAGGCTCTCAGGGCGGCGAGGACAAATAGACTGACTCTCCGTGATGACAG 6121  
 QY 2055 lYleuGlySerArgGlyUlyAspLeuLeuSerGlyValaSerGlyProSerCyAspProLeuTh 2075  
 Db 6122 GCCTGGTATGCCGGGAAACCTGTGTGAGAGTATGAGGCTTCTGCTGCTGACCC 6181  
 QY 2075 rGSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnS 2095  
 Db 6182 GGTCTCATCTTCTTGGGGCGGGTGAAGATTCAGGTGACAGAGGCTTCCGACATCCGA 6241  
 QY 2095 eTyValSerUlyHisIleArgLeuProAlaProCyAspProGlyLeuGlnProSerTrpA 2115  
 Db 6242 GCMAAGTCCCAAGACATCCGCTGCCAGGCCCTTGGCCAGGCTGGAACTGAGTGG 6301  
 QY 2115 lAlaAspProProGluThrArgSerSerLeuGlyLeuAspThrGlyUleuSerTrpIleS 2135  
 Db 6302 CCAAGGACCTTCAGAGACCAAGAACAGCTTAGAGCTGAGACAGAGCTGAGCTGATTT 6361  
 QY 2135 eArgUlyAspLeuLeuProSerSerGlnGlyUglUProLeuPheProArgAspLeuUlyS 2155  
 Db 6362 CAGAGACCTCTCTCCCAAGACCCAGAACAGAACCCCTGTTCACAGGACCTGAAGAACT 6421  
 QY 2155 yETySerValGlyUthrGlnSerCyAspArgArgProGlyPheTrpLeuAspGlyUlna 2175  
 Db 6422 GCTACAGTGTAGAACCCAGACCTCAGAGCGCAGGCGCTGGGTTCTGGCTATGAACAG 6481  
 QY 2175 rGArgHisSerIleAlaValaSerCyLeuAspSerGlySerGlnProArgLeuCyPProS 2195  
 Db 6482 GAGAGACACTCATTCGTGTCACTGTGTGACAGGCGCTCCCAACCCCGCTATGTCCA 6541  
 QY 2195 ePProSerSerLeuGlyGlyGlnProLeuGlyGlyIProGlySerArgProUlySlyVal 2215  
 Db 6542 GCCCTCAAGCTCGGGGCGCAACCTTGTGGGGTCTTGGAGCGCGCTTAAGAAAAAC 6601  
 QY 2215 euSerProProSerIleSerIleAspProProGlyUlySerGlnUlySerArgProCyas 2235  
 Db 6602 TCAAGCCACCAAGTATCTTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCATGCA 6661  
 QY 2235 eEProGlyValaCyLeuArgArgAlaProAlaSerAspSerUlyAspProSerValS 2255  
 Db 6662 GTCTGTGTGTGCTCAGAGAGAGGGCGCGCGAGTCACTTAAGATCCCTCGGTCT 6721  
 QY 2255 eEserProLeuAspSerThrAlaAlaSerProSerProUlySlyAspThrLeuSerLeuS 2275  
 Db 6722 CCAGCCCTTGAACAGACAGGCTGCTCACTCCCTCCAAAGAAAGACAGCTGAGTCTCT 6781  
 QY 2275 eGlyLeuSerSerAspProThrAspMetAspPro 2286  
 Db 6782 CTGGTTGTCTTCTGACCAACAGACATGACCC 6816

RESULT 6  
 ID AAX83486 standard; cDNA; 6795 BP.  
 AAX83486;  
 AC AAX83486;  
 XX  
 XX 07-DEC-1999 (first entry)  
 DT  
 XX  
 XX Rat T-type voltage-gated Ca channel alpha-1-G (rCav1.1b) cDNA.  
 DE  
 XX  
 XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
 KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.  
 XX  
 XX Ratius sp.  
 OS  
 XX PN W0929847-Al.  
 XX

PD 17-JUN-1999.  
XX  
PF 30-OCT-1998; 98WO-US023161.  
XX  
PR 05-DEC-1997; 97US-00985809.  
XX  
PA (LOYO ) UNIV LOYOLA CHICAGO.  
XX  
PI Perez-Reyes E, Cribbs LL;  
DR WPI, 1999-394972/33.  
XX P-PSDB; AAY14591.  
XX  
PT New T-type voltage-gated calcium channels.  
PS  
FS Disclosure: Page 76-85; 138pp; English.  
XX  
XX This sequence represents the coding region for a rat T-type voltage-gated  
CC calcium (Ca) channel alpha-1-G designated rCavTb. Voltage gated channels  
CC are membrane bound glycosylated proteins formed of several subunits. The  
CC large alpha subunits form a pore in the membrane that is selective for a  
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III  
CC and IV) and each domain contains 6 putative transmembrane helical  
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage  
CC than L- or N-type channels. Characteristics of T-type channels include  
CC short current time, slow activation kinetics near threshold, fast  
CC inactivation kinetics and slow tail current. The sequences AAX83481-  
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans  
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region  
CC comprising the amino acid sequence AAY14598. Cells expressing the T-type  
CC voltage-gated calcium channel proteins can be used to screen for drugs  
CC which affect calcium channels. Methods are also disclosed for treating a  
CC disease or disorder associated with a deficiency in a native T-type  
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 6795 BP; 1366 A; 2055 C; 1923 G; 1451 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 0 Length: 6795  
Score: 11751.50 Matches: 2244  
Percent Similarity: 99.07% Conservative: 1  
Best Local Similarity: 99.03% Mismatches: 8  
Query Match: 97.70% Indels: 13  
DB: 2 Gaps: 1  
US-09-611-257a-24 (1-2287) x AAX83486 (1-6795)  
QY 34 TrpThrArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53  
DB 2 TGGAGAGAGAGAGATGGAGCGGCGCGGAGAGACTCGGGACAGCCCGGTACACGC 61  
QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGlyValAsp 73  
DB 62 AGCTCAAGACACTGTCCGGGGCGGGGGCGGCAAGGGCGGGGTCGACGGAAAGGAGCC 121  
QY 73 roG1SerAlaaspSerGluAgiug1yleuProTyProAlaLeuAlaProValAlp 93  
DB 122 CGGGAGCGCGGACTCCAGGCGGAGGGGCTGCCGTAACCGGCGTACGCCGGTGGTTT 181  
QY 93 hePheTyrleuSerGlnaspSerArgProArgSerTrpCysleuArgThrValCysAsp 113  
DB 182 TCTTCTACTGAGCGACGAGCACGCCGCCGAGGTGGGTCTCCGACAGGTCTTAACC 241  
QY 113 roTrpPheGluArgValSerMetLeuValIleleuLeuAsnCysValThrleuGlyMetP 133  
DB 242 CGTGGTTTCGAGGAGATCGATATGCTGTGATCTTCTCAACTGTGTGACTCTGGGTATGT 301  
QY 133 heArgProCysGlnaspIleAlaCysaspSerGlnArgCysArgIleleuGlnAlaPheA 153  
DB 302 TCAGGCGGTGTAGAGACATTGCTGTGACTCCAGCGCTGCCGATCTTGCAGGCGCTTCG 361  
QY 153 spAspPheIlePheAlaPhePheAlaValGluMetValValIlyMetValAlaIleuGlyI 173

DB 362 ATGACTTCATCTTCTTCTTCTGCTGNGAATATGTGTGAAGATGTGGCTTGGGCA 421  
QY 173 IepheGlyLysIyCysTyrleuGlyAspThrTrpAsnArgLeuAspPheheIleValI 193  
DB 422 TCTTTGGGAAAGAAATGTTTACCTGGGAGACACTTGGAAACGGCTTGACTTTTCATGCA 481  
QY 193 IeAlaGlyMetLeuG1UtyzSerleuAspLeuGlnAsnValSerPheSerAlaValArgT 213  
DB 482 TTGCAGGGATGCTCGAGATTCGCTGAGCTCGAGAAAGTACGTTCTCCGCACTCAGGA 541  
QY 213 hrValArgValleuArgProleuArgAlaIleAsnArgValProSerMetArgIleuV 233  
DB 542 CAGTCCGCTGCTCGACCGCTCAGGGCCATTAAACCGGATGCCAGATGCCATTCG 601  
QY 233 a1ThrleuLeuAspThrleuProMetleuGlyAsnValleuLeuLeuCysPhePheV 253  
DB 602 TCACATTACCTGTGACACCTTGCTTATGCTGGGCAACGTCGTGCTGTTCTTCG 661  
QY 253 a1PhePheIlePheGlyIleValGlyValGlnleuTrpAlaGlyleuLeuArgAsnArgC 273  
DB 662 TCTTTTTCATCTTTGGCATGCTGGGCGTCCAGCTGTGGGAGACTGCTTCGCAACCGT 721  
QY 273 ysPheleuProGluAsnPheserleuProleuSerValAspLeuGluProTyTrpGlnT 293  
DB 722 GCTTCTCCCGAGAACTTTCAGCTCCCGCTGAGCGTGACCTGGAAGCTTATTACAGA 781  
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313  
DB 782 CAGAGAAAGAGAGAGAGAGCCCTTCATCTGCTCTCAGCCCTGGAGAAATGGCATGAGAT 841  
QY 313 erCysArgSerSeValProThrleuArgGlyGluGlyGlyGlyProProCysSerleuA 333  
DB 842 CCTCGAGAGAGTGTCACCACTGCGTGGGGAAGCGGTGGGCCACCCGAGTCTCG 901  
QY 333 spTyGluThrTyraSnserserserAsnThrCysValAsnTrpAsnGlnTyTrT 353  
DB 902 ACTATGAGACCTATACAGTTCACGAAACACACCTGTGTCACTGGAAACCACTATATA 961  
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPhesAsnIleG 373  
DB 962 CCAACTGCTGCGGAGGAGCAACCCCTTCAAAAGGCGCATCACTTGCACAACTTG 1021  
QY 373 IyTyraIatrpIleAlaIlePheGlnValIleThrleuGluGlyTrpValAspIleMetT 393  
DB 1022 GCTATGCTGTGATGCCATCTTCCAGGTCATCACTGAGAGGCTGGGTGCATCATGT 1081  
QY 393 yrPheValMetAspAlaHisSerPheTyraSnpheIleTyPheIleleuIleIleV 413  
DB 1082 ACTTCGTATGAGAGCTCACCTCTTCTTACCACTTCATCTTCTCATTCATTCG 1141  
QY 413 a1GlySerPhePheMetIleAsnleuCysleuValValIleAlaThrGlnPheSerGluT 433  
DB 1142 TGGGCTCTTCTTATATATCACTGATGCTGTGGTGTATGCCAGGAGTTCGCCAGA 1201  
QY 433 hrLysGlnArgGluSerGlnleuMetArgGluGlnArgValArgPheleuSerAsnAlas 453  
DB 1202 CCAAAAGCGGGAGAGTACGTATGGGAGAGCGGTATGCATTCCTGTCCATATGCTA 1261  
QY 453 erThrleuAlaSerPheSerGluProGlySerCysTyGluGluLeuLeuLysTyrlEuV 473  
DB 1262 GCACCTTCGGCAAGCTTCTTCTAGCCAGGCAAGCTCTTATGAGACCTTCAAGTACCTCG 1321  
QY 473 a1TyrlIleleuArglyAlaIlaArgArgleuAlaGlnvalSerArgAlaIleGlyValA 493  
DB 1322 TGTACATCTCCGAAAGACACCCGAAAGCTGGGCCAGGTCTTAAGGCTTAAGGCGTGC 1381  
QY 493 rGAlaGlyleuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlys 513  
DB 1382 GGGCTGGGCTGCTCAGACAGCCCACTGGCCGTATGGGAGAGAGCCCAAGCCAGTGCA 1441  
QY 513 erCysThrArgSerHeIaArgArgleuSerValHisIleuValHisHisHisSH 533  
DB 1442 GCTGACATCGCTCAACACGTCGTGTGTGTCCACCACTGGTCCACCACATCACCAACC 1501

QY	533	16H1AHLA1ETRYH1ALEUCLYANGLYTHRLAALVVALPROARGLAAserProGIU	553
Db	1502	ACCATACACATTACCACCTGGAGTAATGGAGCGCTCAGAGTTCCCGGGCCAGCCACAGGA	1561
QY	553	1eG1AAsPArAspAlaAnGLysERaTgLEMeLEuProPobSErThrProT	573
Db	1562	TCGAGACAGGGAATGCCAATGGGTCTGCCGGCTCATCTACACACCTCTACACCCA	1621
QY	573	hrProSErGLYlYProProARGLYAlGLUsErVALHIsErPhETRYH1sAlAsPc	593
Db	1622	CTCCCTCGGGGGCCCTCCGAGGGGTGGAGTCTGTACACAGCTTCTACCATGTCTACT	1681
QY	593	YsH1sLEuGLUProVALrGcYsGlnAlAPrOPrOPrArGcYsPobSErGlnAlAsErG	613
Db	1682	GCCACTTGGAGCCAGTCCGTTGCCAGGACCCCTCCAGATGCCATCGAGGATCTG	1741
QY	613	LYArGThrVALGLYsErGLYsErLYsVALTYrProThrVALHIsThSErProProGIU	633
Db	1742	GTAAGACTGTGGTGTGGAAAGGTACCCCATCTGTCATACAGCCCTCACAGAGA	1801
QY	633	1eLeuLYAsPRLYsAlALEuVALGLUVALAPrOsErPrOGlYrProProThrLEuThrs	653
Db	1802	TACTGAAAGATTAAGCCTAGTGGAGGTGGCCCAAGCCCTGGAGGCCCACTCACCA	1861
QY	653	erPhEAAsH1LAPrOPrOGlYrProPhEsErSErMEH1sLYsLEuLEuGLUThrGlnSErT	673
Db	1862	GCTTCAACATCCCACTGGGCCCTTCACTCCATGCATCACAAGTCTCTGGACACAGAGTA	1921
QY	673	hrgLYAlACyHIsErSErCYsLYsL1EsErSErPrOCYsSErLYsAlAsPSErGLY	693
Db	1922	CGGGAGCCTGGCATAGCTCTGCAAAATCTCCAGCCCTTGCTCCAAAGCAGCACTGGAG	1981
QY	693	1aCYsGL1PrOAsPSErCYsPrOTrCYsAlAsrGThGLYAlGLYlUPrOGlUsErA	713
Db	1982	CCTCGGGGCCGACAGTGTCTCTTACTGTGCCGACAGAGCAGAGAACCAAGTCCG	2041
QY	713	1aAsPHisVALMErProAsPSErAsPSErGLUAlVALTYrGLUThrGlnAsPAlAG	733
Db	2042	CTGACCAATGTCATGCTGACTCAGACAGCGAGCTGTATAGTTCAACACAGGACGCTC	2101
QY	733	1nHIsErAsPRLYsrgArPrOH1sSErArGArGArGLYsHrSErLEuGLYrProAsP	753
Db	2102	AGCACAGTACCTCCGGATCCCAACAGCCGGCGGACGAGGAGCCTGGGCCCAAGTG	2161
QY	753	1aGLUPrOsErSErVALLEuAlAPhETrPArGLUe1LCyAsAPThrPhEAgrLYs1LeV	773
Db	2162	CAGAGCCTAGTTCTGTGCTGGCTTCTGAGGCTGATCTGTACACATTCGGGAAGATCG	2221
QY	773	AlAsPSErLYsTYrPhEGLYArGLY11EMET1eAlAlELEuVALsThrLEuSErM	793
Db	2222	TAGATAGCAAAATACCTTGGCCGGGAAATCATATGATGCCATCTGTGTCAATACATCACA	2281
QY	793	etGLY11eGLYThYH1sGLUGlINPrOGlUGLUeThrAsnAlALEuGLU1sEsErAsH1	813
Db	2282	TGGGATGAGATACCAACAGACGCCCGAGAGCTACCAACCCCTGGAAATCAGACACA	2341
QY	813	1eVALPhEThSErLEuPhEALALEuGLUMETLEuLEuLYsLEuLEuVALTYrGLYrPrOP	833
Db	2342	TCGTCTTACACGAGCTCTTGCCCTTGGAGATCTCTGAAATCGCTTGTCTACAGGTCCCT	2401
QY	833	hEGLTYrT11eLYsArPrOTrYrAsn11ePhAsPGLYAl11eVAL11sEsErALT	853
Db	2402	TTGGCTACATTAAGATCCCTTCAACATCTTGAATGGTGTCAATTGTGTATCAATGTGT	2461
QY	853	rPGLU11eVALGLYGLNGlNGlYGLYGLYLeUsErVALLEuArGThrPhEAgrLEuMEtA	873
Db	2462	GCGAATGTGGGCCACGAGGAGGTGGCTGTCCGTTGTGGACACTTCCCGCTGATGC	2521
QY	873	rGVALLEuLYsLEuVALArGPhELEuPrOAlALEuGLINArGLINLEuVAL11sEMET1	893
Db	2522	GGGTCTGAAGTGTGGCTTCTCGCGGCTCGAGGCGCAGCTCGTGTGTCTCATTA	2581

QY	893	ysrthmclaspasvvalalathrphocyshmetleuMuetleuPheilaPheHlPheS	913
Db	2582	AGACCAATGGACAAAGTGGCCACTTCGCAATGCTCCACATGCTGATATCTTCAATCTTCA	2641
QY	913	erlleauygmehHleuPheglYcyshysPheHlaSergluArgAspglYAspThrL	933
Db	2642	GCATTCCTGGGCAATGCATCTCTTTGGTTGGCAATTCGATCTGAACGGGATGGGACACGT	2701
QY	933	euproAspArgLYAsnPhesAspSerleuEntPrAlaileValThrValPheGlnlleL	953
Db	2702	TGCCAGACCGGAAAGAAATTTGACCTCCTGCTGGGCGCATGCTCATGCTTTGACAGATTC	2761
QY	953	euthrGlnluAspTrpAsnlyValleuYrYranglyMeeAlaSerThSerserTrpa	973
Db	2762	TGACTTCAGGAAGATGGAAATAATCTCTTCAACAACGGCATAGGCTTCCACATGCTTGGG	2821
QY	973	laalaLeuYrPheilaAleuMetThrPheglYAntYrValleuPheAsnleuY	993
Db	2822	CTGCTCTTTACTTATGATGCTCATGACTTTTGGCACTATGCTCTTTAACTTGCTGG	2881
QY	993	alalaileuValGluGlyPheGlnlaGluGlyAspAlaThrLYSerserGluSerGluP	1013
Db	2882	TGGCATTCCTTGTGGAAAGAAATTCAGGACAGAGGGAGATGCCAACAAAGCTGATGACAGGC	2941
QY	1013	roAspPhePheSerProSerValAspglYAspglYAspAArglyLYAsArgleuAlaLeuY	1033
Db	2942	CTGATTTCTTTTCCCCCAAGTGTGATGCTGATGAGGAGACAGAAACACGCTTGCCCTGG	3001
QY	1033	alAlaLeuGluGlnHlaAlGluLeuNrgLYSerserleuLeuProbleuLeileHst	1053
Db	3002	TGGCTTTGGGAGAACAGCGGAACTTAGAAGAGCCTTTTGGCACCCCTCATCATCTATA	3061
QY	1053	hralaAlaThrProMetSerHisProLYSerserSerSerThnglyValGlyluAlaLeuG	1073
Db	3062	CGGCTGGGACACCAATGTCACACCCCAAGCTCAGACACAGTGTGGGGAGAACATCGG	3121
QY	1073	lySerglySerArgArgThSerserSerglySeralAGluProGlyAlaAlaHisHsG	1093
Db	3122	GCTCTGGCTCGACGTAACGTAAGTGGTGTCCGCTGAGCCCTGGAGCTGGCCACCATG	3181
QY	1093	luMclLYsProProSerAlaArgSerSerProHiserProTrpSerAlaIsers	1113
Db	3182	AGATGAATGTCGCCCAAGATGCCGACAGCTCCGACAGTCCCTGGAGTCCGGCAACGA	3241
QY	1113	erTrpThSerserArgSerserSerArgAsnSerleuGlyArgAlaProSerleuYsArgA	1133
Db	3242	GCTGACCAAGAGCGCTCCACAGAAACAGCTCGGCGCGGCCCCACGCTTAAGCGGA	3301
QY	1133	rgSerProSerglyGluArgArgSerleuLeuSerglyGluGlyGlnGluSerglnAspG	1153
Db	3302	GGAGCGGAGCGGGAGGAGGAGTCCCTGCTGTGTGGAGAGGGCAGAGAGTCAAGATG	3361
QY	1153	luGluGluSerSergluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG	1173
Db	3362	AGGAGGAAAGTTCAGAAAGGACCGGGCACCCACGAGGAGGAGTACCATGCCACAGGG	3421
QY	1173	lySerleuGluArgGluAlaLYSerserPheAspLeuProAspThrleuGlnValProG	1193
Db	3422	GTTCTCTTGAAACGTGAGGCCCAAGATTCCTTTGAACCTGCCGACACTGCAAGGCGCGG	3481
QY	1193	lyLeuHisArgThrAlaSerGlyArgSerSeralAsergluHisGlnAspCYsaenglyL	1213
Db	3482	GGCTGCAACCGACACAGCCAGCGCGGAGCTCTGCTCTGACACCAAGACATGTAATGCA	3541
QY	1213	ySerAlaSerGlyArgleuAlaArgThrleuArgThrAspAspProGlnleuAspGlyA	1233
Db	3542	AGTGGGCTTCCAGGCGGTTTGGCCCGCACCTCGAGAGCATGATGAGCCCCCACTGGATGGGG	3601
QY	1233	sPasAspAspAspGluGlyAsnleuSerylGlyGluArgileGlnAlaTrpValArgS	1253
Db	3602	ATGATGACAAATGATGAGGGAATCTTGACCAAGGGGAACGATACAGACCTCGGCTCAGAT	3661
QY	1253	erArgleuProAlaCYeCyshArgluArgAspSerTrpSeralTrYrIlePheProProG	1273

D	3662	CCCCCTTCCTGCTGCTCCGAGAGCGAGATTCCTGGTCCGCTCATATCTTCTCTCTC	3721
Q	1273	InsersrAphsrgLeuLeuCyshIsargIleIethHisIysMecPheaspHisValV	1293
D	3722	AGTCAGAGGTTTCGTCTCTGTCGTCAACCGATCATCAACCAAGATGTTTACCATGTGG	3781
Q	1293	allLeuValIleIlePheLeuancysIleThrIleAlaMetGluabProIysIleAsp	1313
D	3782	TCCTGTCATCATCTTCTCAACTGTATCACTGCTATGAGAGGCCCAAAATGTACC	3841
Q	1313	roHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheL	1333
D	3842	CCCAAGAGCGTGAAGGCATCTTCCGACCCCTCCAACTACATCTTCAACGAGCTTTC	3901
Q	1333	euaIaGluMetThrValIysValValAlaLeuGIYTPCyPheGlyIguIalAlyL	1353
D	3902	TAGCTGAATATGACAGTGAAGGTGGCGCATGGCTGTGGTGGGAGCAGGCTTACC	3961
Q	1353	euaYsSerMetTrpAsnValLeuAspGIYLeuLeuValIleuIleSerValIleAspIleL	1373
D	3962	TGCGCAGAGCTGGAATGTCTGACCGGCTTGCTGTCTCATCTCCGTCAATCCACATCC	4021
Q	1373	euaValSerMetValSerAspSerGIYThrIysIleLeuGIYMetLeuArgValLeuArgL	1393
D	4022	TGCTCTCATGCTCCGACAGCGGCACCAAGATCTTGCGCATGCTGAGGGTGGCGGC	4081
Q	1393	euleuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGIYLeuIysLeuValV	1413
D	4082	TGCTCGGAGCCCTGGTCCACTCAGGATCATCAGCCGGGCCCAAGGACTGAGAGCTGGTG	4141
Q	1413	alGIuThrLeuMetSerSerLeuIysProIleGIYAsnIleValValIleCyScsAlaP	1433
D	4142	TAGAGACTGTATGTATCATCCCTCAAAACCATTTGGCAATGTGTCTATTGTGCTGTCT	4201
Q	1433	hePheIleIlePheGIYIleLeuGIYValGlnLeuPheIysGIYLeuPheValCySG	1453
D	4202	TCTTCATCATTTTGGAAATTCCTCGGGGTGCACTCTTCMAAGGAAATTCTTCGTGTCTC	4261
Q	1453	InGIYGIuAspThrArgAsnIleThrAsnIysSerAspCyAlaGluAlaSerTyrArgT	1473
D	4262	AGGGTGAAGAACCAACGAAACATCACTAACATCGACTGCGCTGAGCGCACTAACCCAT	4321
Q	1473	rPValArgHisIyIstYrAsnPheAspAsnLeuGIYGlnAlaLeuMetSerLeuPheValL	1493
D	4322	GGGTCCGCGCAAGTACAACCTTTGACAACCTGGCGCAGGCTCTGATGTCCCTGTTGTGC	4381
Q	1493	euaIaSerIysAspGIYTrpValAspIleMetTyrAspGIYLeuAspAlaValGIYValA	1513
D	4382	TGGCTCCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGGGTGG	4441
Q	1513	sPrgInGIuProIleuMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuL	1533
D	4442	ATCAGCACCCCATCATGTAAACCAACCCCTGAGTGTCTATACTCAATCCCTTCCCTCC	4501
Q	1533	euiIeValAlaPhePheValLeuAsnMetPheValGIYValValValGIuAsnPheHisL	1553
D	4502	TCATGTGTGGCTTCTTCTTCTGAAACATGTTGTGGSGTGTGGTGAAGAATCTCCATA	4561
Q	1553	ySCyAspArgIuHisGIuGIuGIuGIuValaArgArgArgGIuGIuIysArgLeuArgA	1573
D	4562	AGTGACAGACACACACAGAGAGAGAGAGAGCGGCGCTGAGAGAAAGCACTACGGA	4621
Q	1573	rGLeuGIuIuIysIysArgArg-----SerIysG	1582
D	4622	GGCTGGAGAAAAAGAGAGATCTAATGTGGACGATGTAATGTCCGCGAGCTCAG	4681
Q	1582	IuIysGIuMetAlaGluAlaGlnCyIysProIYrTyrSerAspTyrSerArgPheArgL	1602
D	4682	CCAGGGCTGCTGCAAGGCCAGTGCAGGCCCTTACTGACTGACTGAGATTCGGGC	4741
Q	1602	euleuValIuHisIleuCyThrSerHisTyrLeuAspLeuPheIleThrGIYValIleG	1622

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D	4742	TCCTGTCCACCACTGTATACGAGCACTACCTGACCTCTTCATCATCTGTGTCTATCG	4801
Q	1622	IYLeuAsnValValIleThrMetAlaMetGluHisTyrGIuGIuProGlnIleLeuAspGIuA	1642
D	4802	GGCTGAACGGTGTCACTATGCGCATGGAACTTACCGAGGCCCAATCCTGGACAGAG	4861
Q	1642	IaLeuIysIleCyAsnTyrIlePheThrValIlePheValPheGluSerValPheIysL	1662
D	4862	CTTGAAAGATCTGCATATTAATCATCTTTACGCTCATCTTGTCTTTGACTGATTTCAAC	4921
Q	1662	euaValAlaPheAlaPheArgArgPhePheGluAspArgTrpAsnGlnLeuAspLeuAlaI	1682
D	4922	TYTGCGCTTGTGGCTTCCGCGCTTCTTCAGAGCAGTGAACCAAGCTGACCTGTGCTA	4981
Q	1682	IeValLeuLeuSerIleMetGIYIleThrLeuGIuGIuIleGIuValAsnLeuSerLeuP	1702
D	4982	TTGTCTTCTGTCCATGATGGGCATGCACCTGGAGGAGATGAGGTCAATCTGTGCTGC	5041
Q	1702	roIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuIysL	1722
D	5042	CCATCAACCCCAACATCATCGTATCATGAGGGTGTCCGCAATTGCTCGAGTTCTGAAG	5101
Q	1722	euleuIysMetAlaValGIYMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProG	1742
D	5102	TGTTGAAGATGGCTGTGGGCATGGCGGCACTGTGCACAGGTGATCAGGCCCTGCCCC	5161
Q	1742	IuValGIYAsnLeuGIYLeuLeuPheMetLeuPhePheIlePheAlaAlaLeuGIYV	1762
D	5162	AGGTGGGAACTGGGACTTCTTCATGTATGTITTCATCTTTCAGCTTGTGGGCG	5221
Q	1762	alGIuLeuPheGIYAspLeuGIuCyAspGIuThrHisProCySGIuGIYLeuGIYArgH	1782
D	5222	TGGAGCTCTTTGGAGACCTGGAAGTGTATGAGACACACCTTGGAGAGGCTTGGGTGCG	5281
Q	1782	IaIaIaThrPheArgAsnPheGIYMetAlaPheLeuThrLeuPheArgValIleSerThrGIY	1802
D	5282	ATGCCACCTTGTAGAACCTTTGTATGGCTTGTGACCTTCTCCAGTGTCCACTGTGGT	5341
Q	1802	sPAsnTrpAsnGIYIleMetIysAspProSerArgAspCyAspGIuGIuSerThrCyST	1822
D	5342	ACAACGTGAATGTATATGAGGACACCTCCGGACCTGTGACAGAGATCCACTGCT	5401
Q	1822	YrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValL	1842
D	5402	ACAACACTGTATCTCCCTATCATCTTGTGTCTTCCGTGACGCGCCCAAGTTGTGCG	5461
Q	1842	euaValAsnValValIleAlaValLeuMetIysHisLeuGIuGIuSerAsnIysGIuAlaL	1862
D	5462	TGCTCAACGTGTCTATGCTGTGTGATGAAGCACCTGGAAAGAAAGCAAAAGAGGCCA	5521
Q	1862	YsGIuGIuAlaGluLeuGIuAlaGluLeuGIuLeuGIuMetIysThrLeuSerProGlnP	1882
D	5522	AGAGAGAGCGGAGCTGAGGCGGAGCTGAGAGATGAAAGACCTCAGCCCGGACGC	5581
Q	1882	roHisSerProLeuGIYSerProPheLeuTrpProGIYValGIuGIYValAsnSerThrA	1902
D	5582	CCCACTCCCGCTGGGACGCCCTTCTCTGCGCCCGGGGTGAGGGGTGTCACAACGATCTG	5641
Q	1902	sPserProIysProGIYAlaProHisThrThrAlaHisIleGIYAlaAlaSerGIYPhes	1922
D	5642	ACAACCTTAAGCTGGGGCTTCCACACACACTGCCCATTTGGAGGACCTCGGGCTTCT	5701
Q	1922	eIreuGIuHisProThrMetValProHisProGIuGIuValProValProLeuGIYProA	1942
D	5702	CCCTTGAGCACCCACATGTATCCCAACCCGAGAGGGTGCAGTCCCTTAGAGACAG	5761
Q	1942	sPLeuLeuThrValArgIysSerGIYValSerArgThrHisSerLeuProAsnAspSerT	1962
D	5762	ACCTGCTGACGTGAGGAAGCTGTGTGTACCGCGAGCAGCATCTGTGCCAATACAGCT	5821
Q	1962	YrMetCyAspArgnGIYSerThrAlaGluIuArgSerLeuGIYHisIaArgGIYTrpGIYLeuP	1982
D	5822	ACATGTGCCCAATGGAGGACATGCTGTAGAGATCCCTTAGAGACACAGGGGCTGGGGCTCC	5881

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QY 1982 rplyalaInserglySerIleuSerValHisSerInProAlaapThrSerCysI 2002
DB 5882 CCAMAGCCAGTCAGGCTCATCTTGTTCGTTCACTCCACAGACAGACACAGCTGCA 5941
QY 2002 lAleuGlnleuProlysaapValHisTyrLeuLeuGlnProHisGlyValaProThrTrpG 2022
DB 5942 TCCTACAGCTTCCCAAGATGTCATCTCTCCAGCTTCAAGGCTTCCACCTGGG 6001
QY 2022 lValaIleProlysaProProProGlyArgSerProleuAlaGlnaCpProleuArg 2042
DB 6002 GGGCCATCCCTTAACCTACCCCACTGGCGCTCCCTCCCTGCTGAGAGGCTCTCAGGC 6061
QY 2042 rGlnAlaAlaIleArgThrAapSerLeuAapValGlnGlySerArgGluAapL 2062
DB 6062 GCAGGACCAATTAAGACTGACTCCCTGATGTGAGAGGCTGGGTAGCCGGGAAGACC 6121
QY 2062 euLeuSerGluValSerGlyProSerCysAapProleuThrArgSerSerSerPheThrGlyG 2082
DB 6122 TGTTCAGAGAGTGAAGTGGGCTCTCTGCTGACCCGGCTCTCATCTTCGGGGCG 6181
QY 2082 lYSerSerIleGlnValGlnArgSerGlyIleGlnSerValSerLysHisIleA 2102
DB 6182 GGTTCAGCATTCAGGTGCAGACGCTTCGGGATCCAGACAAAGTCTCCAAAGCACATCC 6241
QY 2102 rGluProAlaProCysProGlyLeuGluProSerTrpAlaYsaapProProGluThrA 2122
DB 6242 GCTGTCAGACCCCTTTCGCCAGGCTTGAAACCCAGCTGGGCAAGAGACCTCCAGAGACCA 6301
QY 2122 rGSerSerleuGlnleuAapThrGlnleuSerTrpIleSerGlyAapleuProSerS 2142
DB 6302 GAAGCGCTTAGAGCTGAGACACGAGACTGAGTGAATTCAGAGACCTTCCTCCAGCA 6361
QY 2142 eGlnGlnGluProleuAapPheProArgAapLeuYsaYsYrYrSerValGluThrGlnS 2162
DB 6362 GCCAGGAAGAACCCCTGTTCCACGGGACTGAAGAGTCTCACTGATGAGAGACCCACA 6421
QY 2162 eCYsaArgArgArgProGlyPheTrpLeuAapGlnGlnArgArgHisSerIleAlaValS 2182
DB 6422 GCTGCAAGGCGAGGCTGGGCTTCGCTGATGAACAGCGAGACACTCCATTCGTGTCA 6481
QY 2182 eCYsaLeuAapSerGlySerGlnProArgLeuCYsaProSerProSerSerleuGlyG 2202
DB 6482 GCTGCTGAGCAAGCGCTCCCAACCCCGCTATGTCAGAGCCCTCAAGCTTCGGGGCC 6541
QY 2202 lmpProleuGlyGlyProGlySerArgProlysaLysLeuSerProProSerIleSerI 2222
DB 6542 AACCTCTTGGGGGTCTCTGGAGCGGCTTAAGAAATACTCAAGCCCAACCAAGTATCTTA 6601
QY 2222 lAapProProGlnSerGlnGlySerArgProProCysSerProGlyValCYsaLeuArg 2242
DB 6602 TAGACCCCGGAGAGAGCGGCTTCGGCCCAAGGATCTCTGGGTCTGCTCAGGA 6661
QY 2242 rGArgAlaProAlaSerAapSerLysAapProSerValSerSerProleuAapSerThrA 2262
DB 6662 GAGGAGCGCGCGGCAAGTCTTAAGATCCCTCGGCTCCAGCCCTTGAGACAGACGG 6721
QY 2262 lAlaSerProSerProlysaYsaPThrleuSerleuSerGlyLeuSerSerAapProT 2282
DB 6722 CTGGCTCAACCTCTCCCAAGAAAGACACGCTGAGTCTCTGTGTGTCTTGAACCA 6781
QY 2282 hrAapMetAapPro 2286
DB 6782 CAGACATGAGCCCC 6795

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RESULT 7  
AAK83488 standard; cDNA; 6741 BP.

XX AAK83488;  
XX AC  
XX 07-DEC-1999 (first entry)  
XX

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DE Rat T-type voltage-gated Ca channel alpha-1-G (rCaV1d) cDNA.
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS Rattus sp.
XX
FN W09929847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98MO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
XX
DR P-PSDB; AAY14593.
XX
PS New T-type voltage-gated calcium channels.
XX
XX Disclosure; Page 94-103; 138pp; English.
XX
XX This sequence represents the coding region for a rat T-type voltage-gated
XX calcium (Ca) channel alpha-1-G designated rCaV1d. Voltage gated channels
XX are membrane bound glycosylated proteins formed of several subunits. The
XX large alpha subunits form a pore in the membrane that is selective for a
XX given ionic species. Each alpha subunit contains 4 domains (I, II, III
XX and IV) and each domain contains 6 putative transmembrane helical
XX segments (S1-S6). T-type Ca channels are activated at a lower voltage
XX than L- or N-type channels. Characteristics of T-type channels include
XX short current time, slow activation kinetics near threshold, fast
XX inactivation kinetics and slow tail current. The sequences AAK83481-
XX K83492 represent novel T-type voltage-gated Ca channel genes from humans
XX and race. Each of the novel Ca-channels contains a putative IVS4 region
XX comprising the amino acid sequence AAY14598. Cells expressing the T-type
XX voltage-gated calcium channel proteins can be used to screen for drugs
XX which affect calcium channels. Methods are also disclosed for treating a
XX disease or disorder associated with a deficiency in a native T-type
XX calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6741 BP; 1355 A; 2041 C; 1908 G; 1437 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 0 Length: 6741
XX Score: 11747.50 Matches: 2242
XX Percent Similarity: 99.47% Conservative: 1
XX Best Local Similarity: 99.42% Mismatches: 3
XX Query Match: 97.67% Indels: 9
XX DB: 2 Gaps: 1
XX
XX US-09-611-257a-24 (1-2287) x AAK83488 (1-6741)
XX
QY 34 TrpThrArgArgArgMetGluArgAlaProArgSerArgAapSerProValaIaSerArg 53
DB 2 TGGAGAGAGAGAGATGAGCGGGCGCGAGAGATCGGAGACGCCCTGACTTCAACGC 61
QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGlnYsaAap 73
DB 62 AGCTCAACGACCTGTCTCCGGGGCGGGGCGCGGAGGGGCGGGGCTGACGAGAAAGAGACC 121
QY 73 rGlySerAlaAapSerGluAlaGlnGlyLeuProTyProAlaLeuAlaProValaP 93
DB 122 CGGCGAGCGCGGACTCCAGAGCGGAGGGGCTCCGTAACCGGCGCTAGCCCGGGTGT 181
QY 93 hApeTyrleuSerGlnAapSerArgProArgSerTrpCYsaLeuArgThrValCYsaAap 113
DB 182 TCTTCTACTTGAAGCCAGACAGCCCGCGGAGGCTGTGTCTCCGACAGGCTGTGAACC 241
QY 113 rGTrpPheGluArgValSerMetLeuValIleLeuLeuAasnCYsaValThrLeuGlyMetP 133

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Db	242	CGTGGTTGAGGAGATCAGTATGCTGGTCAATTCCTTCAACCTGTGACTCTGGGATATGT	301
Oy	133	hEARpRcCyagIuAspIleAlaCyAspSerGlnArgCysArgIleLeuGlnAlaPheA	153
Db	302	TCAGGCCGTGTAGAGACATGCTGTGACTCCACGCGCTGCCGAGATCTCGACAGCTTGG	361
Oy	153	sPAspPheIlePheAlaPhePheAlaValGluMetValIleYsMetValAlaLeuGlyI	173
Db	362	ATGACTTCATCTTGGCTTCTTGGCTGTGGAATAGTGTGGAAGATGTGTGGCTTGGGCA	421
Oy	173	IePheGlyLysAlaCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI	193
Db	422	TCTTTGGGAAAGAAAGTTTACCTGGGAGACACTTGGAAACCGGCTTGCTTTTCATTGTCA	481
Oy	193	IeAlaGluMetLeuGluIuTyrSerLeuAspLeuGluAsnValSerPheSerAlaValArgT	213
Db	482	TTGCAGGGAGTGTGGAGTATTCGTGTGACCTTGACAGAACCTCAAGCTTCTCCGACGTGAG	541
Oy	213	hTValArgValLeuAspArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuY	233
Db	542	CAGTCCGTGTGCTGGGACCGCTCAAGGGCCATTACCGGGGTGCCACATGGCGATTCTCG	601
Oy	233	AlThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheY	253
Db	602	TCACACTTACTGCTGGACACCTTGCCATTATCTGGGCAACCTCGCTGCTGTTCCTTTCG	661
Oy	253	AlPhePheIlePheGlyIleValGlyValGluLeuTrpAlaGlyLeuLeuAspAsnArgC	273
Db	662	TCTTTTTCATCTTTGGCATGTGGGGGTCACTGTGGGCAAGACGTCTTCGACACCGG	721
Oy	273	YsPheLeuPProGluAsnPheSerLeuProLeuSerValAspLeuGluIuProTyrTyrGlnT	293
Db	722	GCTTCTCTCCCGAGAACTTCAGCTCTCCCTGACGTGAGCTGAGACCTTATTACAGA	781
Oy	293	hTGlAsnGluAspGluSerProPheIleCysSerGluProArgGluAsnGlyMetArgS	313
Db	782	CAGAGAAATGAGGACGAGAGACCCCTTCATCTGCTTCAGCCTCGGAGAAATGCGATAGAT	841
Oy	313	erCyAspArgSerAlaProThrLeuAspArgGlyGluGlyValGlyGlyProProCysSerLeuA	333
Db	842	CCTGAGAGAGTGTGCCACACTGCGCGGGGAAAGCGGTGTGGCCACCTCGAGTCTGG	901
Oy	333	sPlyGluThrTyrAsnSerSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrT	353
Db	902	ACTAAGAGACCTTATACATTCACGTTCACGAAACACCACTGTGTCAACTGGAACCACTATTA	961
Oy	353	hTrAsnCysSerAlaGlyGlyIuHisAsnProPheArgGlyValIleAsnPheAspAsnIleG	373
Db	962	CCAACTGCTCTGGGGCGAGCAACACCTTCAAAAGGCCCATCACTTGGACCAACATTG	102
Oy	373	IyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	393
Db	1022	GCTAAGCCTGTGATGCCCATCTTCCAGGTATACATCATGGAGGGCTGGTGTGCATCATGT	108
Oy	393	YrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleY	413
Db	1082	ACTTGATATGAGCGCTCACTCTTCTCAACTTCACTTCACTTCACTTCTTCATCATCG	114
Oy	413	AlGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT	433
Db	1142	TGGGCTCTCTTTCATGATCAACCTGTGCTGGTGTGATTGGCACGAGTTCTCCGAG	120
Oy	433	hTrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS	453
Db	1202	CCAAACACCGGAGAGTCAAGCTGATGCCGAGACAGCGTTCAGATTCTCGTCCAAAGCTA	126
Oy	453	erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuY	473
Db	1262	GCACTCTGGCAAGCTTCTTGTAGCCAGGAGCTGCTATAGAGACTCACTCAAGTACTTGG	132
Oy	473	AlTyrIleLeuAspGlyValAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA	493

Db	1322	TGTAATCTCTCCGAAAAGCAAGCCGGAAGGCTGGCCCAAGTCTCTAAGGAGCTATAGGCTGTC	1381
QY	493	rgalaglyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS	513
Db	1382	GGGCTGGGGCTGCTCAGCAGAGCCCAATGGCCGCTATGGGAGAGAGCCCAAGCCAGTGGCA	1441
QY	513	erCyStrParSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisSh	533
Db	1442	GCTCAGCTCGCTCACACCGTCTGCTGCTCTGCTCCACCACTGGTGCACCAACATCACAC	1501
QY	533	ishHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis	553
Db	1502	ACCATTCACCTATCACCTCGGTGTAATGGAGAGCTCAAGATTCCTCCCGGAGCAGCCAGGA	1561
QY	553	legAnaParGAspAlaasnGlySerArgArgLeuMetLeuProProSerThrProT	573
Db	1562	TTCAGAGACAGGAGATGCCAATGGTCTCGCCGGCTCATGCTACCAACACCTCTACACCCA	1621
QY	573	hrProSerGlyGlyProProArgArgGlyAlaGlnSerValHisSerPheTyrHisAlaApc	593
Db	1622	CTCCCTCGGGGGCCCTCCGAGGGGTGGAGGTCTGTATACAGACTTCTACCATCTGCTACT	1681
QY	593	yHisHisLeuGlnProValArgCyMetGlnAlaProProProArgCyProSerGlnAlaSerG	613
Db	1682	GCCACTTGGAGCCAGTCCGTTGGCCAGGAGACCCCTCCAGATGGCCATCGGAGGACATCTG	1741
QY	613	lyArgThrValGlySerGlyLysValTyrProThrValHisHisHisHisHisHisHisHis	633
Db	1742	GTAAGACCTGTGGTGTAGTGGAGAGGTGTATCCCACTGTGTGCATACCAAGCCTTCACAGGA	1801
QY	633	leLeuLysAspLysAlaLeuValGlnValAlaProSerProGlyProProThrLeuThrS	653
Db	1802	TACTGAAGAGATAAGACACTAGTGGAGGTGGGCCCAAGCCTCGGGCCGCCCACTTCACCA	1861
QY	653	erPheAsnHisLeuProGlyLysProPheSerSerMetHisLysLeuLeuGlnThrGlnSerT	673
Db	1862	GCTTCACATCCCACTCGGGCCCTTCAGCTTCATGACCAAGCTCTGTGAGACACAGAGTA	1921
QY	673	hrGlyAlaCyHisHisSerSerCysLysHisLeuSerProCysSerLysAlaAspSerGlyA	693
Db	1922	CGGAGCCTGCGCAATGCTCTGCAAAATCTCCAGCCTTGTCTCCAAAGCAGACAGTGGAG	1981
QY	693	laCyGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGlnSerA	713
Db	1982	CCTCGGGGCCGAGCAGTGTGCTCTCACTAGTGGCCGGAAGAGAGAGAGAGCAGCAAGTCCG	2041
QY	713	laAspHisAlaMetProAspSerArgAspSerGlnAlaValTyrGlnPheThrGlnAspAlaG	733
Db	2042	CTGACCAATGTCATCCTGACCTGCATCACACAGCGAGCTGTGTATGAACTTACACAGAGCGCT	2101
QY	733	lnHisSerAspLysAlaArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA	753
Db	2102	AGCAACAGATCTCCGGAGATCCCAACAGCGGCGGAGCAGACAGGAGGCTGGGCCCAAGTG	2161
QY	753	laGluProSerSerValLeuAlaPheThrParArgLeuHisCysAspThrPheArgLysHisLev	773
Db	2162	CAGAGCCTAGTCTGCTGCTGCTCTTCTGGAAGGCTGATCTGTGCACATTCGCCGAAGATCG	2221
QY	773	alaAspSerLysTyrPheGlyArgGlyLysMetHisAlaHisLeuValAsnThrLeuSerM	793
Db	2222	TAGATTAGCAAAATACCTTTGGCCGGGGAATCATGATCGGCATCTGTGTCATACCTCAGCA	2281
QY	793	etGlyTyrLeuTyrHisGlnGlnProGlnGlnLeuThrAsnAlaLeuGlnHisLeuSerAsnI	813
Db	2282	TGGGCATCTGATACACAGAGCAGCCGAGAGAGCTACACCAAGCCTGGAAATTCAGCAACA	2341
QY	813	leValPheThrSerLeuPheHisLeuGlnMetLeuLeuLysHisLeuValTyrGlyProP	833
Db	2342	TGCTCTTCCACAGGCTCTTGCCCTTTGGAGAGTGCCTGGAACCTGCTGTACGGTCTCT	2401
QY	833	heGlyTyrTyrLeuAsnProTyrAsnHisPheAspGlyValHisValHisSerValT	853
Db	2402	TTGGCTCATTTAAATATCCCTCAACAATCTTTGATGTGTCATGTGTGTCATCAGTGTGT	2461

QY 853 IPGLIULEVALIGYINGINGIYGIYLYLEUSERVALLEUARGTHRPHEATGLEMETR 873  
DB 2462 GGGAGATTGTGGCCAGCAGGAGGGTGCGCTGTGGTGCTGGCGGACCTTCCGCTGATGTC 2521  
QY 873 TGVALLLEULYSLEUVALAARGPHELEUPROALALEUGINARGINLEUVALVALLLEUMETL 893  
DB 2522 GGGTGCTGAAGCTGGGCGCTTCTGCGCCGCTGAGGCCAGCGCTGGTGCTCATGA 2581  
QY 893 YETThMeCAspAnValAAThRPhCyMeTLeuMeTLeuPheilePhePheS 913  
DB 2582 AATCCATGACAACTGGGCCCACTTCTGCACTGCTCTCATGCTTTCATCTTCA 2641  
QY 913 erileuengiYmeChisleuphegiYalyApheAlaseRgiuArgApGiYAsPThL 933  
DB 2642 GCATCCTGGCATGATCTCTTGTGGTTCAGATTGCAATGCGAGTGGGAGCACGCT 2701  
QY 933 euPProAspArgLySaenPheAspSerLeuLeuTTPAlaleValThRValPheGInIleL 953  
DB 2702 TCCCAAGACCGAAGAAATTCGACTCTGCTGCGGCATTCGCACTGCTTTCAGATTTC 2761  
QY 953 euThRGIuNGIuAsPThRPAuLySValleuTYrAsnGIYmeCAlaseRThRSeRTrPA 973  
DB 2762 TGAATCAGAAAGACTGGAAATTAAGTCTCTTACAAGCGCATGGCTTCCATGCTTGGG 2821  
QY 973 lAlAlaLeuTYrPheileAlaleuMeCThRPheGIYAsnTYrValleuPheAsnLeuY 993  
DB 2822 CTGCTCTTACTTCATCGCCCTCATGATCTTGGCAACTATGCTGCTTAACTGCTGG 2881  
QY 993 AlAlAlaleuValGIuGIYpheGInAlaGIuGIYAspAlaThRlySAsRgiuSeRGIuP 1013  
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QY 1013 rAspPhePheSeRProSeRValAspGIYAspGIYAspArgLySlyAsRLeuAlaleuY 1033  
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QY 1093 lUmeClySProPProSeRAlaArgSeRSeRProHieSeRProTTPSeRAlaAlaSeR 1113  
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QY 1113 erTTPThRSeRArgSeRSeRArgAsnSeRleuGIYArgAlaProSeRleuLyArgA 1133  
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QY 1433 hePheIleIlePheGIYIleuGIYValGIuLeuPheLySlySPhPhePheValCyG 1453  
DB 4202 TCTTCATCATTTTGGAAATTCGCGGGTGACGCTTTCAAAGGAAGTTCTTGTGTGTC 4261  
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DB 4262 AGGTGAGGACACCGAAGCACTACTAACAAATCCGACTGCGCTGAGGCCACACTACGAT 4321  
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RESULT 8  
AAD04756  
ID AAD04756 standard; cDNA; 7741 BP.

AC AAD04756;  
 DT 17-JUL-2001 (first entry)  
 DE Human T-type low voltage activated calcium channel alpha1G-C cDNA.  
 XX  
 XX Human T-type low voltage activated calcium channel alpha1G-C; stress;  
 KW epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease;  
 KW endocrine disorder; respiratory disorder; peripheral muscle disorder;  
 KW muscle excitability; fertilisation; contraception; hypertension;  
 KW neuronal firing regulation; cardiovascular disorder; gene therapy;  
 KW forensic analysis; epidemiological study; neuroleptic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..522  
 FT 5'UTR /tag= a  
 FT CDS 523..7344  
 FT /tag= b  
 FT /product= "Human T-type low voltage activated calcium  
 FT channel alpha1G-C protein"  
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 FT /note= "The CDS is specifically claimed in claim 2 as SEQ  
 FT ID NO.3"  
 FT 7345..7741  
 FT 3'UTR /tag= c  
 XX  
 XX WO200130844-A1.  
 XX  
 XX 03-MAY-2001.  
 XX  
 XX 06-OCT-2000; 2000WO-US027761.  
 XX  
 XX 26-OCT-1999; 99US-00426998.  
 XX  
 XX (ORTH ) ORTHO-MCNEL PHARM INC.  
 XX  
 XX Dublin AE, Galindo JE, Pyatt J, Zhu YJ, Erlander MG;  
 XX  
 XX WPI: 2001-300486/31.  
 XX  
 XX P-PSDB; AAE01019.  
 XX  
 XX New nucleic acid encoding human calcium channel protein, useful for  
 XX identifying specific modulators and potential pharmaceuticals for  
 XX treating e.g. epilepsy.  
 XX  
 XX Claim 2; Page 76-81; 115pp; English.  
 XX  
 XX The invention relates to isoform of human T-type low voltage activated  
 XX calcium channel (alpha1G-C) cDNA and protein. Cells transformed with  
 XX calcium channel DNA to express calcium alpha1G-C channel protein are used  
 XX to identify specific modulators (antagonists or agonists). These  
 XX modulators are useful as therapeutic agents and are used for treating  
 XX wide range of calcium alpha1G-C channel-mediated disorders; e.g. stress  
 XX epilepsy, schizophrenia, depression, sleep disorders, Cushing's disease,  
 XX endocrine disorders, respiratory disorder, peripheral muscle disorder,  
 XX muscle excitability, fertilisation, contraception, disorders involving  
 XX hypertension, neuronal firing regulation, potentiation of synaptic  
 XX signals and cardiovascular disorders (e.g. atherosclerosis, cardiac  
 XX hypertrophy, angina pectoris). Calcium alpha1G-C channel DNA is useful  
 XX for isolating and identifying related molecule mutations. It is also  
 XX optionally used as antisense sequences, in gene therapy. Calcium channel  
 XX alpha1G-C DNA, protein and antibodies are useful for forensic analysis,  
 XX diagnosis and epidemiological studies, by standard hybridisation or  
 XX immunological assays. The present sequence is T-type low voltage  
 XX activated calcium channel alpha1G-C cDNA. This sequence is isolated from  
 XX human thalamus cDNA library  
 XX

SQ Sequence 7741 BP; 1469 A; 2496 C; 2287 G; 1489 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 0 Length: 7741  
 Score: 11066.50 Matches: 2134  
 Percent Similarity: 93.81% Conservative: 33  
 Best Local Similarity: 92.38% Mismatches: 112  
 Query Match: 92.01% Indels: 31  
 DB: 4 Gaps: 5  
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 QY 23 SerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetGluArgAla 42  
 DB 491 CCGGATCCCGCCGGGGCCCCGGCTGGCCAGAGATGACAGAGAGAGATGGAGCGGGCG 550  
 QY 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrCysProGlyProGly 62  
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 QY 102 roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV 122  
 DB 731 CCGGAGGCTGGTGTCCGACGAGTGTAAACCCCTGGTTGAGCGCATCAACATGTTGG 790  
 QY 122 allleleuLeuasnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA 142  
 DB 791 TCATCCTTCTCAACGCGGACCTGGGACATGTCGGGATTCGGGACGAGACATGCGCTGTG 850  
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 DB 1151 TCGTGGGCAACCTCTGCTGCTCTGCTTCTTCTTCACTTCCTTGGCATGCTGGGGG 1210  
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 DB 1211 TCCAGCTGGGGCGAGGGCTGCTTCCGAACCATGCTTCTTACTGAGATTTCAGCTTC 1270  
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Qy	342	snThrThrCysValAsnTPraAsnIntYrYrThrAsnCysSerLaagllygluhisaaen	362
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Db	2291	ATCCACCGTGCAACACAGCCCTCCACCGAGACGCTGAAGAGAGGACCATTAATGAGG	2350
Qy	642	alaIaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPhes	662
Db	2351	TGGCTGCCAGCTTCGGGGCCCCCAACCTTCACCAAGCTCAATGCCACCGGGGCTTACA	2410
Qy	662	erSerMetHisLyLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysIlyS	682

Dd	2411	GCTCCATGACAAAGCTGCTGGAGACACAGATACAGGTGCTGCTGCCAAAGCTCTTGACAGA	2470
Qy	682	leSerSerProCySerSerIysAlaAspSerGlyAlaCySGIyProAspSerCyAspProTyrC	702
Dd	2471	TCTCCAGCGCCCTGCTTGAAAGACAGATGGAGCTGTGGTCCAGACAGCTGCCCTTACT	2530
Qy	702	ysAlaAaGthrGlyAlaGlyGluProGluSerAlaAspHisIvalMetProAspSerAsps	722
Dd	2531	GTGCCCGGGCGGGGAGAGGTGAGGTCCGCCGACCTGTGAATTCCTGACTCAGACA	2590
Qy	722	ergIuAlaIvalTyrGluPheThrGlnAspAlaGlnHisSerAspLeuAlaAspProHis	742
Dd	2591	GCGAGGAGATTATGAGTTTACACAGAGATGCCAGCACAGACTCTGGGAGCCCCACA	2650
Qy	742	erAArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValIleuAlaPheT	762
Dd	2651	GC---CGGCGGCAACGAGGCTGGGCCCAATGAGAGGCCAGTGTGTGCTGGCCTTCT	2707
Qy	762	rpArgLeuIleCyAspThrPheArgLysIleValaAspSerLysTyrPheGlyAArgGlyI	782
Dd	2708	GGAGGCTAATCTGTGACACCTTCGGAAGAATTGGACACAGAACTATTGGCCGGAGAA	2767
Qy	782	leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisIleGluProG	802
Dd	2768	TCAATGATGCCATCTGATCAACACACTTCAGCAATGGGCATCGAATACACAGAGAGCCG	2827
Qy	802	IuGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG	822
Dd	2828	AGGAGCTTACCAAGGCCCTGGAATACGAAACATCGTCTTACACAGCTCTTTGGCCCTGG	2887
Qy	822	IuMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI	842
Dd	2888	AGAGGCTGCTGAGAGCTCTGTGTATGTGCTCCCTTTGGCTACATCAGAAATCCCTACACA	2947
Qy	842	lePheAspGlyValIleIleValIleSerValTropGluIleValGlyGlnGlyGlyG	862
Dd	2948	TCTTCAGATGGTCAATGTGGTCACTCAAGCGTGGGAGATCGTGGGCACAGGGGGGGCG	3007
Qy	862	IlyLeuSerValLeuArgThrPheArgLeuMetArgValIleuLysLeuValArgPheLeuP	882
Dd	3008	GCTGTGGTGCTCGGACCTTCGCGCTGATGCGTGTGCTGMAAGCTGTGCTCTCTGC	3067
Qy	882	roAlaLeuGlnArgGlnLeuValIleuMetLysThrMetAspAsnValAlaThrPheC	902
Dd	3068	CGGCGCTGACGCGGACACTGGTGGTGTCTCATGAAGACCATGACCAAGTGGCCACTTCT	3127
Qy	902	ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisIleuPheGlyC	922
Dd	3128	GCAAGCTGCTTATGCTCTTCACTTCACTTCACTTCAAGCACTCGGCGATGCACTCTTCGGCT	3187
Qy	922	ysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL	942
Dd	3188	GCAAGTTTGCTCTGAGAGGGGATGGGACACCTCTCCAGACCGGAAGAAATTTGACTCTCT	3247
Qy	942	euleuTrrPalaiIleValThrValPheGlnIleleuThrglnIuAspTrrAsnLysValI	962
Dd	3248	TGCTCTGGGCGATGTCACCTGTCTTTCAATCTTGACATCCAGCCAGAGACTGGAAACAAATGCC	3307
Qy	962	eulTrrAsnGlyMetAlaSerThrSerSerTrrPalaiAlaLeuTrrPheIleAlaLeuMetT	982
Dd	3308	TCTTCAATATGATATGGCTCCACAGCTGCTCGTGGGGGGCCCTTATTTCATTTGCCCCCTCA	3367
Qy	982	hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA	1002
Dd	3368	CTTTCGGGACTATAGTCTCTTCAATTTGCTGTGTGCCCATTTCTGGTGGAGGCTTCCAGG	3427
Qy	1002	IaGlu-----	1003
Dd	3428	CGAGAGAAATACAGCAACGGGAAGATGCGATGG9ACAGTTAAGCTGTATTCAGTGCCTG	3487
Qy	1004	-----GlyAspAlaThrLysSerGluSerGluProAspPhePheSerProS	1019
Dd	3488	TCGACTCCAGGGGGGAGATGCCAAACAAAGTCCGAATCAGAGCCCGAATTTCTTCTCACC	3547

QY	1019	erValaBpGlyAaBpGlyAaBpArglyValaBpArglyLeuValaValaLeuGlyValaHisA	1033
Db	3548	GCCTGGATGTGTATGGGGAGACAGAAAGAGCTTGGCGCTTGGTGTCTCTGGAGAGACCC	3607
QY	1039	IaGluLeuAaGlySerSerLeuLeuProProLeuLeuLeuHisThrAlaAaThrPromets	1059
Db	3608	CGAGAGCTCGAGAGAGCTCTGCTGCCCTCTCATATCCACAGGCCGCCACACCATGT	3667
QY	1059	erHisProLySerSerSerThrGlyValaGlyValaLeuGlySerGlySerArgArgT	1079
Db	3668	CGCTGCCCAAGAGACACAGACCGGGCTGGGGCGAGGGCGCTGGGGCTGGCGTGGCGCGCA	3727
QY	1079	hrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCyProProS	1099
Db	3728	CCAGCACACACGGGCTCGCAGAGCTGGGGGGGCGC---CACAGATCAATACACCGGCCA	3784
QY	1099	erAlaAaGserSerProHisSerProThrPseAlaAlaAaSerSerTrpThrSerArgRgs	1119
Db	3785	GCGGCCCGACGCTCCGACAGCCCCCTGAGACCTTGACAGACGCTTGACACAGACGGGCT	3844
QY	1119	erSerArgAaSerLeuGlyAArgAlaProSerLeuLyAaArgArgSerProSerGlyAla	1139
Db	3845	CCAGCCGGAACAGCTCGGCCGTGACCCAGCTCGAAGCGGAGAAAGCCCAAGTGAAGAGC	3904
QY	1139	rgArgSerLeuLeuSerGlyGlyGluGlyGlnGlySerGlnAaBpGluGluGlnSerSerGluG	1159
Db	3905	GCGCGGTCCCTGTGTTCGGAGAAAGCCAGAGAGCCAGAGAGAAAGAGAGCTCAAGAG	3964
QY	1159	IuAaBpArgAlaSerProAlaGlySerAaBpHisAArgHisAaGlySerLeuGluAArgGlyAla	1179
Db	3965	AGGAGCCGGGCCAGCCCTCGGGGAGTGAACATCCGCACAGGGGGTCCCTGAGCGGGAGG	4024
QY	1179	IaLySerSerPheAaBpLeuProAaPThrLeuGlnValProGlyLeuHisArgThrAlaS	1199
Db	4025	CCAAAGAGTTCCTTTGACTGCGACACACACTGACAGTCCAGGGCTGCATGCACTGCCA	4084
QY	1199	erGlyAaGserSerAlaSerGluHisGlnAaBpCyAaGlnGlyAaGlySerAlaSerGlyAaArgL	1219
Db	4085	GTCGCCAGAGGCTCTGCTTCTGAGACACAGCACTCAATGGCAATCGGCTTCAGAGCGCC	4144
QY	1219	euaIaAaGTrhLeuAaGTrhAaBpAaProGlnLeuAaBpGlyAaBpAaBpAaBpGluG	1239
Db	4145	TGCCCCGGGCTCTGGCGCTGATGAACCCCACTGATGGGAGTACCGCGCATGAACAGG	4204
QY	1239	IyAaLeuSerLyGlyGlyAaArgLeuAlaTrpValAaArgSerArgLeuProAlaCysC	1259
Db	4205	GCAACCTGAGCAAGGGGAGCGGGTCCGCGTGGATCCGAGCCGCACTCCCTCGTCT	4264
QY	1259	yAaBpGlyAaArgAaBpSerTrpSerAlaTrpLeuProProGlnSerAaArgPheArgLeuL	1279
Db	4265	GCCCTCGAACCGAGACTCTGGTCAAGCTACATCTTCCCTCAAGTCCAGGTTCCGCTCC	4324
QY	1279	euaCyHisAaGTrIleIleThrHisLysMetPheAaBpHisValaValaLeuValaIleIlePheL	1299
Db	4325	TGTGTACCCGATCATATCACCAACAAAGATTTGACACAGTGTCTTGTATCATCTTCC	4384
QY	1299	euaAaCyAaIleThrIleAlaMetGlyAaArgProLyAaAaBpProHisSerAlaGlyAaArgI	1319
Db	4385	TTAACTGCATCACCATCGCATGAGCGCCCAAAATGACCCCAACGCGCTGAACGCA	4444
QY	1319	IePheLeuThrLeuSerAaAaTrpIlePheThrAlaValaPheLeuAlaGluMetThrValL	1339
Db	4445	TCTTCTCGACCTCTCCAAATTAACATTTACCGCAGTCTTCTTGCTGAATGACAGTGA	4504
QY	1339	yAaValaValaLeuGlyTrpCyAaPheGlyGlyGlnAlaATyrLeuAaGserSerTrpAaAaV	1359
Db	4505	AGGTGTGTGGCACTGGGCTGTGTCTCGGGAGACAGCGTACCTGCGAGCACTTGGAAAGC	4564
QY	1359	aIleuAaBpGlyLeuLeuValaLeuIleSerValIleAaBpIleLeuValaSerMetValSerA	1379
Db	4565	TGCTTGACAGGGCTGTGTGTGTCTCATCTCCGTCATGACATTCGTGTGTCTGTCTCTG	4624

QY	1379	spberGlyThrIysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgP	1399
Db	4625	ACAGCGGACCAAGATCTCTGGCATGTGTAGGGGTCTCGCGCTGTCTCGAGACTCTGGCC	4664
QY	1399	roleuArgValIleSerArgAlaGlnGlyLeuIysLeuValAlaGluThrLeuMetSerS	1419
Db	4685	CGCTCAGGGTGAATCAGCGGGGCCAGGGGCTGAAGCTGGTGGTGAACCGCTGATGTCT	4744
QY	1419	erLeuIysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyT	1439
Db	4745	CACGAAACCATCGGCACATTTGTACTCATCTGTCTGTGCTTCTTCATCATATTTTCGGCA	4804
QY	1439	leLeuGlyValAlaGlnLeuPheIysGlyIysPhePheValCysGlnGlyGluAspThrArg	1459
Db	4805	TCTTGGGGGTGCAGCTCTTTCMAAGGGAAAGTTTTTCGTGTCCAGGGGAGAGATACAGGA	4864
QY	1459	enIleThrAsnIysSerAspCysAlaGlnIleSerTyraArgTyrAlaArgHisIysTyra	1479
Db	4865	ACATCACCAATTAATCGGAATGTGTCCAGGCGCAATTACCGGTGGTCCGCGACAAAGTACA	4924
QY	1479	snPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerIysAspGlyT	1499
Db	4925	ACTTTGACAACTTTGGCGCAGGCCCTGATGTCTCCGTTCGTTTTGGCTCCACAGATGGTT	4984
QY	1499	rpValAspIleMetTyrAspGlyLeuAspAlaValAlaGlyValAspGlnProIleMetA	1519
Db	4985	GGGTGGACATCATGTACATGAGTGGGTGATGTGTGGCGGTGGACACAGCCCATCATGA	5044
QY	1519	snHisAsnProTyrMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheV	1539
Db	5045	ACCAACAACCTTGGATGTCTGTACTTCTCATCTCTGTCTGTCTCATATGTGGCCTTCTTGG	5104
QY	1539	alleuAsnMetPheValGlyValValAlaGluAsnPheHisIysCysArgGlnHisGlnG	1559
Db	5105	TCTCGAACATGTTTGTGGGTGTGGTGGAGAACTTCCAAAGTGTCCGACAGCACCGAG	5164
QY	1559	IuGlnGlnGluAlaArgArgArgGlnGluIysValArgLeuArgArgLeuGlnIysIysArgA	1579
Db	5165	AGGAAGAGAGAGCCCGCGCGGAGAGAGAACCCCTTACGAAAGCTGAGAGAAAAGAA	5224
QY	1579	rgSerIysGlnIysGlnMetAlaGlnIuIaGlnCysIlyProTyrTyrSerAspTyrSerA	1599
Db	5225	GGAGTAAAGAAACAGATGTGCTAAGCCAGTCAAACTTACTTACTTCCAGACTACTCC	5285
QY	1599	rgPheArgLeuLeuValHisHisIleuCysThrSerHisIyTyrLeuAspLeuPheIleThrG	1619
Db	5285	GCTTCCGGCTCTGTCTCCACCATTTGTGTGCACACGCACTACTGAGCCTTCTTATCACA	5344
QY	1619	IyValIleGlyLeuAsnValIleThrMetAlaMetGlnHisIyTyrGlnGlnProGlnIleL	1639
Db	5345	GTGTATCATGGGCTGAACGTGTGTCACTATGTGCATGTAGAGCACTACAGACGCCCA	5404
QY	1639	euaAspGlnAlaLeuIysIleCysAsnTyrIlePheThrValIlePheValPheGlnuSerV	1659
Db	5405	TGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGATCTTGTCTTGGAGTCA	5464
QY	1659	alPheIysLeuValAlaPheAlaPheArgArgPheGlnAspArgTyrAsnGlnLeuA	1679
Db	5465	TTTTCAACTTGTGGCTTGTGGTTTCCGTCCGCTTCTTCCAGAGACAGTGGAAACAGCTGG	5524
QY	1679	spLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGlnIleGluValAsnL	1699
Db	5525	ACGTGGCATTTGTGTGTGTCTTCATCATGGGCGATCACCGCTGAGAGAAATTCAGGTC	5584
QY	1699	eusErLeuProIleAsnProThrIleIleLeuArgIleMetArgValLeuArgIleAlaArgV	1719
Db	5585	CCTGCGTCCCATCAACCCACCAATCATCCGCAATCATGAGGGGTGTGGCATTTGCCCA	5644
QY	1719	alleuIysLeuLeuIysMetAlaValAlaGlyMetArgAlaLeuLeuHisIleThrValMetGlnA	1739
Db	5645	TGCTGAAGCTGTGAAGATGGCTGTGGGCAATCGGGCGCTCTGTGACACGGGTATGACGG	5704
QY	1739	IaleuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaA	1759

Db	5705	CCCGGCCCAAGTGGGGAACCTGGGACTCTCTTCATCTATTGTGTTTCACTTTGAC	5764
Qy	1759	laleuGlYvaGluluePheGlYAspLeuGlucYAspGlulThrhIAsProCysglulYl	1779
Db	5765	CTCGGGGGGTGGAGCTCTTTGGAGACCTGGAGTGTGAGACACACCCCTGTGAGGCC	5824
Qy	1779	euglYlArghIAlArThPheArghAspHeGlYMetAlArPheulThrLeuPheArghAlS	1799
Db	5825	TGGGCGCGTCATGAGCCACTTTTGGGAATTGGACATGGCCCTTCTTAACCTCTTCGAGTCT	5884
Qy	1799	eThrNgIYAspAsnThrAsnGlYlLeMeClyAspProSerArghAspGlnGluS	1819
Db	5885	CCACAGGGGAACAATTGGATGGACATTAGAAGAACCCCTCCGGGACTGTGATCAAGAGGT	5944
Qy	1819	eThrCysTYAsnThrValIlleSerProIleYrPheValSerPheValLeuThralag	1839
Db	5945	CCACTGCTGAACAACAGCGTCACTCGCTTAATCTACTTTGTGTCTCTGCTGACGGCC	6004
Qy	1839	lInPheValLeuValAsnValValIlleAlValleuMeClyHisleuGlulSerAsnL	1859
Db	6005	AGTTCGTCGTAGTCAACGTGGTGTATCGCCGTGTGATGAACACACTGGAGAGAGAACAA	6064
Qy	1859	YsGlulAlArYsGlulGlulAglulLeuGlulAglulLeuGlulLeuGlulMetYsThrLeuS	1879
Db	6065	AGGAGGGCCMAAGAGAGAGCCGACGTAGAGGCTGAGCTGAGACTGAGATGAAAGACCTTCA	6124
Qy	1879	eRProGlnProHIsSerProleuGlYSerProPheLeuTrpProGlYAlSluGlYAlA	1899
Db	6125	GCCCCCAAGCCCACTCGCACTGGGAGACCCCTTCTGTGGCTGTGGGTCCAGGGCCCCG	6184
Qy	1899	snsErThrAspSerProIYsPProGlYAlArProHIsThrThralHisIlleGlYAlAlas	1919
Db	6185	ACAGCGCCCGAAGCCCAAGCTGGGGCTGTGACCCAGCGGCCCAAGAGATGAGCT	6244
Qy	1919	eRGlYPheserleuGlulHisProthrmEtValProHIsProGlulGlulArProValProL	1939
Db	6245	CCCACTTTTCCCTGGAGACCCCAAGAGAGCCCAAGCCCAAGAGAGCTGCA-----	6297
Qy	1939	euglYrProAspLeuLeuThrValArghYsSerGlYValSerArghThrhIsSerleuProA	1959
Db	6298	--GGAACCAAGCTTACTGACTGTGGGAAAGTGTGGGGTGAAGCCAAAGCACTCTTGCCCA	6355
Qy	1959	snaPserTYrMetCysArghAsnGlYSerThralAgluArghSerleuGlYHisArghlYlT	1979
Db	6356	ATGACAGCTACATGTGTGGCATGGAGACACTGCCAGAGGGGCCCTGGGACACAGGGGCT	6415
Qy	1979	rpglYleuProIYsAlAglInsErGlYserIlleuSerValHisErGlInProAlAsPT	1999
Db	6416	GGGGGCTCCCAAAAGCTCAGTCAGAGCTCCGCTGTGCTTCAGTCTCCAGCAGACAGTA	6475
Qy	1999	hrSerCysIlleleuGlInleuProIYsAspValHisTYrleuLeuGlInProHIsGlYAlAr	2019
Db	6476	CCACTCATCTCTGACGCTTCCCAAAAGTGAACCTCATCTCTCTCAAGCCCAAGCCGCC	6535
Qy	2019	roThrTrpGlYAlAlleProIYsleuProProGlYArghSerProleuAlaglnArp	2039
Db	6536	CAACTGGGGGACCATCCCAAACTGCCCCACAGAGAGCGTCCCTTTGGCTCAGAGGC	6595
Qy	2039	roLeuArghArghlnAlAlAlleArghThrAspSerleuAspValGlnGlYleuGlYserA	2059
Db	6596	CACTCAGGCGCCAGAGCAATTAAGACTGACTCTTGGAGCTTCAGGATCTGGGGCAGCC	6655
Qy	2059	rgGlulAspLeuLeuSerGlulValSerGlYrProSerCysProleuThrhArghSerSerP	2079
Db	6656	GGGAAGACCTGCTGCAAGAGGTGATGGGGCTCCCGCCCTGGCCCGGGGCTCACTCTT	6715
Qy	2079	heTrpGlYglYserSerIlleGlnAlGlnGlnArghSerGlYlleglnSerYsValSerL	2099
Db	6716	TCTGGGGGCACTCAAGTACCCAGGACAGACGACTCCCGAGCCACAGCAAGATCTCCA	6775
Qy	2099	YshIsIlleArghleuProAlArProCysPProGlYleuGlulProSerTrpAlAlYsAspProp	2119

Db	6776	AGCAGCATGACCCCGCCAGCCCCCTTGCCAGAGCCAGAACCAACTGGGGAGAGGGCCCTC	6835
Qy	2119	rogiurhrargSerSerleuGluLeuAspThrgluSerTrpIleSerGlyAspLeuL	2139
Db	6836	CAGAGACCAAGAGCAGCTTAGAGTTGGACACGAGAGCTGAGCTGGATTTCAGAGAGACTCC	6895
Qy	2139	eu---ProSerSerGlnGluGluProleuPheProAlaAspLeuValGlyCysEtyrServ	2158
Db	6896	TGCCCCCTGGCGGCGAGAGAGAGCCCCCATCCCAAGGAGCTGAGAGAGTGTACAGCG	6955
Qy	2158	algiurThrgInserCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHis	2178
Db	6956	TGGAGGCCCAAGAGCTGCCAGAGCGCGGCTTACGTCCTGGCTGATGAGACAGAGAGACT	7015
Qy	2178	erilealaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerS	2198
Db	7016	CTATCGCGCGTACGCTGCTGGACAGCGGGCTCCCAACCCCACTGGGCGACAGACCCCTCTA	7075
Qy	2198	erLeuGlyGlyGlnProleuGlyGlyProGlySerArgProGlyGlyValLeuSerProp	2218
Db	7076	ACCTTGGGGGGGACACCTCTTGGGGGGGCGGAGAGCCGGCCAGAAAAAACTCAGCGCCG	7135
Qy	2218	rosertleSerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyV	2238
Db	7136	CTAGATATCACCATGACCCCCCGAGAGCCAGAGTCTCGGACCCCGCCACGCCCTTGTA	7195
Qy	2238	alCysLeuArgArgArgAlaProAlaSerAspSerIlyAspProSerValSerSerProL	2258
Db	7196	TCTGCTCTCGGAGGAGGGGCTCCGTCAGCGACCTCAAGAGATCCCTTGCCCTTGGCCCC	7255
Qy	2258	euAspSerThrAlaAlaSerProSerProIlyGlyAspThrLeuSerLeuSerGlyLeuS	2278
Db	7256	CTGACACAGATGGCTGCTCGCTCGCTCCCAAGAAAGATGTGCTGAGTCTCTCCGGTTTAT	7315
Qy	2278	erSerAspProThrAspMetAspPro	2286
Db	7316	CCTCTGACCCAGCAGACCTGGACCCC	7341
RESULT 9			
ID	AAx83481	AAx83481 standard; cDNA; 6750 BP.	
XX	AAx83481,		
AC	AAx83481,		
XX			
DT	07-DEC-1999	(first entry)	
XX			
DE	Human T-type voltage-gated Ca channel alpha-1-G (hcaV1a) cDNA.		
XX			
KW	Human; T-type voltage-gated calcium channel; membrane; pore; ion;		
KW	activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	W09923847-A1.		
XX			
PD	17-JUN-1999.		
XX			
PF	30-OCT-1998; 98WO-US023161.		
XX			
PR	05-DEC-1997; 97US-00985809.		
XX			
PA	(LOYO ) UNIV LOYOLA CHICAGO.		
XX			
PI	Perez-Reyes E, Cribbs LL;		
XX			
DR	WPI; 1999-394972/33.		
DR	P-PSDB; AAY14586.		
XX			
PT	New T-type voltage-gated calcium channels.		
XX			
PS	Disclosure; Page 31-40; 138pp; English.		
XX			
CC	This sequence represents the coding region for a human T-type voltage-		

CC gated calcium (Ca) channel alpha-1-G designated hCav1.1. Voltage gated  
CC channels are membrane bound glycosylated proteins formed of several  
CC subunits. The large alpha subunits form a pore in the membrane that is  
CC selective for a given ionic species. Each alpha subunit contains 4  
CC domains (I, II, III and IV) and each domain contains 6 putative  
CC transmembrane helical segments (SI-S6). T-type Ca channels are activated  
CC at a lower voltage than L- or N-type channels. Characteristics of T-type  
CC channels include short current time, slow activation kinetics near  
CC threshold, fast inactivation kinetics and slow tail current. The  
CC sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel  
CC genes from humans and rats. Each of the novel Ca-channels contains a  
CC putative IVS4 region comprising the amino acid sequence AAY14598. Cells  
CC expressing the T-type voltage-gated calcium channel proteins can be used  
CC to screen for drugs which affect calcium channels. Methods are also  
CC disclosed for treating a disease or disorder associated with a deficiency  
CC in a native T-type calcium channel nucleic acid, e.g. to treat  
CC cardiomyopathy, epilepsy, etc

SQ Sequence 6750 BP; 1290 A; 2170 C; 1984 G; 1306 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	6750
Score:	10970.00	Matches:	2111
Percent Similarity:	94.99%	Conservative:	32
Best Local Similarity:	93.57%	Mismatches:	105
Query Match:	91.20%	Indels:	8
DB:	2	Gaps:	4

US-09-611-257a-24 (1-2287) x AAX83481 (1-6750)

QY 34 TTPTHARGARGARGMGLUARGALAPROARGSERARGSPSERPROVALAASERARG 53  
DB 2 TGGACGAGAGGAGGATGAGCGCGCGCGAGAGTCCGGGACGCCGCCGAGCTTCATCC 61  
QY 54 SerserThThCyserProGlyPro-GlyAlaAlaGlyAla-GlySerThnGluVysAsp 73  
DB 62 GGCTCAACACCTGTGGGAGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 121  
QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyProAlaAlaAlaAlaAlaAlaP 93  
DB 122 CGGGGCGCGCGGACCTCGAGGGCGGAGGGGCTGCGTACCAGGGGGGGGGGGGGGGGG 181  
QY 93 hepTherYleuSerGlnaAspSerArgProArgSerTrpCyseAlaAlaGlnValVysAsp 113  
DB 182 TCTTCTACTTGAAGCCAGGACAGCGCGCGGAGCTGTGTCTCCACAGGCTCTGAACC 241  
QY 113 roThrPheGluArgValaSerMetLeuValIleleuLeuAlaValIleleuGlyMetP 133  
DB 242 CCGGTTTGAAGCCATCAGCATGTGTCTCTCACTGCGTGAACCTGGGCACTGT 301  
QY 133 hepArgProCyseGluAspIleAlaCyseAspSerGlnaArgCyseArgIleleuGlnAlaPheA 153  
DB 302 TCCGGGCGATCGCAGGACATCGCTGTGATCCCAAGGCGTCCGGATCTCGAGGCTTTGG 361  
QY 153 spaAspPheIlePheAlaPhePheAlaValaGluMetValValIleuMetValAlaAlaGlyT 173  
DB 362 ATGACTTCACTTCTTGTCTTCTTGTCCGTGAGATGTGTGAAGATGTGTGGCTTGGGCA 421  
QY 173 IepheGlyYslyCyseTyTrleuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193  
DB 422 TCTTTTGGGAAAAAGTGTACTGTGGAGACACTTGGAAACCGGCTTGACTTTTATGTGTA 481  
QY 193 IeAlaGlyMetLeuGluTyTrSerLeuAspLeuGlnaAsnValSerPheSerAlaValaArgT 213  
DB 482 TCGCAGGAGATGCTGGAGTACTCGCTGGAACCTGCAAGAACCTTCTAGCTGTGACAGA 541  
QY 213 hrValaArgValaLeuArgProLeuArgAlaIleAlaAlaArgValaProSerMetArgIleLeuV 233  
DB 542 CAGTCCGTGTGTGCGACCGCTCAGGGCCATTAACGGGGTGGCCACACATGCGCATCTTGG 601  
QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAlaValIleuLeuLeuCysePhePhy 253  
DB 602 TCACGTGTGTGTGATGATCGTCCCATGCTGGGCAACGTCTGTGCTGTCTCTTCTG 661

QY 253 alPhePheIlePheGlyIleValaGluValaGluLeuTrpAlaGlyLeuLeuArgAsnArgC 273  
DB 662 TCTTCTTATCTTGGCGATCTGTGGCGCTGTGAGCTGTGGGCGAGGGTGTGTGGAAACCAT 721  
QY 273 ySPheLeuProGluAsnPheSerLeuProLeuSerValaAspLeuGluProTyTrYArgInt 293  
DB 722 GCTTCTTACTGAGAAATTTACGCTCCCTCGAGGTGGACTGGAGGCGTATTAACAGA 781  
QY 293 hrGluAsnGluAspGluSerProPheIleCyseSerGlnProArgGluAsnGlyMetArgS 313  
DB 782 CAGAGACAGAGATGAGAGCCCTTCACTGTCTCCACAGCCAGCAGAGAACGGCAAGCCGT 841  
QY 313 erCyseArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCyseSerLeuA 333  
DB 842 CCGTCAAGAAAGGTGGCCAGCTGCGCGGGGAGCGGGGGGGGGGGGGGGGGGGGGGGGG 901  
QY 333 apTyTrGluThrTyraAspSerSerSerSerSerSerSerSerSerSerSerSerSerSer 353  
DB 902 ACTATGAGGCTTACAAAGCTTCCAGCAACACCTGTGTCACTGGAACCACTGACTACA 961  
QY 353 hrAsnCyseSerAlaGlyGluIleAsnProPheYsGlyAlaIleAsnDheAspAsnIleG 373  
DB 962 CCAACTGCTCAGCGGGGAGGACCAACCCCTTCAAGGGCGGCATCAACTTGAACAATGG 1021  
QY 373 IYTyraAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyTrValaAspIleMet 393  
DB 1022 GCTATGCTGTGATCCCATCTTCCAGTCACTCACTGAGAGGGCTGGGTGCAATCATGT 1081  
QY 393 yrPheValMetAspAlaHisSerPheTyraAspPheIleTyPheIleLeuLeuIleIleV 413  
DB 1082 ACTTGTGATGATCTCAATCTTCTTCAATTTATATCTTCACTTCTCTCATCATCG 1141  
QY 413 aIGlySerPhePheMetIleAsnLeuCyseValaValIleAlaThrnPheSerGluT 433  
DB 1142 TGGGCTCTTCTTCAATGATCAACTGTGCTGTGTGTATTCACAGCATCTCAGAGA 1201  
QY 433 hrYleGlnArgGluSerGlnLeuMetArgGluGlnArgValaArgPheLeuSerAsnAlaS 453  
DB 1202 CCAGACAGGGGAAAGCCAGCTGATGCGGAGACAGGTGTGGTCTCTGTCAACAGCCA 1261  
QY 453 erThrLeuAlaSerPheSerGluProGlySerCyseTyTrGluLeuLeuLeuTyTrLeuV 473  
DB 1262 GCACTCTGCTTACTTCTGTGAGCCCGGAGCTGTATGAGAGCTGTCTCAAGTACCTGG 1321  
QY 473 alTyTrIleLeuArgIysAlaAlaArgArgLeuAlaGlnValaSerArgAlaIleGlyVala 493  
DB 1322 TGTACATCTTGTGAAGGAGCCCGCAGGCTGTCAAGTCTCTCGGGCAGCAGGTGTGC 1381  
QY 493 rGAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513  
DB 1382 GGGTGGGCTGTCTCAGAGCCAGCAGCCCTTGGGGGGCCAGGAGACCCAGCCAGCAGCA 1441  
QY 513 erCyseThrArgSerHisArgArgLeuSerValHisIleValaValHisIleHisIleH 533  
DB 1442 GCTGCTCTGCTCCACCGCCCTTATCCCTTCAACACCTGTGTGACCAACCAACCAACC 1501  
QY 533 IeHisIleHisIleTyTrIleLeuGlyAsnGlyThrLeuArgValaProArgAlaSerProGluI 553  
DB 1502 ATCACCAACACACACACCTGGGCAATGGGAGCTCAGGGGCCCCCGGGGCAACCCGAGA 1561  
QY 553 IeGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573  
DB 1562 TCCAGGACAGGATGCCAATGGTCCCGCGGCTCATGTGTGCAACCTTGAAGCCCTGG 1621  
QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyTrHisIleAsp 593  
DB 1622 CCTCTCCGGGGGCCCTTGTGTGGGAGAGTCTGTGACAGCTTTCACATGCGGACT 1681  
QY 593 yHisIleuGluProValaArgCyseGlnAlaProProProArgCyseProSerGluAlaSerG 613  
DB 1682 GCCACTTAAGGCAAGTCCGCTGCGAGGGGCCCTCCAGGTCCTCCCATGTGAGGATCCG 1741

QY 613 lYArgThrValGlySerGlyLysValIYrProThrValHisThrSerProProProGluI 633  
Db 1742 GCGAGACTGTGGGACCGGGAGAGGTATCCACCGTGCACACGACCCCTCCACCGGAGA 1801  
QY 633 lLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThreLeuThrs 653  
Db 1802 CGCTAGAGGAGAAAGCACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTCACCA 1861  
QY 653 ePheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrTrpIleSerT 673  
Db 1862 GCTCAACAATCCACCCGGGCGCTACAGCTCCATGACACAAGCTGTGGAGACACAGAGTA 1921  
QY 673 hGlyValACysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693  
Db 1922 CAGGTCCTCCCAAGCTCTTTCAGATCTCCAGCCCTTTCCTTGAAGCAGACATGGAG 1981  
QY 693 lACysGlyProAspSerCysProTYrCysAlaArgThrGlyValAGlyGluProGluSerA 713  
Db 1982 CCGTGTGCTCCAGACAGCTGCCCTACTGTGCCGGGCGGAGGAGGTGAGCTCG 2041  
QY 713 lAspHisValMetProAspSerAspSerGluAlaValTYrGluPheThrGlnAspAlaG 733  
Db 2042 CCGACCGTGAATGCTTGACTGACAGACGAGGACAGTTTATGATGATTCACACAGATGCC 2101  
QY 733 lHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753  
Db 2102 AGCACAGCACTCCGGGACCCCCACAGC---CGCGGCAACGAGACCTCGGGCCCAAGTG 2158  
QY 753 lAGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773  
Db 2159 CAGAGCCCGAGCTGTGCTGGCGCTTCTGGAGGCTAATGTGACACCTTCCCAAAAGATTG 2218  
QY 773 aIAspSerLysThrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793  
Db 2219 TGGACGACAGACTTGTGGCCGGGAAATCATATGATGCCATCTGGTCAACACACTGAGA 2278  
QY 793 eGlyIleGluTYrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813  
Db 2279 TGGGACTGGAATACACAGACGAGCCGAGAGCTTACCAAGCCCTAGAAATCACCAACA 2338  
QY 813 lValAlaPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTYrGlyProP 833  
Db 2339 TCGTCTTCCACGAGCTCTTGCCCTGGAGATGCTCTGMAAGCTGTGTGATGTGCTCT 2398  
QY 833 hGlyTYrTrieLysAsnProTYrAsnIlePheAspGlyValIleValIleSerValT 853  
Db 2399 TTGGCTACACTCAAGAAATCCCTCAACATCTTGATGTGTCTATGTGGTCATCACCGTGT 2458  
QY 853 rPGLuileValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873  
Db 2459 GGGAGATCGTGGGCGACAGGGGGGGGGCGGTGTGGGTGTGGGACCTTCCGCGCTGATGC 2518  
QY 873 rGValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValIleLeuMetL 893  
Db 2519 GTGTGTGTAAGCTGGTGGCTTCTGCGCGGCTCAGAGGCGAGCTGTGGTGCATCAGA 2578  
QY 893 ySThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS 913  
Db 2579 ACAACATGACACAGTGGCCACTTCTGCATCTGTCTTATGTCTTTCATCTTCACTTCA 2638  
QY 913 eTrieLeuGluYMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933  
Db 2639 GGATCTGGGCAATGCATCTCTCGGTGCATTTGGCTCTGAGGGAGATGGGACACCC 2698  
QY 933 eUPrAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValIleThrValPheGlnIleL 953  
Db 2699 TCCCAAGACCGGAAGATTGTGACTCTTGCTCTGGGCGCATCTGCACTGCTTTCAGATCC 2758  
QY 953 eUTHrGlnGluAspTrpAsnLysValLeuTYrAsnGlyMetAlaSerThrIleSerSerTPA 973  
Db 2759 TACACCAAGAGGACGTGGAAACAAGTCTCTACAAAGGTATGGCTCCACAGTGTCTTGGG 2818  
QY 973 lAlaLeuTYrPheIleAlaLeuMetThrPheGlyAsnTYrValLeuPheAsnLeuLeuV 993

Db 2819 CGGCGCTTATTTATTCATGGCCCTCATGAACCTTCCGCAACTAGTGCTCTTCAATTGCTGG 2878  
QY 993 aAlaAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluP 1013  
Db 2879 TCGGCATTTCTGTGTGAAGGCTTCCAGGCGAGGAGATGCCAACAGTCCGAATCCAGAGC 2938  
QY 1013 rOAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuV 1033  
Db 2939 CCGATTTCTTTCACCCAGCTCGATGTATGGGAGACAGAAAGATGCTTGGCTTTGG 2998  
QY 1033 aAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuIleIleHisT 1053  
Db 2999 TGTCTCCGAGAGACACCGGAGCTCGGAAAGACCTGTGCTCCGCTCTCATCTCACCA 3058  
QY 1053 hAlaAlaIleThrProMetSerHisProLysSerSerSerThrGlyValGlyLysAlaLeuG 1073  
Db 3059 CGGCGCGCACACCCATGTGCTGCCCAAGACACACACCGGGGCTGGCGAGCGCTGG 3118  
QY 1073 lYSerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyValAlaHisHisG 1093  
Db 3119 GCCCTGCGTCCGCGCGACACAGACGAGGTGGCAGACCTGGGGCGGCG---CAGC 3175  
QY 1093 lUmetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAsers 1113  
Db 3176 AGATGAAGTCAACCGCCAGCGCCGACAGCTCTCCGACAGCCCTGGAGCGCTCAAGCA 3235  
QY 1113 eTTPThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA 1133  
Db 3236 GCTGACCAAGACGCGCTCCAGCGCGAAACAGCTCGGCGGACCCAGCCTTGAAGCGGA 3295  
QY 1133 rGSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnLysSerGlnAspG 1153  
Db 3296 GAAGCCCAAGTGAAGAGCGGCGGTCCCTGTGTGGAGAAAGGCCAAGAGGCCAAGATG 3355  
QY 1153 lUgluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG 1173  
Db 3356 AAGAGAGAGCTCAGAAAGAGAGAGCGGCGCCTCGCGGAGTGAACATGCCACAGAGG 3415  
QY 1173 lYSerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG 1193  
Db 3416 GGTCTCTGAGACGGGAGCGCAAGAGTTCTTTGACCTGGCACACACTGAGAGTGGCAG 3475  
QY 1193 lYLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL 1213  
Db 3476 GGCTGCATCGCACTGCCAGTGGCCGAGGATCTGCTTCTGAGACAACAGACTGCATGGCA 3535  
QY 1213 ySerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGluLeuAspGlyA 1233  
Db 3536 AGTCGGCTTTCAGGGCGCTGGCCCGGCGCTCGCGCTGATGACCCCCCACTGGATGGGG 3595  
QY 1233 sPAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaIleTrpAlaArgS 1253  
Db 3596 ATGACGCCGATGACAGAGGCAACTGAGCAAAAGGGGAAAGGGGTCCGGCGGTGATCCGAG 3655  
QY 1253 eTArgLeuProAlaCysGlyArgGlyLysArgAspSerTrpSerAlaTYrIlePheProProG 1273  
Db 3656 CCCGACTCCCGCTGTGCTGCTGAGGAGACTCTGTGTGACCTTATCATCTTCCCTCTTC 3715  
QY 1273 lUAspArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV 1293  
Db 3716 AGTCAGAGTTCCGCTCCTGTGTCAACCGATCATCACCCACMAAGTGTTCACACACGTTGG 3775  
QY 1293 aLLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspP 1313  
Db 3776 TCTTGTATATATCTTCTTACATGCATCACATGCGCATGAGACGGCCCAAAATGTGACC 3835  
QY 1313 rHisSerAlaGluArgIlePheLeuThrLeuSerAsnTYrIlePheThrAlaValPheL 1333  
Db 3836 CCCACAGGCTGAACGATCTTCTGACCTCTGACCTTCATTAATCTTACCGCAGATCTTTC 3895  
QY 1333 eUAlaGluMetThrValLysValAlaAlaLeuGlyTYrCysPheGlyGluGlnAlaTYrL 1353



Db	3886	TGCGTGAATAACAGCTGAAGGTGGTGGCAGCTGGGCTGGTCTTGGGGAGCAGCGCTAAC	3955
Qy	1353	euAArgSerSerTTPAsnValLeuaspGlyLeuLeuValLeuIleSerValIleAspIleL	1373
Db	3956	TGCGGAGCAGTTGGAAAGTGTGGACGGGCTGTTGGTGTCTATCTCCGTATCGACATTC	4015
Qy	1373	euValSerMetValSerAspSerGlyThrIysIleLeuGlyMetLeuArgValLeuArgL	1393
Db	4016	TGGTGTCATGTGTCTTGCACAGCGGCACCAAGATCTGGGGCATCTGAGGGTGTGGGC	4075
Qy	1393	euLeuArgThrLeuArgProLeuArgValIleSerArgLaGlnGlyLeuIlybLeuValV	1413
Qy	4076	TGCTGGGAGCCCTGGCGCCGCTCAGGGTGATCAGCGGGCCAGGGGCTGAAGCTGGTG	4135
Db	1413	aIGluThrLeuMetSerSerLeuIlybProIleGlyAsnIleValIleCybCybAap	1433
Db	4136	TGGAGAGCCTATGTCTCTACCTGAACCACCTGGCAACATTGTATGTATGTCTGTCTCT	4195
Qy	1433	hepHeIleIlePheGlyIleLeuGlyValGlnLeuPheIlybGlyLysPhePheValCybG	1453
Db	4196	TCTTCATCATTTTGGGCATCTTGGGGGGTGCAGCTCTTCAAGGGAGATTTTTCGTGGCC	4255
Qy	1453	IngIyGluAspThrArgAsnIleThrAnIlybSerAspCybAIGluAlaSerIlyArgT	1473
Db	4256	AGGGGAGAAATPCCAGGAACATCACCAATTAATGGATGTGGCCGAGGCCAGTTAACGGT	4315
Qy	1473	rPValArgHisIlyeTyzAsnPheAspLeuGlyGlnAlaLeuMetSerLeuPheValL	1493
Db	4316	GGGTCCGGCACAAGTACAACTTTGACAACTTTGGCAGGCCCTGTATGTCTCTGTTCGTT	4375
Qy	1493	euAlaSerLysAspGlyTTPValAspIleMetTyrAspGlyLeuAspAlaValGlyValA	1513
Db	4376	TGGCTCTCAAGATGTGTTGGGTGGCACAATGTACATGTACATGTGGCTGTGGCGCTGG	4435
Qy	1513	spGInGInProIleMetAsnHisAsnProTpmLeuLeuThrPheIleSerPheLeuL	1533
Db	4436	ACCAGACCCCATCTATGAAACCAACCCCTGAGATGCTGTACTTCACTCTGTTCTCGC	4495
Qy	1533	euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisL	1553
Db	4496	TCATTGTGGCTTCTTGTCTGTGAACATGTTTGTGGTGTGTGTGGAGAACTTCCACA	4555
Qy	1553	YbCybArgGlnHisGInGlnGlnGlnGluAlaArgArgArgGlnGluLysArgLeuArgA	1573
Db	4556	AGTGTCCGACAGCACGAGGAGAGAGAGAGGCCCGCGCGGAGAGAGAGAGCGCTACGAA	4615
Qy	1573	rGLeuGlnLysLysArgArgSerLysGlnLysGlnMetAlaGlnAlaGlnCybLysProT	1593
Db	4616	GACTCGAAGAAAAGAAAGGAGTAAAGGAGGAAGCATGTGTAAGCCCAAGTGCAAACCTT	4675
Qy	1593	YrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCybThrSerHisIyTrL	1613
Db	4676	ACTACTCCGACTACTCCCGCTTCCGGCTTCTGTCCACCACTTGTGCACCGCCACTTACC	4735
Qy	1613	euAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisT	1633
Db	4736	TGGACCTCTTATCATCAGATGTGCATCGGGCTGAAGCTGTGTCCATCATCGGCATGAGCACT	4795
Qy	1633	YrGlnGlnProGlnIleLeuAspGlnAlaLeuLysIleCybAsnTyrIlePheThrValI	1653
Db	4796	ACCAGACACCCCAAGATTCGTGATGAGGCTCTGAAATCTCGAACAATCTTCACTGCACA	4855
Qy	1653	IlePheValPheGlnSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnA	1673
Db	4856	TCTTTGTCTTGGAGTCAAGTTTCCAACCTTGAGCTTGTGGTTTCCGTGTGTTCTTCCAGG	4915
Qy	1673	spArgTTPAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuG	1693
Db	4916	ACAGGTGAAACACAGCTGAGCCTGGGCATTGTGTCTGTCTCATCATCATGAGGCATACGCTGG	4975
Qy	1693	IngIuIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgV	1713
Db	4976	AGGAATTCAGAGTCAACGCTGTGGTCCCATCAACCCACATCATCTCCGACATCATGAGGG	5035

QY	1713	allLeuArlglleAlaArgValleuLeuLeuLeuLeuLeuMetAlaValGlyMetArgAlaLeuL	1733
Db	5036	TGCTGGCGCATTTGCCCGAGTGTCTGAAGTCTCGAAGATGGCTGTGGGAGATGGGGCGCTGC	5095
QY	1733	euhLsthrValMetGlAlaleuProGlnValGlyAenLeuGlyLeuLeuPheMetLeuL	1753
Db	5096	TGGACACGGTATATCAGGCCCTTGCCCAAGTGGGGAACTGGAGACTTCTCTTCAATGTTGT	5155
QY	1753	euphePheIlePheAlaAlaleuGlyValGluLeuPheGlyValPheGluGlyCysApsGluL	1773
Db	5156	TGTTTTTCATCTTTGCAAGCTCTGGGCGCTGGAGCTCTTTTGGAGACTGGAGTGTACACAGA	5215
QY	1773	hrhLsProCysGluGlyLeuGlyVrohiIsaIthrPheArgAsnPheGlyWheAlaPheL	1793
Db	5216	CACACCCCTTGAGAGGGCTTGGGCGGTATGCACTTTCGGAACTTTGGCATGGCCCTTCC	5275
QY	1793	euthrLeuPheArgValSerThrGlyAspAsnTPaenglyIleMetLysApsProSerA	1813
Db	5276	TAACTCTTTCGAGTGTCCACAGGTGCAATTGGATGGCATATGAAAGGACACCTTCC	5335
QY	1813	rgAspCysApsGlnGlySerThrCysIlyrAenThrValIleSerProIleIyrPheValS	1833
Db	5336	GGGACTGTGACACAGAGATCCACCTGGTACACACAGGTCATCTCCCTATCTACTTTGTGT	5395
QY	1833	erPheValLeuThrAlaGlnPheValleuValAenValIleAlaValLeuMetLysH	1853
Db	5396	CTTTCTGTCTACCGGCCCACTTCTGTCTAGTCAACATGTGTATGTCGGCTGTATGAAGC	5455
QY	1853	IsleuGlnGlySerAsnLysGluAlaLysGlnGluAlaGluLeuGluAlaGluLeuGluL	1873
Db	5456	ACCTGGAGGAGACACACAGAGAGCCCAAGAGGGCGCGAGCTGAGAGCTGACGTGAGGC	5515
QY	1873	eugLmetLysThrLeuSerProGlnProhiIsasrProLeuGlySerProPheLeuTPP	1893
Db	5516	TGGAGATTAAGACCTTCAAGCCGCCAGGCCCACTGGCACTGGGAGACCCCTTCTTGGC	5575
QY	1893	roGlyValGluGlyValAsnSerThrApsSerProLysProGlyValaProhiIsThrThra	1913
Db	5576	CTGGGGTGAAGGGCCCGACAGCCCGACAGCCCAAGCTGGGGCTCTGCACACAGCGG	5635
QY	1913	lahIsIleGlyAlaAlaSerGlyPheSerLeuGluLuhIsProThMetValProhiIsProG	1933
Db	5636	CCCAAGCGAGATACAGCTCCACACTTTTCCCTGGAGACCCCAAGATGAGGCCCAACCCCA	5695
QY	1933	lughValProValProLeuGlyProApsLeuLeuThrValArgLysSerGlyValSera	1953
Db	5696	CGAGACTCCA-----GACCAAGACTTACTGACTGTGGAAAGTCTGGGGTCAAGCC	5746
QY	1953	rgThrHisSerLeuProAsnApsSerIyrMetCysArgAsnGlySerThralaGluArgS	1973
Db	5747	GAAACGCACTCTCTGCCCAATACAGCTACATGTGTGGCATGGAGGACACTCCGAGGGGC	5806
QY	1973	erLeuGlyHisArgGlyThrGlyLeuProLysAlaGlnSerGlySerIleLeuSerValH	1993
Db	5807	CCCTGGGACACAGGGGCTGGGGGGCTCCCAAGCTCAAGTCCGATCTTGTCCCTTC	5866
QY	1993	IsSerGlnProAlaApsThrSerCysIleLeuGlnLeuProLysApsValHisIyTrLeuL	2013
Db	5867	ACTCCACACGACAGATACAGTACATCTGCAAGCTTCCCAAGATGCACCTCATCTGC	5926
QY	2013	eugLInProhiGlyValaProThrThrProGlyAlaIleProLysLeuProProProGlyArgS	2033
Db	5927	TTCAGACCCCAAGCGCCCAACCTGGGGCACATCCCAAACTGCCCCACACAGGACCT	5986
QY	2033	erProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrApsSerLeuApsV	2053
Db	5987	CCCCCTTGGCTCAGAGGCCCACTCAGGCCCCAGGACAGCAATAGAGCTGACTCTTTGAGCG	6046
QY	2053	alGlnGlyLeuGlySerArgLuhApsLeuLeuSerGlyValaSerGlyProSerCysProL	2073
Db	6047	TTCAAGGCTCTGGGCGAGCCGGGAAGCTCTGTGTGTGACAGATAGTGTGGGCTCTCCGAGCC	6106

[illegible]

XX	New T-type voltage-gated calcium channels.
FX	
PS	Disclosure; Page 49-58; 138bp; English.
XX	
CC	This sequence represents the coding region for a human T-type voltage-
CC	-gated calcium (Ca) channel alpha-1-G designated hcaTTC. Voltage gated
CC	channels are membrane bound glycosylated proteins formed of several
CC	subunits. The large alpha subunits form a pore in the membrane that is
CC	selective for a given ionic species. Each alpha subunit contains 4
CC	domains (I, II, III and IV) and each domain contains 6 putative
CC	transmembrane helical segments (S1-S6). T-type Ca channels are activated
CC	at a lower voltage than L- or N-type channels. Characteristics of T-type
CC	channels include short current time, slow activation kinetics near
CC	threshold, fast inactivation kinetics and slow tail current. The
CC	sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel
CC	genes from humans and rats. Each of the novel Ca-channels contains a
CC	putative IVS4 region comprising the amino acid sequence AAAY4598. Cells
CC	expressing the T-type voltage-gated calcium channel proteins can be used
CC	to screen for drugs which affect calcium channels. Methods are also
CC	disclosed for treating a disease or disorder associated with a deficiency
CC	in a native T-type calcium channel nucleic acid, e.g. to treat
CC	cardiomyopathy, epilepsy, etc
XX	
SQ	Sequence 6804 BP; 1301 A; 2186 C; 1998 G; 1319 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	0 Length: 6804
Score:	10946.00 Matches: 2110
Percent Similarity:	94.208 Conservative: 32
Best Local Similarity:	92.798 Mismatches: 106
Query Match:	91.004 Indels: 26
DB:	Gaps: 5
US-09-611-257A-24 (1-22887) x AAX83483 (1-6804)	
OY	34 TTPTThArGArGArGmEtGlUArGAlAPrOArGSerAGApSPPrOVAlAlASerArg 53
Db	2 TGACACAGAGAGGAGGTGGAGCGGGCGCCGAGAGATCGGACACGCCCGAGCTTCATGC 61
OY	54 SeSeSerThThCyAprOGlYPro-GlYAlAlAgLYla-GlySerThGlUnYAspp 73
Db	62 GGCTCAACAACACTGTCGGGGGGCGGGGGGGCGCCGGCGGGCTCAGCAAAAGAAC 121
OY	73 roGLySerAlaapSerGlualagLugLyLeuProTYrProlleuAlaProValalp 93
Db	122 CGGAGCACCGGAGACTCCGAGCGGAGGGAGTGCCGTACCCGGCCCTGGCCCTGGTTT 181
OY	93 heheHYrleuSerGlnaPserAGPrOArGSerTPCYLeuARThThrVAlCYAsnp 113
Db	182 TCYTCTACTTAGCCAGCAAGCACGCCGCCGAGAGCTGATGCTTCGACGGTCTGTACC 241
OY	113 roTrPheglunArgValSerMeLleuValIlleLeuLeuAsnCYeValThrlenuYmeCP 133
Db	242 CCGATTGAGGGCATCAGCATGTTGGTCATCTCTCAATCGGTGAACCTGGGCAATGT 301
OY	133 hearGProCYegLusaplIleaLaCYasappSerGlnarGYArGIlleuGlInalAhea 153
Db	302 TCGGAGCAATGAGGAGCATCGCTGTGATCCCAAGCCGTGCGGATCTTGAGGGCTTTTG 361
OY	153 spAspPheIIePheAlaPhePheAlaValAGImetValIVallyMeCVAlAlaleuGlyI 173
Db	362 ATGACTTCACTTTTGCTTTTGGCTTTTGGCCGTGGAGAAGTGCTGAATGGTGGCCCTTGGCA 421
OY	173 IePheGILyIsLyScYsFYrLeuGILyAspThrTTPaenArgLeuAspPheheIIeValI 193
Db	422 TCTTTGGGAAAAAGGTTAACCTGGGAGACACTTGGAAACGGGCTTGAATTTTTCACTGCA 481
OY	193 IeAlaLIymetLeuGILyTySerleuAsplauGlnanValSerPhSerAlaValalnrt 213
Db	482 TCGAGAGAGAGTGGAGATCTGCTGGACCTGGCAAGAGTGAAGTCTTCAAGCTGTCAAGA 541
OY	213 hrValnrgValleuARGPrOleuARgalAlleAsnArgValProSerMetArgIIleuV 233

[illegible]

Db	1622	CCCTCTCCGGGGCCCCCCTGTGTGGCGAAGTGTGGACAGCTTCTACATCCGACT	1681
QY	593	YSHISLEUGLIPROVALARGYSGLNALAPROPOPOARGYSPROSERGLUALSERG	613
Db	1682	GCCACTTAGAACCCAGTCCGCTGTCCAGGCGCCCCCTCCAGGTCCCACTGAGGACATCCG	1741
QY	613	LYAAGTHVALGLYSERGLYVSTALYRPROTHVALHISTHSEPROPROGLUI	633
Db	1742	GCAGAGCTGTGGGAGCGGGAAAGGTATATCCACCGGTGCACACAGCCCTTCCACGGAGA	1801
QY	633	LELEULYASPLYSALALEUVALGLUVALAPROSERPROGLYPROPROTHRLEUTHRS	653
Db	1802	CGCTGAGAGAAAGCACTAGTATAGAGTGGCTGGCAGCTCTGGGCCCCCAACCTCACCA	1861
QY	653	ERPHEASMLIAPROPROGLYPROPHESERSESMETHLYSLYLEUENGLUHTGINSERT	673
Db	1862	GCCTCAACATCCCAACCGGGGCCCTACAGCTTCCAGTGCACAAAGCTCTGGAGACAGAGTA	1921
QY	673	HRGLYALACYHHISSESERCYSLYSLISESERPROCYSESERLYALASPSERGLYA	693
Db	1922	CAGGCGCTTGCCAAAGCTTTGCAAGATCTTCACGCCCTTGTAAGAAGCACAGTGGAG	1981
QY	693	IACYSGLYPROASPSERCYSPROTYRCYSAIAATGTHGLYALGLYGLUPROGLUSERA	713
Db	1982	CCTGTGTGCCAGACAGCTGCCCTTACTGTGCCGGGCGGGGAGGGAGGTGGAGCTCG	2041
QY	713	IASPHEISVALMECPROASPSERSASPSERGUINALVALTYRGLUPHETHGLINAPALAG	733
Db	2042	CCGACCGTGAAATGCTGACTCAGACAGCGAGGAGATTATGAGTTGCACACAGATGCC	2101
QY	733	INHISSEASPLUARGASPPROHISSEERAGTAGTAGGLINARGSERLEUENLYPROASPA	753
Db	2102	AGCACAGAGCACTCCGGGACCCCAACAGC---CGCGGCAACGAGAGCTTGAGCCACAGT	2158
QY	753	IAGLUPROSESERVALLEUALPHETPRARGLEULIECYASPETHRPHETARGYSLIEV	773
Db	2159	CAGAGCCAGCTCTGTGCTGGCTTCTTGAGAGCTATCTGACACCTTCGGAAGAATGG	2218
QY	773	ALASPSELYTYRPHETGLYARGGLYIEMETLEALILEUENVALASNTHRLEUSERM	793
Db	2219	TGGACAGCAAGTACTTTGGCCGGGGAAATCATGATCGCCACTCTGGTCAACACACTCAGCA	2278
QY	793	ETGLYILEGLUTYRHISGLUGLINPROGLUGLULEUTHRANHALALEUGLUILESERASNI	813
Db	2279	TGGCGATGGAATACCAACAGCAGCGCCGAGGAGCTTACCAAGCCCTTAAATAATCAGCAACA	2338
QY	813	LEVALPHETHSERLEUPHEALALEUGLUMETLEULEULYSELEUENVALTYRGLYPROP	833
Db	2339	TGCTTTTACCAAGCTCTTTGGCCCTGGAGAGCTGCTGACGCTGTTGTATGTCCCT	2398
QY	833	HEGLITYRILEYASAPPROTYRANILPHEASPGLYVALILEVALIIIESERVALT	853
Db	2399	TTGGCTACATCAAGATCCCTTCAACAACATCTTCAGAGGTGATGTTGGTCAATCAGCGT	2458
QY	853	TPGLUIILEVALIGLYGLINGLNGLYGLYILEUSERVALLEUARGTHRPHETARGLEUMETA	873
Db	2459	GGGAGATCGTGGGCGACGAGGGGGCGCGCTGTGCTGCTCGTCCGACCTTCGCGCTGATGC	2518
QY	873	RGVALILEULYSEUVALARPHLEUPROALALEUGLINARGLNULEUVALILEUMETL	893
Db	2519	GTGTGCTGAAGTGTGTGGCTTCCCTGGCGGCGCTGCACAGGCGAGCTGTGTGCTCATGA	2578
QY	893	YETHMETASPAANVALATHRPHETCYSMETLEULEUMETLEUPHEIIPHEIIPHESES	913
Db	2579	AGACCATGGAACAACCTGGCACACCTTCTGCATGCTGCTTATGCTTTCATCTTCATCTTCA	2638
QY	913	ETILEUENGLYMETHISLEUPHEGLYCYSLYSPHEALASERGLUARGASPGLYASPTHRL	933
Db	2639	GCATCTCTGGGCAATGATCTCTTCCGCTGCAAGTTTGGCTCTGAGGGGATGGGACACCC	2698
QY	933	EUPROASPARGLYASAPNHEASPSERLEULEUTPRALILEVALIETHRALPHEGLINILEU	953
Db	2699	TGCCACAGCCGGAAGATTTTGACTCTTGCTGTGGCCATGTGCATCTCTTTCAAGATCC	2758



Db 4916 TTTGGAGTCACTGTTCAACACTGTGGCTTGGCTTCCGTCGCTTCTTCCAGACAGGT 4975  
 1675 rPaSnglInleuAspleuAlaIleValleuLeuSerlleMeGlylleThrLeuGluIu 1695  
 4976 GGAACAGGTGAGCTGGCATTTGCTGCTGCTGCATCATATGGGCATCAAGCTGGAGGAA 5035  
 1695 lAgIuValleuLeuSerlleuProIleAsnProThrIlelleArglleMeAlaGValleu 1715  
 5036 TCGAGGTCAACGCTCGCTGCCATCAACCCACCATTCATCCGCATCAAGAGGGTGTGC 5095  
 1715 KIIlAlaIArgValleuLeuLeuLeuMeAlaValleuLeuArgAlaIleuLeuHleT 1735  
 5096 GCAATGCGCGAGGTGAGAGCTGCTGAAGATGCTGTGGCATGCGGGGCTGTGGACA 5155  
 1735 hValMeGlnAlaIleuProGlnValGlyAsnLeuGlyleuLeuPheMeCtleuLeuPhe 1755  
 5156 CGGTGATGAGAGCCCTGCCAGTGGGAACTTGGACTTCTTTCATGTTGTGTTTT 5215  
 1755 heIlePheAlaIleuGlyValGluLeuPheGlyAspleuGluCyAspGluThrHisP 1775  
 5216 TCATCTTTCACACTCTGGCGCTGGAGCTCTTGGAGACCTGGAGTGTGACGAGACACCC 5275  
 1775 rCCyGluGluIuLeuGlyArgHisAlaThrPheArgAsnPhelGlyMeAlaPheLeuThr 1795  
 5276 CCGTGAAGGGCTGGGCGCTGCATGCGACCTTTCGAACTTTCGATGGCTTCTTACCC 5335  
 1795 euPheArgValSerThrGlyAspAsnTrpAsnGlylleMeClyAspProSerArgAsp 1815  
 5336 TCTTCGCAATCTCCACAGGTGACAAATTGGAATGGCATTTGAAGGACACCTCCGGAGT 5395  
 1815 yAspGlnGluSerThrCysTyraSerThrValIleSerProIleTyPheValSerPheV 1835  
 5396 GTGACAGAGGTCCACTGCTCAACACAGGTCACTCGGCTATCTTGTGTCTCTTGG 5455  
 1835 AlIleuThrAlaGlnPheValleuValAsnValValIleAlaValleuMeClyHisleuG 1855  
 5456 TCGTAGCGGCGCCAGTTCGTAGTCAAGTGTGTATCGCGGTGATGAAGACACTGG 5515  
 1855 lGluSerAsnIuysGluAlaIysGluGluAlaGluIuLeuGluAlaGluLeuGluIuM 1875  
 5516 AGGAGAGCAACAGAGGCGCCAGAGAGGCGAGGTAGAGGTAGAGTGGAGCTGGAGA 5575  
 1875 eEllySerThrLeuSerProGlnProHisSerProIuGlySerProPheLeuTrpProGlyV 1895  
 5576 TGAAGACCTCCAGCCCCCAGCCCCCACTCGCACTGGGAGCCCTTCTGTGGCTGGGG 5635  
 1895 AlGluGlyValAsnSerThrAspSerProIyProGlyValaProHisThrThrAlaHisI 1915  
 5636 TCGAGGGGCGCCGACAGCCCCGAGCCGAGGCTGGGGCTTGACCCAGCGGGCCGACG 5695  
 1915 lAGlyAlaIAserGlyPheSerLeuGluHisIAspProThrMeCValProHisProGluGluV 1935  
 5696 CGAGATCAAGCTTCCACTTTTCCCTGAGACCCCAAGATGACAGCCCCCAGCCGAGAC 5755  
 1935 AlProValProIuGlyProAspLeuLeuThrValaIArgIySerGlyValaSerArgThrN 1955  
 5756 TGGCA-----GGACCAAGACTTACTGACTGTGGGAAGTGTGGGGTCAAGCCGAAAGC 5806  
 1955 lAspLeuProAsnAspSerTyTrpMetCysArgAsnGlySerThrAlaGluAspSerLeuG 1975  
 5807 ACTCTCTGCCAATGACAGTACATGTGTGCGGAGAGACATGTGCGAGGGGCCCTTGG 5866  
 1975 lYHisArgGlyTrpGlyLeuProIyAlaGlnSerGlySerIleLeuSerValHisSerG 1995  
 5867 GACACAGGGGCTGGGGCTCCCAAAGCTCAAGGCTTCGCTTGTCTTCCATTCC 5926  
 1995 lAspThrAspThrSerCysIleLeuGlnLeuProIyAspValHisTyTrpLeuLeuGlnP 2015  
 5927 AGCCACAGATACACAGTACATCTGCAAGTTCGCAAAAGATGACCTCACTTGTCCAGC 5986  
 2015 rOhIAGlyAlaProThrTrpGlyAlaIleProIyLeuProProGlyAspSerProI 2035

Db 5987 CCCACAGGCGCCCAACTGGGGACACATCCCAAACTGCCCCACAGACGCTCCCTT 6046  
 2035 euAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerleuAspValGlnG 2055  
 6047 TGGCTCAAGAGGCACTCAGGGCGCCAGGACGAAATAGGACATGACTCTTGGACGTTCAAG 6106  
 2055 lYleuGlySerArgGluAspleuLeuSerGluValaSerGlyProSerCysProleuThrA 2075  
 6107 GTTGGGACCGGGAGAACCTTGCTGGCAGAGTGAAGTGGGCTTCCCGCCCTGGGCC 6166  
 2075 rGSerSerPheTrpGlyGlySerSerlleGlnValGlnIArgSerGlylleGlnS 2095  
 6167 GGGCTACTCTTCTTGGGGCCAGTCAAGTACCCAGGACAGAGACTCCCGACAGCCACA 6226  
 2095 eTyAsValSerIyHisIleArgLeuProAlaProCyAspProGlyIuLeuGluProSerTrpA 2115  
 6227 GCMAATCTCCAGACATGACCCCGCCAGGCGCTTGGCCAGGCGCCAGAACCAACTGGG 6286  
 2115 lAlYAspProGluThrArgSerSerleuGluLeuAspThrGluLeuSerTrpIleS 2135  
 6287 GCMAAGGCGCTCCAGAGACAGAGACAGCTTGAAGTGAAGAGAGCTGAGCTGGAATTT 6346  
 2135 eRGIYAspleuLeu---ProSerSerGlnGluGluProleuPheProArgAspleuTyL 2154  
 6347 CAGAGACTCTCTGCGCCCTGGCGGCGCAGAGAGAGCCCAATCCCAAGGAGCTGAAGA 6406  
 2154 ySCTySerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluG 2174  
 6407 AGTGCTACAGCTGAGAGGCGCCAGAGCTCCAGCGCGGCTCACTGCTGGCTGAGTAGGC 6466  
 2174 lNArgArgHisSerlleAlaValSerCysleuAspSerGlySerGlnProArgLeuCyP 2194  
 6467 AGAGGAGACACTTATCCCGTCACTGCTGGAGACAGGGCTCCCAACCCCACTGGGCA 6526  
 2194 rOserProSerSerleuGlyGlnProleuGlyGlyProGlySerArgProIyTyL 2214  
 6527 CAGACCCCTCTTAACCTTGGGGGCGAGCCCTTGGGGGGCGCTGGAGCGCGCCAGAA 6586  
 2214 yLeuSerProProSerlleSerlleAspProProGluSerGlnGlySerArgProProC 2234  
 6587 AACTCAGCGCGCTGTATACACATAGACCCCCCGAGAGCCMAAGTCTTCGAGCCCCG 6646  
 2234 ySerProGlyValIuysleuArgArgAlaProAlaSerAspSerIyAspProSerV 2254  
 6647 CCAGCCCTGTATGTGCTCTCGAGAGAGGCTCGTCAAGCATTCGAAAGATCCCTTGG 6706  
 2254 AlSerSerProleuAspSerThrAlaIAserProSerProIySerAspThrLeuSerL 2274  
 6707 CCTTGGGCGCCCTTAACAGCATGGCTGCTGCCCTCCCAAAGAAAGATGTGCTGAGTC 6766  
 2274 euSerGlyLeuSerSerAspProThrAspMetAspPro 2286  
 6767 TCTCCGGTTTATCTCTGACCCAGCAGACCTGAGACCC 6804  
 RESULT 11  
 AAX83482  
 ID AAX83482 standard; cDNA; 6783 BP.  
 AC AAX83482;  
 DT 07-DEC-1999 (first entry)  
 XX XX  
 DE Human T-type voltage-gated Ca channel alpha-1-G (hCavT1b) cDNA.  
 XX XX  
 KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
 XX XX  
 OS Homo sapiens.  
 OS OS  
 PN WO9929847-A1.  
 XX XX  
 PD 17-JUN-1999.  
 XX XX

PF 30-OCT-1998; 98WO-US023161.  
XX 05-DEC-1997; 97US-00985809.  
XX (LOYO ) UNIV LOYOLA CHICAGO.  
PA  
XX Perez-Reyes E, Cribbs LL;  
XX MPI: 1999-394972/33.  
DR P-PSDB; AAY14587.  
XX  
XX New T-type voltage-gated calcium channels.  
XX  
XX Discloure; Page 40-49; 138pp; English.  
XX  
XX This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1G designated hcaV1b. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (SI-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14596. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

50 Sequence 6783 BP; 1294 A; 2182 C; 1990 G; 1317 T; 0 U; 0 Other;

Alignment Scores:

Score: 0 Length: 6783  
Pred. No.: 10923.50 Matches: 2105  
Percent Similarity: 94.31% Conservative: 33  
Best Local Similarity: 92.85% Mismatches: 110  
Query Match: 90.82% Indels: 19  
DB: 2 Gaps: 5

US-09-611-257a-24 (1-2287) x AAX83482 (1-6783)

QY 34 TTPHrAaGaRgAXMeGluARgAlaProARgSerAgaSPSerProValAlaSerArg 53  
DB 2 TGGACGAGGAGGAGATGGAGCGGGCGCGGAGAGTCCGGACAGCCCGAGCTTCATGC 61  
QY 54 SerSerThrThrCysProGluPro-GlyAlaAlaGluAla-GlySerThrGluLysAspP 73  
DB 62 GGCTAACGACCTGCGGGGGCGGGGGGGCGGGGGCGGGGGGTACACAGAAAGAGACC 121  
QY 73 roGlySerAlaaspSerGluAlaGluGlyLeuProTyProAlaLeuAlaProValAlaP 93  
DB 122 CGGGAGCGCGGAGCTCCAGGGGAGGGGCTGCCCTTACCCTGGCCCGGCGTTT 181  
QY 93 hepHeTyLeuSerGlnaSPSerArgProARgSerTyProCysLeuARgThrValCysaSP 113  
DB 182 TCTTCTACTTGAAGCAGGACAGCCCGCGGAGCTGGGTCTCCGACAGGTCTTAACC 241  
QY 113 roTPHrPhGluARgAlaSerMetLeuValIleLeuLeuAsnCysValIleLeuGlyMetP 133  
DB 242 CCTGGTTTGAAGGCAATCAGCATGTTGGTATCTTCTCAACTGCTGAACCTGGGCAATGT 301  
QY 133 hepARProCysGluAspIleAlaCysaSPSerGlnARgCysARgIleLeuGlnAlaPhea 153  
DB 302 TCCGGCCAAATGGAGGACATCGCTGTGACTCCCAAGCGGTGGGATCCGTGACGGCTTTG 361  
QY 153 sPAsPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173  
DB 362 ATGACTTCATCTTTGCTTTTGGCGTGAAGATGGTGAAGATGGTGGGCTTTGGGCA 421

QY 173 lPheGlyLysCysEtyrLeuGlyAspThrTrpAenARgLeuAspPheHeIleValI 193  
DB 422 TCTTTGGGAAAAATGTTTACTGGGAGACACTTGGAAACGGCTTGTATCTTCAATCGTCA 481  
QY 193 leaAGlyMetLeuGluTySerLeuAspLeuGlnaenValSerPheSerAlaValArgT 213  
DB 482 TCGCAGGAGATCTGGAGTACTCGCTGACCTCGAGAACGTCAGCTTCAAGTTCAGAGA 541  
QY 213 hrValARgValLeuARgProLeuARgAlaIleAenARgValProSerMetARgIleLeuV 233  
DB 542 CAGTCCGTGTCTGACCGCTCAGGGCCATTAAACCGAGTCCAGCATGCGCATCTTG 601  
QY 233 aLThrLeuLeuLeuAspThrLeuProMetLeuGlyAenValIleLeuLeuCysaPhePheV 253  
DB 602 TCACTGTCTCTGATGATACGCTGCGCCATGCTGGGCAACGTCCTGCTCTTCTTTCG 661  
QY 253 aPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuARgAsnARgC 273  
DB 662 TCTTCTTCATCTTCGGCATCGTGGCGTCCAGCTGTGGGACGGCTCTTCGAAACCGAT 721  
QY 273 ySPheLeuProGluAsnPheserLeuProLeuSerValaSPLeuGluProTyTrpGlnT 293  
DB 722 GCTTCTTAACTGAGAAATTTACGCTCCCGGACCGTGAAGCTGAGCGCTATTACAGA 781  
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProARgGluAsnGlyMetARgs 313  
DB 782 CAGGAAACGAGAGATGAGAGCCCTTCACTGCTCCAGCCAGCGGAAACCGCATGCGGT 841  
QY 313 eTyARgSerValProThrLeuARgGlyGlyGlyGlyGlyGlyProProCysSerLeuA 333  
DB 842 CCTCAGAAAGGTGCCACGCTGCGGGGACGGGGCGGGGCGGCCACCTTGGCGGTCTTG 901  
QY 333 sPyTyrgluThrTyraSPSerSerSerSerSerSerSerSerSerSerSerSerSerSer 353  
DB 902 ACTATGAGGCTTACAAACAGCTCCAGCAACACACTGTGTCACTGAGAACCAAGTACTACA 961  
QY 353 hrAenCysSerAlaGlyGlyIleAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373  
DB 962 CCAACTGCTGCGGGGGGAGACAAACCTTTCAAGGGCGGCATCAACTTTCAGAAACATTTG 1021  
QY 373 lTyTyraIleTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyTrpValaSPleMet 393  
DB 1022 GCTATGCTGGATGCGCATCTTCCAGGTATCAAGCTGAGGGCGGTGGCTTCACATCATGT 1081  
QY 393 yrPheValMetAspAlaHisSerPheTyraSPheIleTyrrPheIleLeuLeuIleIleV 413  
DB 1082 ACTTGTGATGATGCTCATCTCTTCTTCAATTTCACTTCACTTCACTCTCTCATCATCG 1141  
QY 413 aAGlySerPhePheMetIleAsnLeuCysLeuValIleAlaIleThrGlnPheSerGluT 433  
DB 1142 TGGGCTCTTCTTATGATATCACTGACCTGTGCTGTGTGATGGACCAAGTTCACAGAGA 1201  
QY 433 hrLysGlnARgGluSerGlnLeuMetARgGluGlnARgValARgPheLeuSerAsnAlaS 453  
DB 1202 CCAAGCAGCGGGAAGCAGAGCTGATGCGGAGCAGCGTGTGGCTTCTGTCACCAACCCA 1261  
QY 453 eThrTrleuAlaSerPheSerGluProGlySerCysTyrgluGluLeuLeuLysTyrrLeuV 473  
DB 1262 GCACCTGGCTAAGCTTCTCTAAGCCCGGACGCTCTATGAGAACTGCTCAAGTAACTGG 1321  
QY 473 aLTyrrIleLeuARgAlaAlaIleARgARgLeuAlaGlnAlaIleSerARgAlaIleGlyAla 493  
DB 1322 TGTACATCTTCTGTAAGGACCCGAGCTGCTCAGGTCTCTCGGGACAGAGTGTGTC 1381  
QY 493 rGlaAGlyLeuLeuSerSerProValAlaARgSerGlyGlnGluProGlnProSerGlyS 513  
DB 1382 GGGTTGGGCTGTCAAGAGCCAGCAACCCCTCGGGGGCCAGGAACCCAGCCGACGCA 1441  
QY 513 eTyTrThrARgSerHisARgARgLeuSerValHisIleLeuValHisHisHisHisHis 533  
DB 1442 GCTGCTCTGCTCCACCGCGCTATTCCTGTCACACACTGTGTGACACACACACACACC 1501





Db 3656 CCCGACCTCCCTGCTGCTGCTCGACGAGACACTCTGGTCAGCTTACATCTTCCCTCTC 3715  
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Db 3716 AGTCAGAGGTTCCGCTCCCTGTCACCGGATCATACCCAGAAAGTTCGACACGTCGG 3775  
Qy 1293 alLeuVal1le1lePheLeuAuCysh1leThr1lealameG1uArghProly1leAsp 1313  
Db 3776 TCCTGTATCATCTTCTTCTTAATCATCATCATGCGCATGAGGCGCCCAAAATTGAC 3835  
Qy 1313 roH1seSer1aG1uArG1lePheLeuThrLeuSerAsnTr1lePheThralaValPheL 1333  
Db 3836 CCCAGAGCGCTGAAGCAATCTTCTCGACCTCTCCAAATTACATCTTCAACCGGAGCTTTTC 3895  
Qy 1333 euAlaG1uMeThrThrallysVal1aleuG1yTrpCyshPheG1yG1uG1na1aTyrl 1353  
Db 3896 TGGCTGAATGACATGTGAAGGTCGTGACCTGGGCTGGTCCTCGGAGACGCGTCACC 3955  
Qy 1353 euArGSeSerTrpAsnVal1leuAspG1yLeuLeuVal1leu1leSeVal1leap1leL 1373  
Db 3956 TCCGAGAGAGTTGGAACGTGCTGGAAGGCTGTGTGTCATCTCCGTCAATCGACATTC 4015  
Qy 1373 euVal1seTMeVal1seArSpSerG1yThrLys1leuG1yMeLeuArGVal1leuArGL 1393  
Db 4016 TGGTGTCCATGTCCTCTGACACCGGACCAAGATCTGGGCATGCTGAGGGTCGCGGC 4075  
Qy 1393 euLeuArGThrLeuArghProleuArGVal1leSeArG1aG1uG1yLeuLysLeuVal 1413  
Db 4076 TCCTGGAGACCTCGGACCGGCTGACGAGGTATGACCGGGCGAGGGCTGAAAGCTGGTGG 4135  
Qy 1413 alG1uThrLeuMeSeSerLeuLysPro1leG1yAsn1leVal1leCyCyAs1aP 1433  
Db 4136 TGGAGACGTGTATGTCTCTACGAAACCATGCGAACATTTGATCATCTGCTGTGCT 4195  
Qy 1433 hepHe1le1lePheG1yleuG1yVal1G1uLeuPheLysG1yLysPhePheVal 1453  
Db 4196 TCTTATCATCTTTCCGACATCTTGGGGGTGCAGCTTTCAAAGGGAAGTTCGTGTGCC 4255  
Qy 1453 1nG1yG1uAspThrArghAsn1leThrAsnLysSeArSpCysh1aG1u1aSeTrYrArGT 1473  
Db 4256 AGGGGAGAGATCCAGGAACATCACAAATAATGGAATGTCGAGGCGAGTTACCGGT 4315  
Qy 1473 TrpValArGHis1y1sTyArSpPheAsnLeuG1yG1na1aleuMeSeSerLeuPheVal 1493  
Db 4316 GGGTCGGGACAAAGTACAATTGACAACCTTGGCACGGCCCTGATGTCCGTTCGTTT 4375  
Qy 1493 euAl1seSerLysAspG1yTrpVal1aSp1leMeTrYrAspG1yLeuAspAlaVal1aG1yVala 1513  
Db 4376 TGGCTCTCCAAAGATGTTGGGTGACATCATGTACATGGGTGATGCTGTGGCGCTGG 4435  
Qy 1513 spG1uG1uPro1leMeArasn1saSnProTrpMeLeuLeuThrPhe1leSePheLauL 1533  
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Qy 1553 yScYArG1uH1sG1uG1uG1uG1uAlaArGArGArG1uG1uLysArG1eLeuArGa 1573  
Db 4556 AGTGTCCGACGACCAAGAGAGAGAGGCGCGCGGAGGAGAGAAAGCCCTACACAA 4615  
Qy 1573 rGLeuG1uLysLysArGArG-----SeTrLysG 1582  
Db 4616 GACTGGAGAAAGAGAGAAATCTAATGCTGACGATGTAATTCCTTCGCGACCTGAG 4675  
Qy 1582 1uLyG1uMeAlaG1u1aG1uCyLysProTyTrYSeArSpTrYSeArGPhearGL 1602  
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Db 4736 TCCTGTGTCACCACTTGTGACCAAGCCACTGGAACCTTTCATCAACAGGTGTCAATCG 4795

Qy 1622 1yLeuAsnVal1a1ThrMeAlaMeG1uH1sTyTrG1uG1uProG1u1leuAspG1uA 1642  
Db 4796 GGTGAACGTGTATCAATGAGCATGAGCATGAGCATGAGCACTGACAGACCCCAATTCGATGAG 4855  
Qy 1642 1aleuLys1leCyAsnTr1lePheThrVal1lePheVal1PheG1uSerVal1PheLysL 1662  
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Qy 1682 1eVal1leuSeSer1ameG1y1leThrLeuG1uG1u1leG1uVal1AsnLeuSeSerLeup 1702  
Db 4976 TTTGTCTGTCTCATCATGAGGCATCAAGCTGAGAGAAATGAGTCAACCCCTCGCTGC 5035  
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Qy 1742 1nVal1G1yAsnLeuG1yLeuLeuPheMeLeuLeuPheAla1aleuG1yV 1762  
Db 5156 AGTGGGGAACCTGGACCTTCTTCAATGTTGTTTTCATCTTTGACAGCTTGCGGC 5215  
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Qy 1782 1sa1aThrPheArghAsnPheG1yMeAlaPheLeuThrLeuPheArGVal1SeThrG1yA 1802  
Db 5276 ATGCACCTTTCGGAACCTTGGACATGACCTTTCACCTTTCGAGTCTCCACAGTGG 5335  
Qy 1802 spAsnTrpAsnG1y1leMeLysAspProSeArGAspCyshAspG1uG1uSeThrCyST 1822  
Db 5336 ACAATTGGAATGGCATTTGAAAGACACCTCCGGAGCTGAGACAGAGATCCACTGCT 5395  
Qy 1822 YrAsnThrVal1leSePro1leTyTrPheVal1SeThrPheVal1leuThralaG1uPheVal 1842  
Db 5396 ACAACACGTCATCTCCCTATCTTACCTTGTGTCTTCGTCGACGCGCCACAGTTCGTGC 5455  
Qy 1842 euValaSnVal1leAlaVal1leuMeLysH1sLeuG1uG1uSeArAsnLysG1uAla 1862  
Db 5456 TAGTCACGTGTATGCGCGTGTGATGAAAGCACTGAGAGAGACAAGAGAGGCA 5515  
Qy 1862 ySG1uG1uAlaG1uLeuG1uAlaG1uLeuG1uLeuG1uMeLysThrLeuSeProG1uP 1882  
Db 5516 AGAGAGAGCGGACCTGAGGCTGAGCTGAGCTGAGATGAAACCTCGAGCCGCCAGC 5575  
Qy 1882 roH1seSerProleuG1ySeProPheLeuTrpProG1yVal1G1uG1yVal1aSnSerThra 1902  
Db 5576 CCCACTCGCACTGGGAGGCCCTTCTGTGCTCGGCGTGCAGAGGCCGACGCCCG 5635  
Qy 1902 spSeTrProLysProG1yAlaProH1sThrHrAlaH1s1leG1yAla1aSeSerLysPheS 1922  
Db 5636 ACAAGCCCAAGCTGGGAGCTTGCACCAAGCGGCCACGAGATCAAGCTCCCACTTT 5695  
Qy 1922 eTrLeuG1uH1sProThrMeVal1ProH1sProG1uG1uVal1ProVal1ProleuG1yProA 1942  
Db 5696 CCTCGAGACCCCAACATGAGGCCCAACCCCAAGAGCTGCCA-----GAGCAG 5746  
Qy 1942 spLeuLeuThrVal1aArG1ySeSerG1yVal1SeArArGThrH1sSeTrLeuProAsnAspSeTr 1962  
Db 5747 ACTTACTGACTGTGCGAAGCTGTGGGTCAAGCCAAAGCACTCTCTCCCAATATACAGCT 5806  
Qy 1962 yTrMeCyshArGArG1ySeThrThralaG1uArGSeTrLeuG1yH1sArG1yTrpG1yLeup 1982  
Db 5807 ACATGTGTGCGATGGAGACCTGCGAGGGGCCCTGGAGACACAGGGGCTGGGGGCTCC 5866

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QY 1982 10LYGALAGLISERGLYSERILELEUSERVALHISERGLINPROALAAPRTHRSERYSI 2002
DB 5867 CCAAAAGCTCAGACGGCTCCGTTGTCCTCACCACCCAGACGACGATACAGCTACA 5926
QY 2002 1ELEUGLNULEUPROLYSAPRVALHISERILELEUGLNULEUPROHISGLIYALAPRTHRTFG 2022
DB 5927 TCTTCAGCTTCCCAAGATGCACCTCATCTGCTCCAGCCCAAGACGCCCAACTGSG 5986
QY 2022 1YALA11EPROLYSLEUPROPROPROGLIYARISERPROLEUALAGINARPROLEUARGA 2042
DB 5987 GGAACATATCCCAAACTGCCCAACAGACGCTCCCTTGGCTCAGAGCCACTCAGGC 6046
QY 2042 TGGGALAA1A11EATGTHRASPSEERLEUASPRVALGINGLYUENGLYSERARGLIUAAPL 2062
DB 6047 GCAGGACCAATTAAGACTGACTCTTGGACGTTACGAGGTCTGGCACCCGGGAAGACC 6106
QY 2062 EULEUSERGLIUALISERGLYPROSERCYSPROLEUTHRARGSERSESERPHETRGLYG 2082
DB 6107 TCTTGGCAGAGGTGAGTGGGCTCTCCCGCCCTTGGCCGGGCTTACTCTTCTGGGGCC 6166
QY 2082 1YSESERILEGLINVALGININARISERGLY11EGLINSELYSVALSERLYSHISLEA 2102
DB 6167 ACTCAAGTACCCAGACGACGACGACACTCCCGACGACCAAGATCTCAAGACACATGA 6226
QY 2102 TGLUENPROALAAPROCYSPROGLYUENGLUPROSETRTPALALYAPAPROPROGLIUTHA 2122
DB 6227 CCCCCGCACTTTCGCCAGGCGCCAGAACCCCACTGGGCGAAGGGCCCTCCAGACCA 6286
QY 2122 TGSERSEIRLEUGLNULEUAPRTHRGULSESERTRPILESERGLYAPPLUEN---PROS 2141
DB 6287 GAAGCAGCTTAAGTTGAGACACGAGACTGAGCTGGAATTCAAGAGACCTTCGCCCTTG 6346
QY 2141 ESESEGLINGLUJLUPROLEUPHEPROARASPLEULYSYCYSTRYSERVALGLUTHRG 2161
DB 6347 GCGGCGCAGAGAGAGCCCATCCCAAGGGAAGCTGAAGAGTCTACAGGTGAGAGCC 6406
QY 2161 1NLSERCYARARGARGARGPROGLYPHERTRPLEUAPGLINATGARGHISERILEALAY 2181
DB 6407 AGAGCTGCAGCCCGGCTACCTCTGCTGATGATGAGACGAGACACACTCTATGCGCG 6466
QY 2181 1LSERCYELEUAPRSEIRGLYSEIRGLINPRARGLEUCYSPROSERPROSEIRLEUGLYG 2201
DB 6467 TCAGCTGCCTGGACACGGCTCCCAACCCCACTGGGACACACCCCTTACCTTGGGG 6526
QY 2201 1YGLINPROLEUGLYGLYPROGLYSEARARGPROLYSILYSLEUSERPROPROSERILES 2221
DB 6527 GCCAGGCTCTTGGGGGGGCTCGGAGCCGCCCAAGAAAACCTCACGCCGCTAGATCA 6586
QY 2221 EXILEAPPROPROGLIUSERGLINGLYSEARARGPROCYSPERPROGLIYVALCYALEUA 2241
DB 6587 CCATAGACCCCGGAGAGCCAGATCTCTGAGACCCCGCCCACTGGATATCTGCTCC 6646
QY 2241 TGAARGARGALAPROALASERASPRSERLYSAPRSEIRVALISERSEIRPROLEUASPR 2261
DB 6647 GAGAGGAGGCTCGCTCGACGACTCCAGAGATCTTGGCTTGGCCCTCGACAGCA 6706
QY 2261 HVALA1ASERPROSERPROLYSLEUASPRTHRLEUSERLEUSERGLYLEUSERSEIRASP 2281
DB 6707 TGGCTGCTTGCCTCTCCCAAAAGATGTGCTGATCTCTCGGTTATCTCTGACC 6766
QY 2281 ROTHRAPMETAPPRO 2286
DB 6767 CAGCAGACCTGAGACCC 6783

```

RESULT 12  
 AAX83484 standard; cDNA; 6729 BP.  
 ID AAX83484  
 XX AAX83484;  
 AC  
 XX  
 DT 07-DEC-1999 (first entry)  
 XX Human T-type voltage-gated Ca channel alpha-1-G (hcaVT1d) cDNA.

```

XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KM activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
KW
XX
XX Homo sapiens.
OS
XX MO9929847-A1.
PN
XX
XX 17-JUN-1999.
PD
XX
XX 30-OCT-1998; 98WO-US023161.
PF
XX
XX 05-DEC-1997; 97US-00985809.
PR
XX (LOYO ) UNIV LOYOLA CHICAGO.
PA
XX
XX Perez-Reyes E, Cribbs LL;
PI
XX
XX WPI: 1999-394972/33.
DR
XX P-PSDB; AAY14589.
DR
XX
XX New T-type voltage-gated calcium channels.
PS
XX Disclosure; Page 58-67; 138pp; English.
XX
XX This sequence represents the coding region for a human T-type voltage-
CC gated calcium (Ca) channel alpha-1-G designated hcaVT1d. Voltage gated
CC channels are membrane bound glycosylated proteins formed of several
CC subunits. The large alpha subunits form a pore in the membrane that is
CC selective for a given ionic species. Each alpha subunit contains 4
CC domains (I, II, III and IV) and each domain contains 6 putative
CC transmembrane helical segments (SI-S6). T-type Ca channels are activated
CC at a lower voltage than L- or N-type channels. Characteristics of T-type
CC channels include short current time, slow activation kinetics near
CC threshold, fast inactivation kinetics and slow tail current. The
CC sequences AAX3481-X83492 represent novel T-type voltage-gated Ca channel
CC genes from humans and rats. Each of the novel Ca-channels contains a
CC putative IVS4 region comprising the amino acid sequence AAY14598. Cells
CC expressing the T-type voltage-gated calcium channel proteins can be used
CC to screen for drugs which affect calcium channels. Methods are also
CC disclosed for treating a disease or disorder associated with a deficiency
CC in a native T-type calcium channel nucleic acid, e.g. to treat
CC cardiomyopathy, epilepsy, etc
XX
XX
XX Sequence 6729 BP; 1283 A; 2168 C; 1975 G; 1303 T; 0 U; 0 Other;
SQ
XX
XX Alignment Scores:
XX
XX Pred. No.: 0 Length: 6729
XX Score: 10919.50 Matches: 2103
XX Percent Similarity: 94.68% Conservative: 33
XX Best Local Similarity: 93.22% Mismatches: 105
XX Query Match: 90.78% Indels: 15
XX DB: 2 Gaps: 5
XX
XX US-09-611-257A-24 (1-2287) x AAX83484 (1-6729)
XX
XX 34 TPTTHARGARGARGMETGLUARGALAPROARGSERARGASPRPROVALASERARG 53
DB 2 TSGACGAGAGGAGATGAGCGGGGCGGAGAGATCGGAGACGCCCGGACCTTCATCC 61
QY 54 SERSERTRTHCYSPROGLYPROGLYALAAAGLYAAGLYSERTRHGLUYSAPR 73
DB 62 GGCTCAACGACCTGCTGGGGGCGGGGGGCGGGGCGGGGGGCTGAGCAAGAAAGGACC 121
QY 73 ROGLYSER1AASPRSERGLIAGLUGLYLEUPROTYRPROALALEUALAPROVALP 93
DB 122 CCGGCGAGCCCGGACTCCGAGGCGGAGGGGCTCCGATCCCGGCGCTGGCCCGGGTGT 181
QY 93 hEPHERYLEUSERGLIUAAPRSEIRARGPROARGSERTRPCYLEUARGTHRVAlCYAASP 113
DB 182 TCTTCTACTTGAAGCCAGACACGCCCGCGGAGAGCTGGGTCTCCGCAAGGCTGTGAAC 241
QY 113 ROTRPHNEGLUARGVALISERMETLEUVALILEUULEUASNYCYVALTHRLUGLYMETP 133

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|||||:::|||||  
242 CCTGTTTGAGGCGATCAGCATGTTGTCATCTTCAACGCGTGACCCGCGCATGT 301  
QY hehYrProCysGluAspIleAlaCysAspSerGlnAryCysArgIleuLeuGlnAlaPheA 153  
Db TCCGGCCATGCGAGAGACATCGCTGTGACTCCACGCGTGCGGATCCTGACAGGCTTTG 361  
QY sPAspPheIlePheAlaPhePheAlaValAlaGluMetValAlaLeuGlyI 173  
Db ATGACTTCATCTTCCCTTCTTGGCCGTGAGATGGTGTAAAGATGGTGGCTTTGGGCA 421  
QY 1epheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleAla 193  
Db TCTTTGGGAAAAAGTTACCTGGGAGACATTGGAAACGGGCTTGACTTTTTCATGTCGA 481  
QY 1eAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213  
Db TCGCAGGGATGCTGGAGTACTCGCTGGAACCTGCAGAACGTCGCTTCAGCTGCAGAGA 541  
QY hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233  
Db 542 CAGTCCGTGTGCTGGACCGCTCAGGGCCATTAAACGGGTGCCCGCATGCGCATCTTG 601  
QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253  
Db 602 TCACGTTGCTGTGATACGCTGCCCATGCTGGCAACGTCCTGCTGTGCTTCTTCG 661  
QY 253 alPhePheIlePheGlyIleValGlyValAlaGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273  
Db 662 TCTTCTTCATCTTGGCATGCTGGCGCTGCACAGTGTGGCAGGGGCTGCTGGAAACCAT 721  
QY 273 ySPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293  
Db 722 GCTTCTTCACCTGAGAAATTTCAGCCCTCCCTGAGGCTGGACCTGGAGGCGTAATTAACGA 781  
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313  
Db 782 CAGAAAGACAGAGATGAGAGCCCTTCATCTGCTCCAGCACGCGAAGAACGCGCATGCGGT 841  
QY 313 eCYAspSerValProThrLeuArgGlyGlyGlyGlyGlyProProCysSerLeuA 333  
Db 842 CCTGAGAAAGCGTGGCCACGCTGCCGGGGAGGGGGGGGTGGCCACCTTGGGCTGG 901  
QY 333 sPYrGluThrTyrAsnSerSerSerAsnThrTyrCysValAsnTrpAsnGlnTyrTyrT 353  
Db 902 ACTATGAGGCGCTACAAACAGCTCCACCAACACCACTGTGTCAACTGGAACCAAGTACTACA 961  
QY 353 hrAsnCysSerAlaGlyGlyLysAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373  
Db 962 CCAACTGCTCAGCGGGGAGCACAAACCCCTCAAGGGCGCCATCAACTTTGACAAACATTG 1021  
QY 373 1yTyrAlaATrPileAlaIlePheGlnValIleThrLeuGluGlyTyrTrpAlaAspIleMet 393  
Db 1022 GCTATGCGCTGAGTCCCATCTTCCAGGTATCACCTGAGGGGCTGGGTGCACATCAATGT 1081  
QY 393 yRPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413  
Db 1082 ACTTTGTGATGATGATCTCATCTTCTTCAAAATTTTCATCTACTTCATCTTCCATCAATCG 1141  
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433  
Db 1142 TGGGCTCCTCTTCTTCATGATCAACCTGTGCTGGTGTGATTTGCCACGAGTTCACAGAGA 1201  
QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453  
Db 1202 CCMAACACCGGGGAAAGCCAGCTGATGCGGAGACACGCTGTGGTTCCTGTCCAAACGCGCA 1261  
QY 453 eRThrLeuAlaSerPheSerGluProGlySerCysTyrGlyGluLeuLeuLysTyrLeuV 473  
Db 1262 GCAACCTTGGCTAGCTTCTCTGAGCCCGGAGCTGTATGAGAGAGTGTCTCAAGTACCTGG 1321  
QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493  
|||||:::|||||

Db 1322 TGTAATCTTTCGTAAAGCAGCCCGCAGGCTGAGTCTCGAGTCTCGGAGCAGAGTGTGC 1381  
QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513  
Db 1382 GGGTTGGGCTGTGAGACGCCACACACCCCTCGGGGGGCGAGAAACCGACGCCAGCGACA 1441  
QY 513 eCYsThrArgSerHisArgArgLeuSerValHisIleValAlaHisIleHisIleHisI 533  
Db 1442 GCTGCTCGCTCCACCGCGGCTTATCCGTCCACCAACCTGTGTACACACACACACACACC 1501  
QY 533 1shIshIshIshTyrHisIleuGlyAsnGlyTyrThrLeuArgValProArgAlaSerProGlu 553  
Db 1502 ATCACACACCTTACCTACCTGGGCAATGGAGCGCTCAGAGGCCCCCGGAGCGCCGAGA 1561  
QY 553 1eGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573  
Db 1562 TCCAGAGAGGGAATGCCAATGGATCCCGCGGCTCAATGTCGACCAACCTTCAGCGCTTG 1621  
QY 573 hrProSerGlyGlyProProArgGlyAlaGlySerValHisSerPheTyrHisAlaAspC 593  
Db 1622 CCGTCTCGGGGCCCCCGCTGTGTGGCGAGTGTGTGACAGCTTCTACCATCGCAGACT 1681  
QY 593 ySHIleuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613  
Db 1682 GCCACTTAAAGCCAGTCCGCTGCGCAGAGGCCCCCTCCAGGTCCCATCTGAGGCAATCCG 1741  
QY 613 1yArgThrValGlySerGlyLysValTyrProThrValHisIshSerProProGluI 633  
Db 1742 GCAGGACTGTGGGAGCGGGAGAGTGTATCCACCGTGCAACAGCCCTTCACCGGAGA 1801  
QY 633 1eLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs 653  
Db 1802 CGCTGAAGAGAAAGCAGCTAGTAGAGGTGCTGCCACTCGGGGCCCAACCTTCACCA 1861  
QY 653 eRPheAsnIleProProGlyProPheSerSerMetHisLysLysLeuGluThrGlnSerT 673  
Db 1862 GCTCAACATTCACCCCGGCTTACAGCTTCACAGCAACAGCTGCTGAGACACAGAGTA 1921  
QY 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693  
Db 1922 CAGGTGCTGCCAAAGCTCTTGCAGAGATCTTCAGCCCTTGTGAAAAGCAGACAGTGGAG 1981  
QY 693 1AcysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713  
Db 1982 CCGTGGGTCCAGACAGCTGCCCTTACTGTGCCGGGCGGGGAGGAGGTGAGTCTCG 2041  
QY 713 1aAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733  
Db 2042 CCGACCGTGAATCTGTGACTCAGACACAGCGAGGAGTTTATGAGTTTCAACACAGATGCC 2101  
QY 733 1nhIserAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753  
Db 2102 AGCACAGGACCTTCGGGAGCCCCCAGAC--CGGCGGCAAGGAGCTGGGCCAATG 2158  
QY 753 1agIuProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773  
Db 2159 CAGAGCCAGCTGTGTGCTGGCTTTCGAGGCTTAATCTGTGACACCTTCGAAAGATTG 2218  
QY 773 alAspSerLysTyrPheGlyArgGlyLleMetIleAlaIleLeuValAsnThrLeuSerM 793  
Db 2219 TGGACAGCAAGTACTTTTGGCCGGGGAAATCATGATCGCATCTGTGTAAACACTTCAGCA 2278  
QY 793 eTGlyIleGluTyrHisGlyGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813  
Db 2279 TGGGCAATCGAATACAGAGAGGCCCGAGAGCTTACCAACGCCCTTGAATACGCAACA 2338  
QY 813 1eValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProP 833  
Db 2339 TCGTCTTACACAGGCTCTTGGCTTGGAGATGTGTGAGAGCTGCTGTGTATGTGCTCCT 2398  
QY 833 heGlyTyrTyrIleLysAsnProTyrTrpAsnIlePheAspGlyValIleValValIleSerValT 853  
Db 2399 TTGGCTCATTCMAAAGATCCCTACAAACATCTTCATGGGTGTCTATTTGTGTATCAGCGTGT 2458  
|||||:::|||||

Qy	853	rrgllulllevalglvnglndlyvglvlyleuservallleuarxthPharxgumeta	873
Db	2459	GGGAGATCGTGGGCGACGAGGAGGAGGCGGCTGTGGTGTGGGACCTTCGCTGATGC	2518
Qy	873	rgVallleuLyLeuValArpPheleuPProAlaleuGlnArGlnLeuValLeuMetL	893
Db	2519	GTGTGCTGAAGCTGTGTGGCTTCTTCGCGGCGCTGCAAGCGGCACTGTGTGCTATGA	2578
Qy	893	lyrthmetAspAsnValAlathrPheCywMetLeuMetLeuPheIlePheS	913
Db	2579	AGACCATGACAACGTGGCCACCTTGTGCATGCTGATTACTCTTCATCTTCATCTTCA	2638
Qy	913	erlleleuGlYmetHiEleuPheGlCyblySPhenAlaserGluArxAspGlyAspThrL	933
Db	2639	GCAATCTGGGATCATCTTCTTGCGCTGCAGATTGCTCTGACCGGAGATGGGACACC	2698
Qy	933	euproAspArgLyAsnPhenAspSerLeuLeuTrrAlleValThrValPheGlnIleL	953
Db	2699	TGCCAGACCGGAAGATTTCATCTCTGTGCGCATGTGCATCTCTTCAGATCC	2758
Qy	953	euthrGlnGluAspTrrAsnLyValLeuTyraGlnYmetAlaserThrsSerTrrPa	973
Db	2759	TGACCCAGAGAGATCGAACAAAGCTCTCAATAGATGAGCTTCACGTCGTGGG	2818
Qy	973	laAlaleuTyrrPheIleAlaleuMetThrPheGlyAsnTyrrValLeuPheAsnLeuTy	993
Db	2819	CGGCGCTTATTTATTCATGGCCCTCATGACCTTCGGCACTACGTGTCTTCATTTGCTGG	2878
Qy	993	AlAlAlleuValGlnGlyPheGlnAlaglnGlyAspAlaThrLySerGlnSerGlnP	1013
Db	2879	TCCGCATCTCTGTGGAGGGCTTCCAGCGGAGGAGAGTCCACAAGTCGGAATCAGAGC	2938
Qy	1013	roAspPhePheSerProSerValAspGlyAspArgLyAspArgLyLeuArgLeuAlaLeuV	1033
Db	2939	CCGATTTCTTCTCACCCAGCTGTGATGTGGGACAGAGAACGATGCTTGGCTTGGC	2998
Qy	1033	AlAlAlaleuGlyGlnHiAlaGluAlaGlyLySerLeuLeuProProleuIleIleHsT	1053
Db	2999	TGTCCCTGTGGAGAGACCCGGAGCTGGGAAAGCTGTCTCCGCTTCATCATCCACA	3058
Qy	1053	hrrAlaAlaThrProMetSerHiAspProLySerSerSerThrGlyValGlyGlnAlaLeuG	1073
Db	3059	CGGCGGCCACACCATGTCTGCTGCCCAAGACACACAGCACGGGCTGGGCGAGGCGCTGG	3118
Qy	1073	lySerGlySerArxArgThrSerSerSerGlySerAlaGlnProGlyValAlaHiShiSg	1093
Db	3119	GCCCTGCGTCCGCGCGCACACAGACACGGGATCGGACAGACTGGGCGGCGCC--CACG	3175
Qy	1093	lumerLyCyAspProSerAlaArxSerSerProHIsSerProTrrSerAlaIAsers	1113
Db	3176	AGATGAATCACCGGCCAGCGCGCGACACTCTCCGACAGCCCTCGAGGCGCTGTACACA	3235
Qy	1113	erTrrThrSerArxArgSerSerArxAsnSerLeuGlyArxAlaProSerLeuLyAsrGa	1133
Db	3236	GCTGACCAAGAGGGGCTTCCAGCGGAAACAGCTCGGCGGTGACCCAGCCTGAAGCGGA	3295
Qy	1133	rgSerProSerGlyGlnArxArgSerLeuLeuSerGlyGlnGlyGlnIuSerGlnAspG	1153
Db	3296	GAAAGCCCAAGTGAAGAGCGGCGGTCTCTGTTGTTCGGAGAAAGCCAGGAGGCCAGATG	3355
Qy	1153	luguGlnuSerSerGlnGluAspArgAlaSerProAlaGlySerAspHiAsrGlnAsrG	1173
Db	3356	AAGAGGAAGCTCACAAGAGAGCGGGGCGAGCTTCGGGCGAGTGAACATGGCCACAGGG	3415
Qy	1173	lySerLeuGlnuArgGlnAlaLySerSerPheAspLeuProAspThrLeuGlnValProG	1193
Db	3416	GCTTCCTGGAAGGGAAGGCMAAGATTCTTTGACTCGACACACATGCACGGTGCAG	3475
Qy	1193	lyLeuHiAsrGThrAlaSerGlyArxSerSerAlaSerGlnuHiGlnAspCyAsnGlyL	1213
Db	3476	GGCTCATCTGCATCCAGTGGCGCAGAGGATGTGCTTCTGAGACCAAGAGATGCATATGCA	3535

QY	1213	ysSerAlaSerGIyArGLeuAlaArGhrLLeuArGhrThraPaPaAPProGInLeuAspGIyA	1233
Db	3536	AGTCGGGCTTACAGGGCGGCTG3CCCGGCGCTGCGGCTGATGACCCCCCAGTCGATGGG	3595
QY	1233	spAPaPaPaAmaAspGIuGIyAsnLeuSerLySGIuArGIeGlnAlaTrpValArGs	1253
Db	3596	ATGACGCCCGATGACAGAGGCAACTGAGCAAAAGGGAAACGGTCCGGCGGTGATCCGAG	3655
QY	1253	erArGLeuProAlaCySArGArGIuArGAspSerTrpSerAlaTrpIlePheProProG	1273
Db	3656	CCGAGACTCCCTGCGCTGCTGCTGAGGAGACTCTGGTCAGCTTACATTCATCTCCCTCTC	3715
QY	1273	InSerArGhrPheArGLeuLeuCyShiSaRgIleIleThrHislyrMetPheAspHisValY	1293
Db	3716	AGTCAGAGTTCGGGCTCTGTGTCAACGGATTCATCACCCAAAGATGTTCACACAGCGG	3775
QY	1293	alleuValIleIlePheLeuAsnCySileThrIleAlaMetGIuArGProLySileAsp	1313
Db	3836	CCCAACAGCGTGAACGATCTTCTCTGACCCCTCCATTCATCTTACATCCGAGCTTTTC	3895
QY	1333	euaIaGIuMetThrValIlySaValAlaIleuGIyTrpCySPheGIyGIuGlnAlaTrpL	1353
Db	3896	TGCGTGAATGACAGTAAAGGTGTGTGCACCTGGGCTGGTGTGGGAGAGAGCGTACC	3955
QY	1353	euaGAspSerTrpAsnValIleuAspGIyLeuLeuValIleuIleSerValIleAspIleL	1373
Db	3956	TGCGAGAGAGTTGAAAGCTGTCTGACAGGGGCAACAAAGATCTGGGATCTGAGGGTCTGGCG	4015
QY	1373	euaIleSerMetValSerAspSerGIyThrLySileuGIyMetLeuArGValIleuArGL	1393
Db	4016	TGCTGTCCATGTGTCTGACAGGGGCAACAAAGATCTGGGATCTGAGGGTCTGGCGG	4075
QY	1393	euleuArGhrThrLeuArGProLeuArGValIleSerArGAlaGInGIyLeuLySleuValY	1413
Db	4076	TGCTGCGGAGCCCTGCGCCGCTCAAGGTGATCACCCGGGCGCACGGGTGTGAAGCTGGTGG	4135
QY	1413	alGIuThrIleuMetSerSerIleuLySProIleGIyAsnIleValIleCySAspAlaP	1433
Db	4136	TGGAGACCGTATGTCTCTCACTGAACCCCATCGGCAACATTGATGTCATCTGCTGTGCT	4195
QY	1433	hePheIleIlePheGIyIleuGIyValGIuLeuPheLySGIyAspPhePheValCySG	1453
Db	4196	TCTTCATCATTTTGGGCATCTTGGGGGTGCGAGCTTTCMAAGGGAAGTTTTCGTGTCC	4255
QY	1453	InGIyGIuAspThrArGAsnIleThrAsnLySserAspCySaIeGIuAlaSerTrpArGT	1473
Db	4256	AGGGCGAGAGATACAGGAACATCAACCAATAATGTGAGCTGCGAGCGCAGTTACCCGT	4315
QY	1473	trpValArGhrHisLyGTrpAsnPheAspAsnLeuGIyGlnAlaLeuMetSerIleuPheValI	1493
Db	4316	GGGTCGCCGCAACAAGTAACTTTTGAACAACCTTGGCGACAGCCCTGATGTCCCTGTGCTT	4375
QY	1493	euaIleSerLyAspGIyTrpValAspIleMetTrpAspGIyLeuAspAlaValGIyValA	1513
Db	4376	TGGCTTCCAAAGATGTGTGGGTGACATCATGTACATGAGCGGCTGATGCTGTGGCGGTGG	4435
QY	1513	spGIuGIuProIleuMetAsnHisAsnProTrpMetLeuLeuTrpPheIleSerPheLeuL	1533
Db	4436	ACGACAGCCCATCATGAAACACAAACCCCTGAGTGTGTCTACTTCATCTCGTGTCTCGC	4495
QY	1533	eulIleValAlaPhePheValIleuAsnMetPheValGIyValValIleGIuAsnPheHisL	1553
Db	4496	TCATTTGTGGCTTTCTTGTCTCTGAACATGTTGTGGGTGTGTGTGGTGAACATTCACA	4555
QY	1553	ysCySArGAspGIuHisGIuGIuGIuGIuAlaArGArGArGIuGIuLySArGLeuArGA	1573
Db	4556	AGTGTGGCAGACACCAAGAGAAAGAGAGGCCCGCGCGGGAAGAAAGCGCTACGAA	4615
QY	1573	rgLeuGIuLySlyArGhrSerLySGIuLyGIuMetAlaGIuAlaGIuCySlySProT	1593

Db	4616	GACCTGGAGAAAAAGAGAAG-----AAAGCCCAAGCAAACTTT	...	4654
Qy	1593	YRTYRSeAspTYSeSerApPheArpPheArpLeuLeuValHISHisLeuCYsThrSerHisTYRLeu		1613
Db	4655	ACTACTCCGACTTACTCCCGCTTCGGCGCTCTCTGCTCCACCACTTGTGACACCGACCACTTACC		4714
Qy	1613	euaApLeuPheIleThrGIYValIIleGIYLeuAsnValValThrMetAlaMetGIuHisT		1633
Db	4715	TGACACTCTTCATCAACAGGTGTCACTCGGGCTGAAGTGTGTCAACATGAGCCATGAGAGCACT		4774
Qy	1633	YRGINginProGlnIIleLeuAspGIuIIaIeLeuYsIIleCYsAspTYRllePheThrValII		1653
Db	4775	ACCAGACAGCCCCCAATTCTGGATGAGGCTCGAAGATCTGGAACTCAACTTCACCTGCA		4834
Qy	1653	IePheValPheGIuSerValPheIYsLeuValAlaPheAlaPheArgArpPhePheGlnA		1673
Db	4835	TCTTTGTCTTGGAGTCAAGTCTTTCAAACTCTTGAGCCTTTGGTTTCCGTGGTCTTCCAGG		4894
Qy	1673	sPArGTTPAsngInLeuAspPheuAlaIleValIleuLeuSerIleMetGIYIleThrLeuG		1693
Db	4895	ACAGGTGGAAACAGCTGGACCTGGCCATTGTGTGTCTGTCCATCATGAGGCATCAAGCTGG		4954
Qy	1693	IuGIuIIleGIuValAsnLeuSerIeuProIIeAsnProThrIIleIleArgIIleMetArgY		1713
Db	4955	AGGAATTCGAGAGTCAAACCGCTCGCTGCCATCAACCCCAACATCATCCGACATCATGAAGG		5014
Qy	1713	AlIeAsuArgIIleAlaArgValLeuIYsLeuLeuIYsMetAlaValGIYMetArgAlaLeuI		1733
Db	5015	TGCTGCGCATTTGCCCGAGTGCCTGAAGCTCTGMAAGATGCTGTGGGATGCGGGCGCTGC		5074
Qy	1733	euhIsthrValMetGIuAlaLeuProGlnValGIYAsnLeuGIYLeuLeuPheMetLeuI		1753
Db	5075	TGGACACGGTGATGAGGCCCTCGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTGT		5134
Qy	1753	eupPhePheIlePheAlaAlaLeuGIYValGIuLeuPheGIYAspLeuGIuCYsAspGIuT		1773
Db	5135	TGTTTTTCATCTTTGCACTCTCGGCGGTGGAGCTCTTTGGAGAACCTGGAGTGTGACGGA		5194
Qy	1773	hrHISProCYsGIuGIYLeuGIYArgHISAlaThrPheArgAsnPheGIYMetAlaPheI		1793
Db	5195	CACACCCCTGTGAGAGGCTGTGGCCGTCAATGCCACTTTCCGAACTTTGGCATGAGCTTCC		5254
Qy	1793	euthrLeuPheArgValSerThrGIYAspAsnTPAsnGIYIleMetIYsAspProSerA		1813
Db	5255	TAAACCTCTTCCGAGTCTCCACAGGTGACAAATTGGAAATGGACATTATGAAGACACCTCC		5314
Qy	1813	rgAspPCYsAspGIuGIuSerThrCYsTYRAsnThrValIIleSerProIleTYRPhenAlS		1833
Db	5315	GGGACTGTGACAGAGAGTCCACTGTCTACAAACAGGTATCTCGGCTATCTTCAACTTGTGT		5374
Qy	1833	erPheValIleuThrAlaGlnPheValIleuValAsnValValIIleAlaValIleuMetIYsH		1853
Db	5375	CCTTCGTGCTACAGCCGCCAATTCGTGCTAGTCAACGTGTGATCCGCTGCTGATGAAGC		5434
Qy	1853	IstLeuGIuGIuSerAsnIYsGIuAlaIaIYsGIuGIuAlaGIuLeuGIuAlaGIuLeuGIuI		1873
Db	5435	ACCTGGAGAGAGCAACAAGAGGCCCAAGAGAGGCCGAGCTGAGAGGCTGAGCTGAGGC		5494
Qy	1873	eugIuMetIYsThrIleuSerProGlnProHISerProLeuGIYSerProPheLeuTTP		1893
Db	5495	TGGAGATTAACAACCTTCAGCCGCCCACTGCCACTGGGCGAGCCCTTCCTTCCTGGCC		5554
Qy	1893	roGIYValGIuGIuValAsnSerThrAspSerProIYsValAlaProHISThrThra		1913
Db	5555	CTGGGGGTGAAGGGCCCCGACAGCCCCCGACAGCCCCCAACCTTGGGGCTTGGACCCAGGGG		5614
Qy	1913	IaHISleGIYAlaIaIaSerGIYPheserLeuGIuHISProThrMetValProHISProG		1933
Db	5615	CCCAAGCGAGATCAAGCTCCCACTTTTCCCTGGAGACACCCACATGACAGGCCCAACCCCA		5674
Qy	1933	IuGIuValProValProLeuGIYProAspLeuLeuThrValArgIYsSerGIYValSerA		1953

Db	5675	CGAGGCTGCCA-----GACCAAGACTTACTGACTGTGCGGAAGTCTGGGGTCAACC	5725
QY	1953	IGTTHHISSELeuProAsnAspSerTYrMetCysArgaenglySerThralaGluArgS	1973
Db	5726	GAAGCACTCTCTGCCAATGACGACTACATGTGTGGCATGGGAGACATGCCAGAGGGCC	5785
QY	1973	erLeuGlyHlaArgGlyTYrTrpGlyLeuProIySalagInserGlySerHlaLeuSerHlaH	1993
Db	5786	CCCTGGGACACAGGGGGGTGGGGGGCTCCCAAGCTCAGTACGCTCGTGTTCCTGC	5845
QY	1993	ISserGlnProAlaAspThrSerCysIleLeuGlnLeuProIyAspValHISTYrLeuL	2013
Db	5846	ACTCCCAAGCCAGCAATACAGACTACATCTCTGCAGCTTCCCAAGATGACACTCATCTGC	5905
QY	2013	eugInProHISglYAlaProThrTrpGlyAlaIleProIyLeuProProProGlyIyArgS	2033
Db	5906	TTCAGCCCCACAGGGGCCCAACTGCGGGGACACATCCCAACTGTGCCCAACAGAGAGCT	5965
QY	2033	erProLeuAlaGlnArgProLeuArgGlnAlaAlaIleArgThnAspSerLeuAspY	2053
Db	5966	CCCCCTTGGCTCAGAGGCCACTCAGGGGCCAGGAGGAATPAGAGACTCTCTTGGAGC	6025
QY	2053	alGlnGlyLeuGlySerArgGluAspLeuLeuSerGlyValISerGlyPProSerCysProL	2073
Db	6026	TTTCAGGCTCTGGGAGCCCGGAGAGACTCTGCTGGACAGGTGATGAGTGGCCCTCCCGGCC	6085
QY	2073	euthrArgSerSerSerPheTrpGlyIySerSerIleGlnValGlnGlnArgSerGlyI	2093
Db	6086	TGGCCCGGGCTACTCTTCTTGGGGGCCAGTCAAGTACCCAGGACACAGCACACTCCGCA	6145
QY	2093	IeGlnSerIyValSerIyHISIleArgLeuProAlaProCysPProGlyIyLeuGlnProS	2113
Db	6146	GCCACAGCAAAATCTCCAGACATGACCCCGCAGCCCTTGGCCAGGGCCGAGAACCA	6205
QY	2113	erTPAlaIyAspPProGlnIyHrArgSerSerLeuGlnLeuAspThGlyIuLeuSert	2133
Db	6206	ACTGGGGCAGAGGGCCCTCCAGAGCCAGAAAGACCTTAGAGTTGACACGAGAGTGAAGT	6265
QY	2133	TPleSerGlyAspLeuLeu---ProSerSerGlnGlnGlnIyProLeuPheProArgAspL	2152
Db	6266	GGATTTACGAGGACCTCTGCTGGCCCTGGCGGCGCAGAGAGACCCCACTCCCAAGGAGAC	6325
QY	2152	eulYslyCySfTYrSerValGluThrGlnSerCysaGlaGlaGArgProGlyIyPheTrpLeuA	2172
Db	6326	TGAAGAAGTGTCTACAGGTGAGGCGCCAGAGCTGCCAGCCCGGCTTACCTGCTGG	6385
QY	2172	spGlnGlnArgArgHISerIleAlaValSerCysLeuAspSerGlyISerGlnProArgL	2192
Db	6386	ATGAGCAGAGAGACACTCTATGCCCTCAGCTGCTGGACAGGGGCTCCCAACCCACAC	6445
QY	2192	eucYsProSerProSerSerLeuGlyIyGlnProLeuGlyIyGlyProGlyISerArgProL	2212
Db	6446	TGGGACACAGACCTCTTACCTTGGGGGCGCAGCTCTTGGGGGGGCTGGGAGCGCGCCA	6505
QY	2212	YslySlyLeuSerProProSerIleSerIleAspProProGlnSerGlnGlySerArgP	2232
Db	6506	AGAAAAAACTCAGCGCCGCTAAGTATCAACATPAGACCCCCCGAGAGCAAGAGTCTTGGGA	6565
QY	2232	roPProCysSerProGlyValCysLeuArgArgArgAlaProAlaSerAspSerIyAspP	2252
Db	6566	CCCCGCCAGCGCTGATGTGCTCTCCGAGAGAGAGGCTCGGTCCAGGCACTCCAGGATC	6625
QY	2252	roSerValSerSerProLeuAspSerThralaIalaserProSerProIySlyAspThrl	2272
Db	6626	CCTTGGGCTCTGGGCCCTCCGACAGCATGGGTGCTGGCCCTCCCAAGAAAGATGTGC	6685
QY	2272	eusSerLeuSerGlyLeuSerSerAspProThrAspMetAspPro	2286
Db	6686	TGAATCTCTCCGATTATCTCTGACCCAGACAGACCTGGAACCC	6729

XX AAF31684;  
 AC  
 XX  
 DT 09-APR-2001 (first entry)  
 XX  
 DE Human alpha-IG T-type calcium channel cDNA.  
 XX  
 KW Human; antiarrhythmic; anticonvulsant; hypotensive; cardiant; nootropic;  
 KW T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;  
 KW hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel;  
 KW 85.  
 XX Homo sapiens.  
 OS  
 XX  
 PN W0200102561-A2.  
 XX  
 PD 11-JAN-2001.  
 XX  
 PF 04-JUL-2000; 2000MO-CA000794.  
 XX  
 PR 02-JUL-1999; 99US-00346794.  
 XX  
 PA (NEUR-) NEUROMED TECHNOLOGIES INC.  
 XX  
 PI Snutch TP, Baillie DL;  
 XX  
 DR MPI; 2001-123111/13.  
 XX  
 DR P-PSDB; AAB66481.  
 XX  
 PT Novel T-type calcium channel alpha-1 subunit gene useful for treating  
 PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and  
 PT epilepsy.  
 XX  
 PS Example 3; Fig 6; 103bp; English.  
 XX  
 CC The present sequence is given in a specification providing sequences and  
 CC partial sequences for three types of mammalian (human and rat) T-type  
 CC calcium channel subunits. An expression cassette has been generated which  
 CC comprises a nucleotide sequence encoding a T-type calcium channel alpha-1  
 CC subunit operably linked to control sequences to effect its expression.  
 CC The novel calcium channel nucleic acids and proteins are useful for  
 CC treating conditions characterised by undesirable levels of T-type calcium  
 CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,  
 CC hypertension, sleep disorder and epilepsy  
 CC  
 SQ Sequence 6892 BP; 1315 A; 2223 C; 2017 G; 1337 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 0 Length: 6892  
 Score: 10916.00 Matches: 2109  
 Percent Similarity: 93.42% Conservative: 34  
 Best Local Similarity: 91.94% Mismatches: 113  
 Query Match: 90.75% Indels: 38  
 DB: 5 Gaps: 6  
 US-09-611-257a-24 (1-2287) x AAF31684 (1-6892)  
 QY 19 AAlaArgProSerSerSerProProGlyProArgLeuAlaArgGlyTrpThrArgArgArg 38  
 DB 7 GCTTGCCTCTCTCCGATTCGCCCGGGGCCCGGCTGGCCAGAGATGACGAGAGAGG 66  
 QY 39 MetGluArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrCys 58  
 DB 67 ATGAGCGGCGCCGAGGAGTCCGAGCAGCCCGGAGCTTCAGCGGCTCAAGACCTGT 126  
 QY 59 ProGlyProGlyAla-AlaGlyAla-GlySerThrGlyLysArgProGlySerAlaAsp 78  
 DB 127 CGGAGGCGCGGAGCGCGCGCGGCGCGGAGTCAAGCAAAAGACCCGCGGACGCGGACT 186  
 QY 78 erGluAlaGluGlyLeuProTyrrProAlaLeuAlaProValAlaPhePheThrLeuSerG 98  
 DB 187 CCGAGGCGGAGGAGGCTGCGGATCCCGGCGCTGGGCCCGGTGGTTTCTTCTACTTGACC 246

QY 98 lnaSerSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgV 118  
 DB 247 AGGAGCGCGCCCGGAGGCTGGTGTCTCCGACAGGTCTGAAACCCCTGGTTGAGCCCA 306  
 QY 118 alSerMetLeuValIleLeuLeuAsnCysValTrpLeuGlyMetPheArgProCysGluA 138  
 DB 307 TCAGCATTTGGTATCTCTTCAACTGCGTGAACCTGGCATGTTCCGGCCATGCGAGG 366  
 QY 138 epIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheA 158  
 DB 367 ACATCGCTGTGACTCCGAGGCTGCCGATTCGACAGCCCTTGATATCACTTCTTG 426  
 QY 158 lAphePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysC 178  
 DB 427 CTTCTTTCGCGTGGAGATGGTGTGAAGATGAGTGGCTTGGGCATCTTGGGAAAAAGT 486  
 QY 178 yTyTrLeuGlyAspTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuG 198  
 DB 487 GTTACTCGGAGACACTTGGAAACCGGCTTGACTTTTCATGTCATCCAGGAGATGCTGG 546  
 QY 198 lTyTrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuA 218  
 DB 547 AGTACTCGCTGGACCTGCAGAAACGTCACTTCTCAGCTGTGCAGGACAGTCCGTGTGCTGC 606  
 QY 218 rGProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuA 238  
 DB 607 GACCCCTCAGGGCCATTAAACGGGTGCCAGATCGGACTCTTCTACAGTTGCTGCTGG 666  
 QY 238 spThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheG 258  
 DB 667 ATACGCTGCCATGCTGGGCAACGTCGTGCTCTGCTTCTTCTGCTTCTTCACTTCTG 726  
 QY 258 lYleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluA 278  
 DB 727 GCATCGTGGCGCTCAGCTGTGGGCGAGGCTGCTTCCGAAACCGATGCTTCTTCACTGAGA 786  
 QY 278 snPheSerLeuProLeuSerValAspLeuGluProTyrrTyrrGlnThrGluAsnGluAspG 298  
 DB 787 ATTTACGCTTCTCCCTGAGCGTGAACCTGAGCCGCTATTACAGACAGAAAGAGAGATG 846  
 QY 298 lUSeProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValP 318  
 DB 847 AAGAGCCCTTCACTGTCTCCAGCCAGGAGAAAGGATGCGTCTCAGAAAGGCTGC 906  
 QY 318 roThrLeuArgGlyGluGlyGlyGlyGlyProProCysSerLeuAspTyrrGluTrpTyrrA 338  
 DB 907 CCAGCGCTGGCGGAGACGGGGCGGCTGGCCCACTTGCCTGAGCTTGAATGAGGCTTACA 966  
 QY 338 snSerSerSerSerSerThrCysValAsnTrpAsnGlnTrpTyrrTrpAsnCysSerAlaG 358  
 DB 967 ACAGCTCCAGCAACACCACTGTGTCACTGAGAACCAAGTACTACACCACTGCTCAGCGG 1026  
 QY 358 lYGlUhiAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrrAlaATPILeA 378  
 DB 1027 GGGAGACAAACCTTCAAGGGCGCATCACTTGAACAACATTGGCTATGCTGGATG 1086  
 QY 378 lAllePheGlnValIleThrLeuGluGlyTyrrValAspIleMetCysPheValMetAspA 398  
 DB 1087 CCATCTTCAGGATCATCAGCTGAGGGCTGGGTGCACATCATGTACTTGTGATGATGATG 1146  
 QY 398 lAhIserPheTyrrAsnPheIleTyrrPheIleLeuLeuIleIleValGlySerPhePheM 418  
 DB 1147 CTCATTCCTTCAACATTCATTCATCTTATCTCTCATCATCGGGCTCTTCTTCA 1206  
 QY 418 erIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgLus 438  
 DB 1207 TGATCAACTGCTGCTGGTGGTATGATGCAACGAGTTCTCAAGACCAAGACGCGGAGAA 1266  
 QY 438 erGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerP 458  
 DB 1267 GCCAGCTGATGCGGAGGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326  
 QY 458 heserGluProGlySerCysTyrrGluGluLeuLeuLysTyrrLeuValTyrrIleLeuArgL 478

Db	1327	TCTGTGAGCCCGGAGAGCTGCTATAGAGAGCTGCTCAAGTACTGCTGTAACCTTGCTGTA	1386
QY	478	ysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuLeu	498
Db	1387	AGGAGAGCCCGGAGAGCTGAGTCAAGTCTCTCGGGGAGAGAGGTGTGGGTGGGCTCTCA	1446
QY	498	erSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerH	518
Db	1447	GCAGCCGACGACCCCTCGGGGGCCAGAGACCCAGCCAGCAGAGAGCTGCTCGCTCC	1506
QY	518	IsaArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHis	538
Db	1507	ACCGCGGCTTACCGTCCACACACCTGGGACACACACACACACACATCACCACTAC	1566
QY	538	IsLeuGlyAsnGlyThrIleuArgValProArgAlaSerProGluIleGlnAspArgAspA	558
Db	1567	ACCTGGCGAAAGGAGCGCTACAGGGCCCCCGGGCCAGCCCGAGATTCAGAGACGAGATG	1626
QY	558	IaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyP	578
Db	1627	CCAAATGGGTCCCGGAGCGCTCAATGCTGACACACACCTGACGCGTCCCTCCGGGGCC	1686
QY	578	roProArgGlyValAlaGluSerValHisSerPheIleHisAlaAspCysHisLeuGluProV	598
Db	1687	CCCCGTGGGCGCAGAGTCTGTGACACACTTCTACCAATGCGAGCTGCACCTTAGCGCAG	1746
QY	598	aIArgCysGlnAlaProProProArgCysProSerGlnAlaSerGlyArgThrValGlyS	618
Db	1747	TCCGTGCGCAGGCGCCCCCTCCAGAGTCCCAATCTGAGGCAATCCGGAGAGACTGTGGCA	1806
QY	618	erGlyIleValTyrProThrValHisIsthSerProProProGluIleLeuIleAspIlyS	638
Db	1807	GCGGGAAGTGTATCCACCGGACACACAGCCCTCCACCGAGACGCTGAAGAAGAGAG	1866
QY	638	IaLeuValGluValAlaProSerProGlyProProThrIleuThrSerPheAsnIleProP	658
Db	1867	CACATGTAGAGGTGGCTCCAGCTCTGGGGCCCCCAACCTCACACGCTTCAACATCCAC	1926
QY	658	roGlyProPheSerSerMetHisIleIleLeuGlnThrGlnSerThrGlyIleCysHisS	678
Db	1927	CCGGGCGCTTACAGCTTCATGCACAGACTGCTGGAGACACAGAGTACAGGTGCTCCAA	1986
QY	678	erSerCysIleIleSerSerProCysSerIlySalaAspSerGlyValaCysGlyProAspS	698
Db	1987	GCTCTTGCAAGTCTCCAGCCCTTGCTTGAAGAAGACAGTGGAGACGTGTGGTCCAGACA	2046
QY	698	erCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetP	718
Db	2047	GCTGCGCTTACTGTGTCGCCGGGCGGGGAGGTGGAGTGTCCGCCACCGTGAAGAAGC	2106
QY	718	roAspSerAspSerGluValaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuA	738
Db	2107	CTGACTCAGACAGCCAGAGAGTTTATGAGTTTACACAGAGATGCCAGACAGCAGACTTC	2166
QY	738	rGAspProHisSererArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerV	758
Db	2167	GGGAGCCCCACAGC---GGGGGGAACGGAAGCTGGGGCCAGATGCAGAGCCCAAGCTCTG	2226
QY	758	AlleuAlaPheThrPArgLeuIleCysAspThrPheArgIlySileValaAspSerIlyP	778
Db	2224	TGCTGCGCTTCTGGAGAGCTAATCTGTGACACCTTCGGAAGAATTTGGACAGCAAGTACT	2283
QY	778	heGlyArgGlyIlyIleMetIleAlaIleuValAsnThrLeuSerMetGlyIleGluTyrH	798
Db	2284	TTGGCGGGGAATTCATGATCGGCATCTCGGTAAACACTCAGCATGGGCATCGAATACC	2343
QY	798	IeGluGlnProGluIleuLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerL	818
Db	2344	ACGAGCAGCCCGAGAGAGCTTACCAAGCCCTTGAATATGACAACTGCTTTCACACAGCC	2403
QY	818	euphAlaIleuGluMetLeuLeuIleuIlySleuLeuValTyrGlyProheGlyIlyIleIyS	838

Dd	2404	TCCTTGCCCTGGAGATGCTGCTGAAGCTGCTTGTAATGATCCCTTGGCTACATCAAGA	2463
Qy	838	snProTyAsnIleIpheAspGlyValIleValIleSerValTyrGluIleValGly	858
Dd	2464	ATCCCTCAACATCTTGCATGATGTGCATTTGATGGCATCACAGTGTGGAGATCTGTGGCC	2523
Qy	858	IngInGlyGlyValLeuSerValLeuArgThrPheArgLeuMetArgValLeuIleu	878
Dd	2524	AGCAGGGGGGGGGCTTCGGTGTGGGACCTTCCGCTGATGCGTGTCTGAAGCTGG	2583
Qy	878	AlaXArgPheLeuProAlaLeuGluArgIleuValIleLeuMetTyrMetAspAsn	898
Dd	2584	TGCCTCTTCGCGCGCGCTGCAGCGGAGAGCTGGTGGTGCATATGAACATCATGACAAAG	2643
Qy	898	AlaIArgPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMet	918
Dd	2644	TGGCACTCTTGATGCTGCTTATGCTTTCATCTTCATCTTCAGCATCTCGGAGCATGC	2703
Qy	918	IleuPheGlyCysIlePheAlaSerGluArgAspGlyAspThrLeuProAspArgIys	938
Dd	2704	ATCTCTTCGGCTGCAGATTGCTCTTACGGGGATGGAGACCTTCGACGACCGAGAGA	2763
Qy	938	snPheAspSerLeuLeuTyrAlaIleValThrValPheGluIleLeuThrGluAsp	958
Dd	2764	ATTTTGACTCTTGTCTCTGCGGCATCTGCATCTCTTTCAGATCTTACCCAGAGAGACT	2823
Qy	958	TPAsnIysValIleuTyrAsnGlyMetAlaSerThrIleSerSerTyrAlaIleuTyrPheI	978
Dd	2824	GGACAAAGCTCTCTCAATAGTATGGCTTCACGTGCTGGGGGCGCTTATTTATTTCA	2883
Qy	978	IleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleuValG	998
Dd	2884	TTGGCTTCATACCTTGCGGCAACTACGTCCTTCAATTGCTGTGTGCCATTTGTGTGG	2943
Qy	998	IuGlyPheGluAlaGlu-----	1003
Dd	2944	AGGCTTCACGGCGGAGGAATCAAGCAACGGGAAAGTGCAGTGCAGTAAAGCTGTA	3003
Qy	1004	-----GlyAspAlaThrIleYsSerGluSerGluProAsp	1015
Dd	3004	TTCAAGCTCGCTGTGCATCTCCACGAGGGGGAGATGTCCAACAAGTCCGAATTCAGAGCCGATTT	3063
Qy	1015	hePheSerProSerValAspGlyAspGlyAspArgGlyIleValArgLeuAlaIleValAlaI	1035
Dd	3064	TCCTTCTCACCCAGCGCTGGATGTATGGGGCAGAGAAAGAAAGCTTGGCTTGGTGTCC	3123
Qy	1035	eugIyGluHisAlaGluIleuArgIysSerLeuLeuProProLeuIleIleHisThrAlaA	1055
Dd	3124	TGGAGACACCCGAGAGCTGCGGAAAGACCTGTGCGGCTCTCATATCATCCACAGCGCG	3183
Qy	1055	IaThrProMetSerHisProIysSerSerSerThrGlyValGlyAlaLeuGlySerG	1075
Dd	3184	CCACACCCATGTGGTGCCCAAGAGCACACAGACGGGCTGGCGAGGCGCTGGGGCCTGT	3243
Qy	1075	IySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisIleGluMetL	1095
Dd	3244	CGTCGCGCGGCACAGCAGCAGCGGGTGCAGAGACCTGGGGCGGCGC---CACAGAGTA	3300
Qy	1095	YsCysProProSerAlaIleArgSerSerProHisSerProTyrSerAlaIleSerSerTPT	1115
Dd	3301	AGTACACCCCAAGGCGCCGACGCTTCCGACAGACCCCTGAGAGCGCTGCAAGCACTGGA	3366
Qy	1115	hrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuIyAsnArgSerP	1135
Dd	3361	CCAGAGGCGCTCCAGCCGGAACAGCTCGGCCGAGCACCCAGCTGTAAGCGGAGAACCC	3420
Qy	1135	roSerGlyIleuArgArgSerLeuLeuSerGlyIleGlyIleGluSerGluAspGluGlu	1155
Dd	3421	CAAGTGGAGAGACGGCGGTCTCTGTTGTTCGGAGAGAAAGCCAGAGAGCCAGATGAAAGG	3480
Qy	1155	IuSerSerGluGluAspArgIleSerProAlaGlySerAspHisArgHisArgGlySerL	1175
Dd	3481	AGAGCTCAAGAGAGCGGCGGCGCTTGGCGGAGAGTGAACATATGCCACAGGGGGGTCC	3540



QY	1175	euGLuAArgGLuAlAlvSerSerPheAspLeuProAspThrLeuGLuValProGLyLeuH	1195
Db	3541	TGGAGCGGAGGCGCMAAGTTCCTTTACCTCGGACACACTGCACCTGCACAGGGCTGC	3600
QY	1195	IsaArgThrAlaSerGlyArgSerSerAlaSerGluHISGLnAspCysAsnGLyLysSerA	1215
Db	3601	ATGCCACTGCCAGTGGCGCGAGGGCTCTCTCTGTAGACACAGAGACTGCATTCGAAAGTCCG	3660
QY	1215	IsaSerGlyA-gLeuAlaArgThrLeuArgThrAspAspProGLnLeuAspGlyAspAspa	1235
Db	3661	CTTCAGGGCGCGCTGGCCCCGGGCGCTGGCGGCTGTAGACCCCCCACTGGAATGGGGATACG	3720
QY	1235	bpAsnAspGluGLyAsnLeuSerLysGlyGLuAGLISGLnAlaTrpValArgSerArgL	1255
Db	3721	CCGATGACAGAGGACACTGTAGACAAAGGGAGACGGGCTCCGGCGTGATCCGAGCCCGAC	3780
QY	1255	euProAlaCysCysArgGLuArgAspSerTrpSerAlaTrpLLePheProProGlnSerA	1275
Db	3781	TCCCTGCTGCTTACCTCGAGCGAGACTCTTGTCACCTTACCTTCTCTCTCTCAGTCCA	3840
QY	1275	rgPheAlaGluLeuLeuCysHisArgLLeIleThrHisLysMetPheAspHisValValLeuV	1295
Db	3841	GGTTCGCCCTCTCTGTGTACCGGATCATCACCCACAAAGATGTTGACCGAGGTGCTCTTG	3900
QY	1295	AlIleIlePheLeuAsnCysLLeThrLLeAlaMetCGLuArgProLysLLeAspProHis	1315
Db	3901	TCAATCATCTTCTTAACTGCATCACATCCGCATCGAGCGGCCCAAAATGACCCCA	3960
QY	1315	erAlaGLuArgLLePheLeuThrLeuSerAsnTrpLLePheThrAlaValPheLeuAlaG	1335
Db	3961	GCGCTGAAGCATTTCTCTGACCTCTTCCAAATTCATCTTTCACCGCAGTCTTCTGCTG	4020
QY	1335	LuMetThrValLysValValAlaLeuGLyTrpCysPheGLyGLuGLnAlaTrpLeuArgS	1355
Db	4021	AAATGACAGTAAAGTGTGTGCACTGGGCTGTGTCTTGGGGAGACAGCGTACTCGCGA	4080
QY	1355	erSerTrpAsnValLLeuAspGLyLeuLeuValLeuLLeSerValLLeAspLLeLeuValS	1375
Db	4081	GCACTTGGAAAGTGTCTGTGACGGGCTGTGGTGCATCTCCGTATGCACATTTCTGTGTGT	4140
QY	1375	erMetValSerAspSerGlyThrTrpLLeLeuGLyMetLeuArgValLLeuArgLeuLeuA	1395
Db	4141	CCATGGCTCTGACAGCGGACCAAGATCTCGGCGATGTGAGGGTGTGTGGCTGTGCTGC	4200
QY	1395	rgThrLeuArgProLeuArgValLLeSerArgAlaGLnGLyLeuLysLeuValValGLuTr	1415
Db	4201	GGACCTCTGCGCCCTCAGGGGTGATCAGCCGGCGCAGGGGCTAAGCTGTGTGTGAGA	4260
QY	1415	hrLeuMetSerSerLeuLysProLLeGLyAsnLLeValValLLeCysCysAlaPhePheI	1435
Db	4261	CGCTGATGTCTCTCACTGAAACCATCGGCAACATTTAGTATCTGCTGTGTCTTCTTCA	4320
QY	1435	LeIlePheGLyLLeLeuGLyValGLnLeuPheLysGLyLysPhePheValCysGLnGLyG	1455
Db	4321	TCAATTTTCGCAATCTTGGGGGTGACGCTCTTCAAAGGGAAGTTTTCGTGTGCCAGGGCG	4380
QY	1455	LuAspThrArgAsnLLeThrAsnLysSerAspCysAlaGLuAlaSerTrpArgTrpValA	1475
Db	4381	AGGATTAACAGAAATCTCAACATTAATGTGACTGTGCGGAGCGCAGTAACTCGGTGGCTCC	4440
QY	1475	rgHisLysTrpAsnPheAspAsnLeuGLyGLnAlaLeuMetSerLeuPheValLLeuAlaS	1495
Db	4441	GGCACAAGTAACTTGTGACAACTTGGCGCAGGCGCTGATGTCTCTGTGCTTTTGGGCTT	4500
QY	1495	erLysAspGLyTrpValAspLLeMetTrpAspGLyLeuAspAlaValGLyValAspGLn	1515
Db	4501	CCAAAGGATGTTGGGTGTGACATCATGTACATGGGTGTGATGCTGTGGCGGTGGACGACG	4560
QY	1515	LnProLLeMetAsnHisAsnProTrpMetLeuLeuTrpPheLLeSerPheLeuLeuLLeV	1535
Db	4561	AGCCCATATAAACCAACACCTCGGAATGCTGTATCTTATCTCTGTTCTGTCTCATTTG	4620

QY	1535	alAlaPhePheValLeuAsnMetPheValGlyValValValGluAspPheHisIleGlyCysA	1555
Db	4621	TGGCTTCCTTGTTCCTGAACATGTTTGTGGGTGGTGGTGAACCTTCCACAAAGTGA	4680
QY	1555	rgGlnHISgInGluGluGluLalaArgArgArgGluGluValArgLeuArgArgLeuG	1575
Db	4681	GGCGACACCGAGAGAGAGAGAGAGCCGGCGGGAGAGAGAGCCCTACGAGAGACTGG	4740
QY	1575	IuLysIlyArgArgSerIlyGluIlyGlnMetAlaGluAlaGlnCysIlyAspProTyrTyrS	1595
Db	4741	AGAAAAAGAGAGG-----AAAGCCCACTGCAAACTTACTACT	4779
QY	1595	erAspTyrSerArgPheArgLeuLeuValHisIleCysLeuCyETHSerHisIlyTyrLeuAspL	1615
Db	4780	CCGACTACTCCCGCTCCCGGCTCTCGTCCACCACTTGTCAGACAGGCACACTCCAGACC	4839
QY	1615	eupHeIIeTHGluValIIleGluLeuAsnValValIThrMetAlaMetGluHisIlyArgInG	1635
Db	4840	TCTTCATACAGGAGTGTCACTGGAGCTGAACCTGTGCACCAATGGCCATGGAGACTACACG	4899
QY	1635	InProGlnIIleLeuAspGluAlaLeuLeuLysIleCysAsnTyrIlePheThrValIIlePheV	1655
Db	4900	AGCCCAAGATTCTGGATGAGGCTGTGAAGATCTGCAACTACATCTTCACTGTACTCTTGG	4959
QY	1655	aIPheGluSerValPheIlyLeuValAlaPheAlaPheArgArgPheGlnAspArgT	1675
Db	4960	TCTTGGAGTCAAGTTTCAACTGTGTGGCTTTGGTTTCCGTCGGTTCTTCCAGACAGGT	5019
QY	1675	rPaenGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluI	1695
Db	5020	GGAAACAGCTGGACCTGGCCATTGGCTGCTGTTCATCATATGGGATCATACGCTGAGAGAA	5079
QY	1695	IeGluValAsnLeuSerIleuProIleAsnProThrIleIleArgIleMetArgValLeuA	1715
Db	5080	TGAGAGTCAAGCCTCGCTGCCATCAACCCACATCATCATCCGATCATGAGGGGTGCG	5139
QY	1715	rgIIeAlaArgValLeuIlyLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisT	1735
Db	5140	GCATTGGCCCGAGTCTGTGAAGCTGTGTGAAGTGGCTGTGGGCTGTCTGTGACA	5199
QY	1735	hrValMetGlnAlaLeuProGlnValGlyAsnLeuGluIlyLeuLeuPheMetLeuLeuPheP	1755
Db	5200	CGGAGATGACAGCCCTGCCCAAGGTGGGAAACCTGGGACTTCTCTTCATATGTTGTTGTTT	5255
QY	1755	heIlePheAlaIleLeuGluValGluLeuPheGluAspLeuGluCysAspGluThrHisP	1775
Db	5260	TCACTTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTACGAGACACACCC	5319
QY	1775	roCyBgIuGluIlyLeuGluYArgHisIalThrPheArgAsnPheGlyMetAlaPheLeuThrL	1795
Db	5320	CCTGTGAAGGGCCTGGGCGCTCATGCCACTTTCGGAACCTTGGGATGCGCTTCCTAACC	5379
QY	1795	eupHeArgValSerThrGluAspAsnThrPaenGlyIleMetIlyAspProSerArgAspC	1815
Db	5380	TCTTCCGAGTGTCCACAGTGTACATTTGAATATGAGATATAGAAGACACCTCCGGGACT	5433
QY	1815	YAspGlnGluSerThrCysTyrAsnThrValIIleSerProIleTyrPheValSerPheV	1835
Db	5440	GTGACACGAGATCCACTCGCTACCAACACGCTCATCTGCGCATATCATCTTGTGCTCTTGG	5499
QY	1835	aIleuThrAlaGlnPheValLeuValAsnValValIIleAlaValLeuMetLysHisIleuG	1855
Db	5500	TGCTGACGGCCCAAGTTCGTCTAGTCAACGTTGGTATGCGGTGCTGTATGAAGACACTGG	5555
QY	1855	IuGluSerAsnIlyGluAlaIlyGluGluIlyArgIuLeuGluGluAlaGluLeuGluIlyuM	1875
Db	5560	AGGAGAGCAACAAGAGGCGCAAGAGAGGCGCAGACTGAGAGCTGAGCTGGAGCTGGAGA	5619
QY	1875	eIlySThrLeuSerProGlnProHisSerProLeuGluIlySerProPheLeuTrpProGluY	1895
Db	5620	TGAAGACCTTACGCCCCCAAGCCCACTGCCACTGGGAGGCGCTTCTCTGGGCTGGGG	5679
QY	1895	aIgluGluValAsnSerThrAspSerProIlySProGluValaProHisThrThrAlaHisI	1915

Db	5680	TCGAGGGCCCGCAGACGCCCCGACAGCCCGACGCTGGGGCTCTGCACCCAGCGGCCACG	5739
Qy	1915	leglYlaaLaSerGlyPheSerLeuGlnHisProThrMetValProHisProGluGluV	1935
Db	5740	CGAATCAAGCTCCCACTTTTCCCTGGAGACACCCCAAGATCAAGCCCAACCCACGAGC	5799
Qy	1935	aLProValProLeuGlyPProAspLeuThrValArgLysSerGlyValSerArgThrH	1955
Db	5800	TGCCA-----GACACAGACTTACTGACTGTGGCGAATCTGGGGGTACGCCGAAGC	5856
Qy	1955	insertLeuProAsnAspSerTyrtMetCysArgAsnGlySerThrAlaGluLysSerLeuG	1975
Db	5851	ACTCTGCGCCCAATGACAGCTACATGTGTGGCATGGAGGACATGCCACGAGGGCCCTGG	5910
Qy	1975	lyHlsArgGlyTrpGlyLeuProLysAlaGlnSerGlySerLileuSerValHisSerG	1995
Db	5911	GACACAGGGGCTGGGGGCTCCCCCAAGCTCAGTCAAGGCTCGCTGTTCGCTTCACTCC	5970
Qy	1995	lnProAlaAspThrSerCysLileuGlnLeuProLysAspValHisTyrlLeuLeuGlnP	2015
Db	5971	AGCCAGCAGATACCAAGTACATCTGTGAGCTTCCCAAGATGACACTCATCTGTCTCAGC	6030
Qy	2015	roHlsGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyLysSerProL	2035
Db	6031	CCCAAGGGCCCAACCTGGGGCACAATCCCAACCTGCCCAACAGAGAGCTCCCTT	6090
Qy	2035	euaLaglnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspAlaGlnG	2055
Db	6091	TGGCTCAGAGCCACTCAGGGCCAGGACGACGACGACATAGGACTGACTCTTGGACGTTACG	6150
Qy	2055	lyLeuGlySerArgGluAspLeuLeuSerGlyValSerGlyProSerCysProLeuThrA	2075
Db	6151	GTCGAGGAGCCGGGAAGACTGTGCTGGCAGAGGTGAAGTGGGCCCTCCCGCCCTGGGCC	6210
Qy	2075	rgSerSerSerPheTrpGlyGlySerSerLileGlnValGlnGlnArgSerGlyIleGlnS	2095
Db	6211	GGGGCTACTTTTCTGGGGCCAGTCAATGATCCACGACACACAGCACTCCGACGCCACA	6270
Qy	2095	eLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluGlnProSerTrpA	2115
Db	6271	GCAAGATCTCAAGACACATGACCCCGCCAGCCCTTGTGCCAGGCCACGACCCCACTGGG	6330
Qy	2115	lalyAspProProGluThrArgSerSerLeuGlnLeuAspThrGlnLeuSerTrpLies	2135
Db	6331	GCAAGGGGCCCTCCAGAGACAGAGACAGCTTAAAGATTGGAACCGAGCTGAGCTGGAATT	6390
Qy	2135	erGlyAspLeuLeu--ProSerSerGlnGluGluProLeuPheProArgAspLeuLysL	2154
Db	6391	CAGAGACCTCTCTCCCTCGCGCCAGGAGAGGCCCCCAATCCCAACGGACCTGAAGA	6450
Qy	2154	ysCysTyrrSerValGluThrGlnSerCysAspArgArgProGlyPheThrLeuAspGluG	2174
Db	6451	AGTCTACAGGTGAAGGCCCAAGACTGACAGCGCGGCTTACGTCCTGGCTGAGTGAAGC	6510
Qy	2174	lnArgArgHisSerLileAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysP	2194
Db	6511	AGAGAGACACTCATAGCCCTCAGCTGCTCGACAGAGGCGCTCCCAACCCACCTGGGCA	6570
Qy	2194	roSerProSerSerLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysL	2214
Db	6571	CAGACCCCTCTAACTTGGGGGCCACAGCTTGGGGGGCTGTGGGAGCGCGCCCAAGAAA	6630
Qy	2214	ysLeuSerProProSerLileSerLileAspProProGlnLysGlnGlySerArgProProC	2234
Db	6631	AACTCAGCGCCCTAGATACACATAGACCCCCCGGAAGGCCAAGAGTCTTGAGACCCCGC	6690
Qy	2234	ysSerProGlyValCysLeuArgArgArgAlaProLysAspSerLysAspProSerV	2254
Db	6691	CCAAGCCCTGGATCTGCTCCGAGAGAGGCTCCGTCAAGGACTCCAAAGATCCCTTGG	6750
Qy	2254	alSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerL	2274

Db	6751	CCCTGGCCCCCTGCACAGCATGCTCCTCGCCCTCCCAAGAAAGATGTCTAGTGC	6810
Qy	2274	eUSerGlyLeuSerSerAspProThrAspMetAspPro	2286
Db	6811	TCTCGGGTTTATCCTCTGCACCCAGCACACCTGGACCCC	6848
RESULT 14			
ADQ89063			
ID	ADQ89063	standard; cDNA; 7648 BP.	
AC	ADQ89063;		
XX			
XX	21-OCT-2004	(first entry)	
DE			
XX	Human urological disorder related protein 4421 encoding cDNA SEQ.15.		
XX	urological disorder; uropathic; cytostatic; urinary incontinence;		
KW	benign prostatic hyperplasia; human; gene; ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..7134	
FT		/tag= a	
FT		/product= "urological disorder related protein 4421"	
PN	WO2004065576-A2.		
XX			
PD	05-AUG-2004.		
XX			
PF	14-JAN-2004;	2004WO-US000750.	
XX			
PR	15-JAN-2003;	2003US-0440318P.	
PR	04-FEB-2003;	2003US-0444783P.	
PR	27-MAR-2003;	2003US-0457901P.	
PR	08-MAY-2003;	2003US-0458775P.	
PR	19-MAY-2003;	2003US-0471614P.	
PR	16-JUN-2003;	2003US-0478742P.	
PR	18-JUL-2003;	2003US-0488529P.	
PR	30-JUL-2003;	2003US-0491156P.	
PR	02-SEP-2003;	2003US-0495594P.	
PR	26-SEP-2003;	2003US-0506332P.	
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Karicheti V, Silos-Santiago I, Eliasof SD;		
XX			
XX	WPI; 2004-562167/54.		
DR	P-PSDB; ADQ89064.		
XX			
PT	Use of polypeptides related to urological disorders, e.g. 44390, 54181,		
PT	211 or for identifying a compound capable of treating a urological		
PT	disorder or identifying and treating a subject having a urological		
PT	disorder.		
XX			
PS	Claim 1; SEQ ID NO 15; 542bp; English.		
XX			
XX			
CC	The present invention describes the use of polypeptides related to		
CC	urological disorders for identifying a compound capable of treating a		
CC	urological disorder, identifying a subject having a urological disorder,		
CC	or treating a subject having a urological disorder. Also described: (1) a		
CC	method for identifying a compound capable of treating a urological		
CC	disorder; (2) a method for identifying a subject having a urological		
CC	disorder; and (3) a method for treating a subject having a urological		
CC	disorder. The compound has uropathic and cytostatic activities. The		
CC	polypeptides related to urological disorders are useful for identifying a		
CC	compound capable of treating a urological disorder, identifying a subject		
CC	having a urological disorder, or treating a subject having a urological		
CC	disorder. Disorders include urinary incontinence and benign prostatic		
CC	hyperplasia. The present sequence encodes a human urological disorder		
CC	related protein, which is used in the exemplification of the present		
CC	invention.		
XX			

Sequence 7648 BP, 1492 A, 2419 C, 2205 G, 1532 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 7648  
Score: 10845.50 Matches: 2105  
Percent Similarity: 89.72% Conservative: 33  
Best Local Similarity: 88.33% Mismatches: 110  
Query Match: 90.17% Indels: 135  
DB: 13 Gaps: 7

US-09-611-257a-24 (1-2287) x ADQ89063 (1-7648)

34 TTPTHAARGAARGHMETGLUARGALAPROARGSERARGASERPROVALASERARG 53  
2 TGGACGAGAGGAGGATGAGCGGGCGCGAGAGATCGGAGACGCCCGAGATTTCATGC 61  
54 SERSERTHTHCYAPPROGJUPROGJYALA-ALAGJYALA-GJYSERTHTGJULYEAASP 73  
62 GGCTCAACACCTCTCGGGGGCCGGGGCCGGCCGGGGCCGGGGTCAAGAAAAGAAC 121  
73 roGlySerAlaaspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValaP 93  
122 CGGGCAGCGCGGACCTCGAGGGCGGAGGGGCTGCCATACCGGGCGTGGCCCGGTGTT 181  
93 hePheTyrLeuSerGlnaPserArgProaRgSerTTPCySleuAqThrValCyAsn 113  
182 TCTTCTACTTGAGCCAGGACAGCGCGCGCGGAGCTGTCTCCACAGGCTCTGAAC 241  
113 roTThPheGluArgValaSerMetLeuValaIleuLeuAnaGlyValaThrLeuGlyMetP 133  
242 CCGGTTTAAAGCCATCAGATGTGTATCTTCTTCACTGCGGACCTGGGCAATG 301  
133 heaRgProCySgluaPAlaAlaCyAspSerGlnaRgCySargIleLeuGlnAlaPhea 153  
302 TCCGGGCAATCGCAGACATCGCTGTGATCCACAGGCTGGCGATCTCGAGGCTTTGG 361  
153 spAsPheIlePheAlaPhePheAlaValaGluMetValaValaLysMetValaAlaLeuGlyT 173  
362 ATGACTTCACTCTTGGCTTCTTGGCGGTGAGATGTGTGAGAAAGATGTGGCTTGGGCA 421  
173 lePheGlyLysLysCySgTyrLeuGlyAspThrThPheAnaRgLeuAspPheIleValaI 193  
422 TCTTTGGAAAAAGTGTACTGTGGAGACACTTGGAAACGGGCTTGACTTTTATGCTCA 481  
193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAnaValaSerPheSerAlaValaArgT 213  
482 TCGCAGGAGATGCTGGAGTACTGCTGGAACCTGCAGAACGTCAAGCTTCTCAAGCTGACGA 541  
213 hrValaRgValaLeuArgProLeuArgAlaIleAnaRgValaProSerMetArgIleLeuV 233  
542 CAGTCCGTGTGCTGCACCGCTCAGGGCCATTAACGGGGTCCACACATGCGCATCTTGG 601  
233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAnaValaLeuLeuLeuCySphPheV 253  
602 TCAAGTGTGCTGTGATACGCTGCCATGTGGGCAACGCTCGTGTCTTCTTCTTGG 661  
253 alPhePheIlePheGlyLeValaGlyValaGlnLeuTPrAlaGlyLeuLeuArgAsnArgC 273  
662 TCTTCTTCACTCTTGGCATGTGGGCTCCAGCTGTGGGCAAGGCTGCTTCCGAACCGAT 721  
273 yePheLeuProGluAnaPheSerLeuProLeuSerValaAspLeuGluProTyrTyrGlnT 293  
722 GCTTCTCACTGAGATTTTCAGCTCCCTCGAGCGGTGACCTGAGCGCTATTACAG 781  
293 hrGluAnaGluuArguLeuSerProPheIleCySgSerGlnProaRgGluAnaGlyMetArgS 313  
782 CAGAGAACGAGATGAGAGCCCTTCACTGTCTCCACGCAACCGAGAAAGGATGGGT 841  
313 erCyAsnRgSerValaProThrLeuArgGlyGlnGlyGlyGlyGlyProProCySgSerLeuA 333  
842 CCTGCAAGACGCTGCCACCGCTGGCGGGGACCGGGGCGGTGGCCACCTTGGGCTGG 901  
333 spTyrGlnThrTyrAnaSerSerSerAnaThrThrCySValaAnaTPrAnaGlnTyrTyrT 353

DB 902 ACTATGAGGCTTACACAGCTCTCCAGCAACACCACTGTGTCACTGAGAACAGTACTACA 961  
353 hrAnaCySserAlaGlyGlnuHisaenProPheLysGlyValaIleAnaPheAsnIleG 373  
962 CCAACTGTCTAGCGGGGAGACAAACCCCTTCAAGGGCGCATCAACTTTCACAACTTGG 1021  
373 lYTYrAlaTPrAlaIlePheGlnValaIleThrLeuGluGlyTyrValaAspIleMetC 393  
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393 yrPheValMetAspAlaHisSerPheTyrAnaPheIleTyrPheIleLeuLeuIleLeV 413  
1082 ACTTTGTATGATCTATCTATCTTCTTCAATTTCACTTCACTTCTCTCCATCATCG 1141  
413 alGlySerPhePheMetIleAnaLeuCySleuValaValaIleAlaThrGlnPheSerGluT 433  
1142 TGGGCTCTTCTTCACTGATCAACCTGTGCTGTGTATTTGCCAGCAGTTCTCAGAGA 1201  
433 hrLysGlnaRgGluSerGlnLeuMetArgGluGlnaRgValaArgPheLeuSerAnaIas 453  
1202 CCAGCAGCGGGAAGCCAGCTGATGCGGAGACAGCTGTGGGTCTGTCTCAAGCCA 1261  
453 erThrLeuAlaSerPheSerGluProGlySerCySgTyrGlyGluLeuLeuLysTyrLeuV 473  
1262 GCACTTGGCTAGCTTCTTCTAGACCCGGCAGCTGCTATAGAGAGCTGCTCAAGTACTGG 1321  
473 alTyrIleuAnaRgLysAlaAlaArgArgLeuAlaGlnValaSerArgAlaIleGlyVala 493  
1322 TGTATCATCTTGTATAGGAGCCGACAGCTGTGCTCAAGTCTCTGGCAGACAGGTGTGC 1381  
493 rGAlaGlyLeuLeuSerSerProValaAlaArgSerGlyGlnGluProGlnProSerGlyS 513  
1382 GGGTTGGGCTGTCCAGCAGCCACGACCCCTGGGGGGCAGAGACCCAGCCACAGCA 1441  
513 erCySgThrArgSerHisArgArgLeuSerValaHisIleLeuValaHisIleHisIleH 533  
1442 GCTGCTGTGCTCCACCGCGCTATCTGCTACACCACTGTGTGCACCAACCAACCAACC 1501  
533 lshIshIshIshIshIshIshIshIshIshIshIshIshIshIshIshIshIshIshIsh 553  
1502 ATCACCACACACACACACCTGGGCATGGAGCGCTCAGGGCCCCCGGGCAGCCGGAGA 1561  
553 leGlnaPArgAspAlaAnaGlySerArgArgLeuMetLeuProProProSerThrProT 573  
1562 TCCAGAGACGAGATGCCAATGGGTCCCGAGCTCATGTGTGCACACCCCTGAGCGCTG 1621  
573 hrProSerGlyGlyProProArgGlyValaGluSerValaHisSerPheTyrHisAlaAspC 593  
1622 CCTCTCCGGGGCCCCCTGTGGCGCAGAGTGTGTGCACAGCTTCTTACATGGCCGACT 1681  
593 yeHisIleuGluProValaArgCySgluaAlaProProProArgCySProSerGluAlaSerG 613  
1682 GCCACTTGAAGCAGATCCGCTGCCAGGGCCCCCTCCAGATGCCCATGTAGGGATCGG 1741  
613 lYArgThrValaGlySerGlyLysValaTyrProThrValaHisIshSerProProProGluT 633  
1742 GCAGAGCTGTGGGACGGGGAAGGTGTATCCACCGTGCACACAGCCCTCCACCGGAGA 1801  
633 leLeuLysAspLysValaLeuValaGluValaAlaProSerProGlyProProThrLeuThS 653  
1802 CGCTGAAGAGAAAGACATGATGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTTCACCA 1861  
653 erPheAnaIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673  
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693 laCyGlyProAspSerCySProTyrCySAlaArgThrGlyValaGlyGluProGluSerA 713

Dd 1982 CCTGTGTCAGACAGACTGCCCTTACTGTGCCCCGGGCGAGGGAGGTGAGTCTG 2041  
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Dd 2042 CCGACCGTGAATGCTGACTGACAGACAGCGAGGATTATGATGATTCACACAGGATGCGC 2101  
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Dd 2159 CAGAGCCACAGCTCTGTGCTGGCTCTTGAGAGGCTATCTGTACACCTTCGAAAGATTG 2218  
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Dd 2219 TGGACAGCAAGACTTGTGGCCGGGGAATCATGATGCCATCCTGTGTAAACAACATCAACA 2278  
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Dd 2339 TCGCTCTTACACAGCCTCTTGCCCTGGAGATGCTGTGAAGCTGCTGTGTGATGCTCCCT 2398  
Qy 833 heGlyTyrIleIlyAsnProTyrAsnIlePheAspGlyValIleValIalleSerValT 853  
Dd 2399 TTGGCTACATCAAGAAATCCCTAACATCTTCGATGTGTCTATGTGTCAACAGCGGT 2458  
Qy 853 rPgIuIleValGlyGlnGlnIlyGlyGlyLeuSerValLeuArgThrPheArgLeuMeCa 873  
Dd 2459 GGGAAATCGTGGGCGACAGGAGGGGGCGGCTGTGGTGTGGGACCTTCGCCCTGATGTC 2518  
Qy 873 rGValLeuIlyLeuValArgPheLeuProAlaLeuGlnhArgIleuValIalleuMeCtL 893  
Dd 2519 GTGTCTGAAGCTGTGGCTTCTCTGCGGCGCTGACAGGCGAGCTGTGTGGTCTCATGA 2578  
Qy 893 ySThMeCAspAsnValAlaThrPheCySMetLeuLeuMetLeuPheIlePheIlePheS 913  
Dd 2579 AGACCATGAGACAACGTGGCCACTTGTGATGCTCTTAAGCTTCTTCACTTCATCACTTCA 2638  
Qy 913 eErlleuGlnIyMeHi5leuPheGlyCysIySPheAlaSerGluArgAspGlyAspTrL 933  
Dd 2639 GCATCTGGGCGATGATCTCTTCGCGTGCAGATTGGCTCTGAGGGGATGGGGACACCC 2698  
Qy 933 eUpProAspArgIlyAsnPheAspSerLeuLeuTrpAlaIleValIThrValPheGlnIle 953  
Dd 2699 TCCAGACCGGAAATTTTGACTCCTTGCTGTGGGCCATCGTCACTGCTTTCAGATCC 2758  
Qy 953 eUThrGlnGluAspTrPheAsnIlyValLeuTyrAsnGlyMeCaIaSerThrSerSerTrPA 973  
Dd 2759 TCACCCAGAGAGACTGGAAACAAAGTCTCTTACAAATGTGATGGCTTCACGTCGTCTGAG 2818  
Qy 973 1aAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993  
Dd 2819 CGGCGCTTATTCTATTCATGCGCTCATGACCTTGGGCACTACGTGCTTTCANTTTGTCTG 2878  
Qy 993 a1AlaIleuValGluGlyPheGlnIaGlu----- 1003  
Dd 2879 TCGGCATTCGTGTGGAGGGCTTCCAAGCGGAGAAATCAGAAACGGGAAGTGGAGTg 2938  
Qy 1004 -----GlyAspAlaThrIlySerG 1010  
Dd 2939 GACAGTTAAGCTGTATTCACTGCGCTGTGACTCCAGGGGGGAATGCAACAAGTCCG 2998  
Qy 1010 1uSerGluProAspPhePheSerProSerValAspGlyAspGlyAspArgIlySLyAspGly 1030  
Dd 2999 AATTCAGAGCCCAATTTCTTCTACCCAGCGCTGTGATGTGATGGAGACAGAAAGAGTGT 3058  
Qy 1030 eUAlaLeuValAlaLeuGlyGluHISa1aGluLeuArgIlySerLeuLeuProProLeuI 1050  
Dd 3059 TGGCTTGTGTGTCCCTGGGAGAGCAACCGGAAGCTCGGGAAGAGCCTGCTGCGCTCTCA 3118

Qy 1050 1eIleHi5ThrAlaAlaThrProMeSerHi5ProIlySerSerSerThrGlyValaGlyG 1070  
Dd 3119 TCATTCACAGGCGCGCCACACCATGTCTGCTGCCCAAGACACACAGACGGGCTGGCGG 3178  
Qy 1070 1uAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAla 1090  
Dd 3179 AGGCGTGGGCGCTGCGTGGCGCGCACAGACAGACAGCGAGTGGGCGAGACTTGGGGCGG 3238  
Qy 1090 1aHi5Hi5GluMetIlyCysProProSerAlaArgSerSerProHi5SerProTrPserA 1110  
Dd 3239 CC---CACAGATTAAGTCAACCGCGCCAGCGCCGCACTCTCCGCAACGCGCTGGAGCG 3295  
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Dd 3296 CTGCAGAGACTGGAACCAAGAGGGGCTCCAGCCGGAACACGCTGGCGCTGCACCCAGCC 3355  
Qy 1130 eUlyAsArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnIus 1150  
Dd 3356 TGAAGCGGAGAGGCCAAGTGAAGAGCGCGGTCCCTGTGTGGAGAAAGCCAGGAGA 3415  
Qy 1150 eErGlnAspGluGluIlySerSerGluIlyAspArgAlaSerProAlaGlySerAspHi5A 1170  
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Qy 1170 rGHi5ArgGlySerLeuGluArgGluAlaIlySerSerPheAspLeuProAspThrLeuG 1190  
Dd 3476 GCCACAGGGGTCCTCTGAGCGGAGGCCCAAGACTTCTTGAACCTCCAGACACACATGC 3535  
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Dd 3536 AGGTGCCAGGGCTCATTCGCACTGCCAGTGGCCGAGGGGTCTGCTTTCAGAGCACAGGACT 3595  
Qy 1210 ySaAsnGlyIlySerSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL 1230  
Dd 3596 GCAATGGCAATCGCTTCAGGGGCGCTGGCGCGGCTTGCGGCTGTAGTAAACCCGCCAC 3655  
Qy 1230 eUAspGlyAspAspAspAspAspGluGlyAsnLeuSerIlySGlyGluArgIleGlnAlaT 1250  
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Qy 1270 heProProGlnSerArgPheArgLeuLeuCySHISaGlyIleIleThHi5IyMetPhea 1290  
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Dd 3836 ACACAGTGTCTCTGTATCATCTTCTTAACTGCATCACATGCGCATGGAGGGCCCA 3895  
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Dd 3896 AAATTGAACCCCAACAGCGCTGAACGATCTTCCGACCCCTTCCAATTCACTTTCACCG 3955  
Qy 1330 1aValPheLeuAlaGluMetThrValIlySValAlaLeuGlyTTPCyPheGlyGluG 1350  
Dd 3956 CAGCTTTCCTGGCGAAATGACATGAAGGTGTGGGACTGGGGTGTGTTCGGGGAGC 4015  
Qy 1350 1nAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValI 1370  
Dd 4016 AGCGGTACTCGGAGACGATTGGAACTGTGAGACGGGCTTGTGTCTATCTCCGTCA 4075  
Qy 1370 1eAspIleLeuValSerMetValSerAspSerGlyThrIlySIleuGlyMeMetLeuArgV 1390  
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QY 1410 ybLeuValValGluThrLeuMetSerSerLeuLeuProIleGlyAsnIleValIleValIleC 1430  
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QY 1470 eTyTrArgTrpValArgHisIleValTyrAsnPhePheAsnLeuGlyGlnAlaLeuMetSerL 1490  
| | | | |  
Db 4376 GTTACCGGTGGGTCCGGCAACAAGTCAACCTTGGCCAGGCGCCGTGATGTCTCC 4435  
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QY 1490 euPheValLeuAlaSerIleValAspGlyTrpValAspIleMetValAspGlyLeuAspAlaV 1510  
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Db 4436 TGTTCCTTGGCTCTCAAGATGTTGGGTGGATCATGTCATGATGGGGCTGGATGCTG 4495  
| | | | |  
QY 1510 aIGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleS 1530  
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Db 4496 TGGGGCTGGACCAAGCCCATCATCAACCAACCCCTGGATGCTGCTGATCTCATCT 4555  
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QY 1570 rgLeuArgIleGluGluGlyIleValArgArg----- 1579  
| | | | |  
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QY 1580 --SerIleGluIleValMetAlaGluAlaGlnCysIleValProTyrTyrSerAspTyrSerA 1599  
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| | | | |  
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QY 1719 aLeuIleValLeuLeuValMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA 1739  
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Db 5156 TGTCTGAAGCTGTGAAGATGT 5215  
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QY 1739 laLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1759  
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Db 5216 CCGTGGCCCAAGGTGGGAACTGGGACTTCTTTCATGTGTGTGTGTGTGTGTGTGTGTGT 5275  
| | | | |  
QY 1759 laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL 1779  
| | | | |

Db 5276 CTCTGGGCTGGAGCTCTTTGGAGACCTGGAGCTGAGAGACACACACCCCTGTAGGGGCC 5335  
| | | | |  
QY 1779 euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValS 1799  
| | | | |  
Db 5336 TGGGCGGTCAAGCCACTTTTGGAACTTGGCATGTGGCTTCTTAACCTCTTCCAGACT 5395  
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QY 1799 eThrGlyAspAsnTrpAsnIleGlyIleMetIleValAspProSerArgAspCybAspGlnIus 1819  
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QY 1859 ybGluAlaIleGlyGluGluAlaGluLeuGluAlaGluLeuGluLeuMetIleThrLeus 1879  
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Db 5576 AGGAGGCCAAGAGAGAGCCGAGCTGAGAGCTGAGCTGAGAGTGAAGTGAAGACCTCA 5635  
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QY 1879 ePProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGlyValA 1899  
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QY 1899 snSerThrAspSerProIleValAlaProHisThrAlaHisIleGlyAlaAlaS 1919  
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QY 1919 eGlyPheSerLeuGluHisProThr----- 1927  
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QY 1927 ----- 1927  
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QY 1928 -----MetValProHisProGluGluValProValProLeuGlyProAspLeuLeuThrV 1946  
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Db 6056 GCAAATATGAGGCCCAACCCACAGAGCTGCCA-----GACCAAGCTTACTGACTG 6106  
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Db 6167 ATGGAGAGCACTCGAGGGGCCCTTGGACACAGGGGCTGGGGGCTCCCAAGCTCACT 6226  
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QY 1986 eGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuP 2006  
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Db 6227 CAGGCTCCGTCTTGTCTGTTCACTCCAGCCAGAGATCAAGCTACATCTGCAAGCTTC 6286  
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QY 2006 roIleAspValHisTyrIleLeuGlnProHisGlyAlaProThrTrpGlyAlaIlePro 2026  
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QY 2026 ybLeuProProGlnArgSerProLeuAlaGlnArgProLeuArgArgIleAlaI 2046  
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Db 6347 AACTGCCCCACGAGGAGCTCCCTTGCTCAGAGGCCACTCAGCGCCAGGACGAA 6406
Qy 2046 |eArGThrAAspSerleuAspValGlnGlyLeuGlySerArgGlnAspLeuLeuSerGluV 2066
Db 6407 TAAAGACTGACTCTTGAGCTTGAGGGTCTGGGAGCGGGAAGACCTGCTGGCAGAGG 6466
Qy 2066 aISerGlyProSerCysProLeuThrArgSerSerPheTrpDlyGlySerSerIleG 2086
Db 6467 TGAAGGGGCGCTCCCGCGCCCTGGCGCCGCTACTCTTTCTGGGGCCAGTCAAGTACC 6526
Qy 2086 InValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaP 2106
Db 6527 AGGCACACAGAGACTCCCGCAGCCACCAAGATCTCAAGACACATGACCCCGCAGGCC 6586
Qy 2106 roCySProGlyLeuGlnProSerTrpAlaLysAspProProGlnThrArgSerSerIleuG 2126
Db 6587 CTGGCCAGGGCCCAACCCCACTGGGGCAAGGGCCCTCCAGAGCCCAAGACAGCTTAG 6646
Qy 2126 IuLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeu---ProSerSerGlnGluG 2145
Db 6647 AGTTGGACACGAGCTGAGCTGATTCAGAGAGACTCTCCGCCCTGGCGGCGCAGAGG 6706
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Qy 2185 sPSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlnProLeuG 2205
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Qy 2205 IyGlyProGlySerArgProLysLysLysLeuSerProProSerIleSerIleAspProP 2225
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Qy 2225 roGluSerGlnGlySerArgProProCysSerProGlyValCysleuArgArgAlaP 2245
Db 6947 CCGAAGGCCAAGAGTCTCGAGACCCCGCCAGCCCTGATGCTCCTCGAGAGAGGGCTC 7006
Qy 2245 roAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaIleAsp 2265
Db 7007 CGTCAAGGAGCTCCAGAGATCCCTTGCGCTCTGGCCCCCTGACAGCAGTGGCTGCTGC 7066
Qy 2265 roSerProLysLysAspThrIleuSerIleuSerGlyLeuSerSerAspProThrAspMetA 2285
Db 7067 CCTCCCAAGAAAGATGTGAGTCTCTCCGGTTATCTCTGAGCCACAGACGACTGG 7126
Qy 2285 sPPro 2286
Db 7127 ACCCC 7131
RESULT 15
ADSI6298
ID ADSI6298 standard; DNA; 7648 bp.
AC ADSI6298;
ADSI6298;
DT 02-DEC-2004 (first entry)
DE Human voltage-dependent alpha 1G subunit calcium channel (CACNA1G) DNA.
XX Voltage-dependent ion channel; drug candidate;
XX aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;
XX anticonvulsant; antiarrhythmic; human; alpha 1G subunit; ds.
OS Homo sapiens.
XX
XX US2004175761-A1.
XX
XX 09-SEP-2004.
PD
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XX 01-MAR-2003; 2003US-00377139.
PF
XX 01-MAR-2003; 2003US-00377139.
PR
XX (MACK/) MACKINNON R.
PA (MACK/) MACKINNON A L.
PA (JIAN/) JIANG Y.
PA (RUTA/) RUTA V.
XX
XX Mackinnon R, Mackinnon AL, Jiang Y, Ruta V,
XX WPI: 2004-642122/62.
XX
XX REFSEQ: NM_018896.
XX
XX Screening drug candidates that target voltage dependent ion channel
XX protein, involves contacting screening protein with chemical compound,
XX PT which is drug candidate and determining whether chemical compound binds
XX to screening protein.
XX
XX PS Disclosure; SEQ ID NO 10; 61pp; English.
XX
XX CC The invention relates to the composition of matter suitable for use in
XX CC identifying chemical compounds that bind to voltage-dependent ion channel
XX CC proteins. The composition comprises a screening protein that consists of
XX CC an ion channel voltage sensor domain of the ion channel protein
XX CC immobilised on a solid support. The invention is useful for identifying
XX CC chemical compounds (drug candidate) that bind to voltage-dependent ion
XX CC channel proteins. The drug candidate of the invention is utilised for
XX CC treating a condition mediated by aberrant electrical activity that
XX CC initiates uptake or release of neurotransmitters and contraction of
XX CC muscles. The drug candidate of the invention is also utilised for
XX CC treating epilepsy and arrhythmia. The present sequence is a voltage-
XX CC dependent calcium channel DNA.
XX
XX SQ Sequence 7648 BP; 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0 Length: 7648
XX Score: 10845.50 Matches: 2105
XX Percent Similarity: 89.72% Conservative: 33
XX Best Local Similarity: 88.33% Mismatches: 110
XX Query Match: 90.17% Indels: 135
XX DB: Gaps: 7
XX
XX US-09-611-257a-24 (1-2287) x ADSI6298 (1-7648)
Qy 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db 2 TGAAGAGAGAGAGATGAGAGCGGCGCCGAGAGTGGGACAGCCCGGAGCTTCATGC 61
Qy 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGlnLysAsp 73
Db 62 GGCCTCAACGACTGTGCGGGGCGCGGGGCGGGGCGGGGCTCAGCAAAAAAGAAC 121
Qy 73 roGlySerAlaAspSerGluAlaGlnGlyLeuProTyrProAlaLeuAlaProValAlaP 93
Db 122 CGGCAAGCGCGACTCCGAGGCGGAGGGGCTGCGTACCCGGCGCTGCGTGGTTT 181
Qy 93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsp 113
Db 182 TCTTCTACTTGAGCCAGAGAGCGCGCGCGAGCTGTCTCCGACGCTGTAAAC 241
Qy 113 roTTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 182 CTGTGTTTGAGCGCATGAGATGTGTGTCCTTCTCAACTGCGTACCCCTGGGCAATG 301
Qy 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db 302 TCCGGCATGCGAGGAGATGCGCTGTGACTCCAGCGCTCCGGATCTCTCAGGCCCTTG 361
Qy 153 sPAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyT 173
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D 362 ATGACTTCACTCTTGGCTTCTTGGCGTGGAGATGCTGTAAGATGTCGGCTTGGGA 421  
Q 173 IepheGlyYublyscYsTytleuGlyAspThrTrpAsnArgleuAhpheIleValI 193  
D 422 TCTTTGGGAAAAAGGTTACTCTGGGAGACACTTGGAAACGGGCTGACTTTTCATGCTCA 481  
Q 193 IeAlGlyMetleuGlyYrSerleuAspLeuGlnAsnValSerPheSerAlaValArgT 213  
D 482 TCGCAGGGAGTGTGGAGTACTCGCTGGACTGTGAGAACGTCTTCACTGCTGACGGA 541  
Q 213 hVValArgValIleuArgProleuArgAlaIleAsnArgValProSerMetArgIleLeuV 233  
D 542 CAGTCGCTGTGCTGACACCGCTCAGGGCCATTACCGGGGTGCCACAGTCCGATCTTGG 601  
Q 233 aThrleuLeuLeuAhpThrleuProMetleuGlyAsnValIleuLeuLeuCySphePheV 253  
D 602 TCACGTGGCTGTGGATAGCTGCTGCCATGCTGGGCAACGTCCTGCTGCTTCTTGG 661  
Q 253 aIphePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyleuLeuArgAsnArgC 273  
D 662 TCTTCTTCACTTCCGCTCATGCTCGCGCTCAGCTGTGGCAGGGGCTGTCGGAACCGAT 721  
Q 273 yPheLeuProGluAenPheSerleuProleuSerValAspLeuGluProTyTYrTYrGlnT 293  
D 722 GCTTCTTACCTGAGAAATTCAAGCTTCCCTGAGCGTGAACCTGGAGCCGCTATTACAGA 781  
Q 293 hrgGluAenGluAhpGluSerProPheIleCySerGlnProArgGluAenGlyMetArgS 313  
D 782 CAGAGAACAGAGATGAGAGACCCCTTCACTGCTCCAGCCAGCCAGGAACGGGATCGGT 841  
Q 313 eCyAArgSerValProThrleuArgGlyGlyGlyGlyGlyProProCySerleuA 333  
D 842 CCTGCGAAGACCGTCCACGCTGCGCGGGAGCCGGGGCGGTGCGCACCTTGGGCTCG 901  
Q 333 gPTyGluThrTyraSerSerSerSerAsnThrCysValAsnTPAsnGlnTyTYrTYT 353  
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Q 353 hAsnCySerAlaGlyGluHleAsnProPheIleGlyAlaIleAsnPheAspAsnIleG 373  
D 962 CCAACGCTCAGGGGGGGAGACAAACCCCTTCAAGGGCGCCATCACTTGGCAACATTG 1021  
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Q 393 yPheValMetAspAlaHisSerPheTyraAsnPheIleTyrrheIleleuLeuIleIleV 413  
D 1082 ACTTGTGTGATGATGCTCATCTCTTCACAATTTCATCTTCACTTCTCATCATG 1141  
Q 413 aGlySerPhePheMetIleAsnLeuCySerleuValIleAlaThrGlnPheSerGluT 433  
D 1142 TGGGCTCTCTTCTTCAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1201  
Q 433 hrlYsglnArgIleuSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453  
D 1202 CCAAGCAGCGGGAAGCAGCTGATCGGGAGCAGCTGCGGTTCTGTCCAAAGCCCA 1261  
Q 453 eThrleuAlaSerPheSerGluProGlySerCystrYrGluGluLeuLeuTyTYrleuV 473  
D 1262 GCACCTGTGCTACTTCTTGAAGCCCGGAGCTGTGATAGAGAGCTGTCAAGTACTCTG 1321  
Q 473 aLYrIleleuArgValAlaAlaArgArgleuAlaGlnValSerArgAlaIleGlyValA 493  
D 1322 TGTACATCTTCTGTAGGAGCCCGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1381  
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Q 513 eCythrAArgSerHleArgArgleuSerValHisIleleuValHisIleHisIleH 533  
D 1442 GCTGCTCTGCTCCACCGCGCTATCTGTCACCACTGTGTGACCAACACCAACCAACC 1501

Q 533 IeHisIleHisIleTyrrHisleuGlyAenGlyThrleuArgValProArgAlaSerProGluI 553  
D 1502 ATCACACCACTTACCACTGGGCAATGGAGCGCTAGGGCCCCCGGGCCAGCCGGAGA 1561  
Q 553 IeGluAspArgAspAlaAsnGlySerArgArgleuMetleuProProSerThrProT 573  
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Q 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrrHisAlaApc 593  
D 1622 CCTCTCCGGGGCCCCCTGGTGGCGCAGATGTGTGACAGACTTTCATCAATGCGGACT 1681  
Q 593 yHisleuGluProValArgCyseGlnAlaProProProArgCyAProSerGluAlaSerG 613  
D 1682 GCCACTTGAAGCAATCCGCTGCGCAGGGCCCCCTCCAGGTCCTCATGTAGGGATCCG 1741  
Q 613 IYArgThrValGlySerGlyysValTYrProThrValHisThrSerProProGluI 633  
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D 1802 CGCTGAGAGAGAGGACCTAGTAGAGTGGCTGCAGACTTGGGCCCCCAACCTCACCA 1861  
Q 653 ePheAsnIleProProGlyProPheSerSerMetHisLyLeuLeuGluThrGlnIserT 673  
D 1862 GCCTCAATATCCACCCGGGCTTCACTCATGTGCAACAAGCTGTGGAGACACAGAGTA 1921  
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D 1922 CAGGTGCTGCGAAGCTTCTGCAAGATCTCCAGCCCTTCTTGAAGCAGACATGGAG 1981  
Q 693 IaCyGlyProAhpSerCyProTyCyAlaArgThrGlyAlaGlyGluProGluSerA 713  
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Q 713 IaAspHisValMetProAhpSerAhpSerGluAlaValTYrGluPheThrGlnAspAlaG 733  
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QY 913 eTlLeuGlywMeThsleuPheGlyCySlySPheAlAsErGluArgApGlyAspThL 933  
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QY 953 euThGlnGluAspTrpAsnlySValleuTyAsnGlywMeAlAsErThRSeSerTrPA 973  
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QY 973 lAlAlLeuTyRheIleAlAlEuMeTThRPhEglyAsnTyRValleuPheAsnleuTy 993  
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QY 1004 -----GlyAspAlAThRlySerg 1010  
| | | | |  
DB 2939 GACACTTAAGCTGATTCAGCTGCTGTGACTCCAGGGGGGAGATGCCAACAAGTCCG 2998  
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QY 1010 lAsErGluPAspAAspPheSerProSerValAspGlyAspGlyAspAArglySlyAsArgL 1030  
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DB 2999 AATCAGAGCCGATTTCTTCTCACCCAGCCTGATGTGATGGGAGCAGAAAGAGTCTCT 3058  
| | | | |  
QY 1030 euAlAlleuValAlAlleuGlyGlnHsAlAGluLeuArglySserleuEuPAspPheL 1050  
| | | | |  
DB 3059 TGGCCTTGCTGTCCCTGGAGAGCACCAGAGCTGGAAAGCCTGTGCGCCTCTCA 3118  
| | | | |  
QY 1050 lElleHsEThRAlAlThRProMetSerHsProLySserSerThRgLyAlGlyG 1070  
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DB 3119 TCATCCACAGGCCGCCACACCATGTGCTGCTGCCAAAGACACAGCACGGGCTGGGCG 3178  
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QY 1070 lAlAlLeuGlySerglySerArgArgThRSeSerSerGlySeraAGluProGlyAla 1090  
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DB 3179 AGGCCCTGGGCCCTCGTCGCGCCGCCACAGCAGCGAGCGGTGCGCAAGCTCGGGGCGG 3238  
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DB 3535 AGGTCCCAAGGGGTGCATGCACACTGCCAGTGGCGAGGCTGTGCTTCTTAAGCACCGAGACT 3595  
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QY 1310 ySllleAspProHsSerAlAGluArglllePheLeuThRleuSerAsnTyRllePheThR 1330  
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QY 1350 lNAlATyLeuAsRSeSerTrpAsnValleuAspGlyLeuLeuValleuLleSeraYl 1370  
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QY 1430 ySCyAlAlPhePheIlellePheGlylleuGlyValGlnleuPheLyGlySypheP 1450  
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DB 4256 GCTGTGCTTCTTATCATATTTGCGCATCTTGGGGGTGACAGCTTTCAAAAGGAAAGTTTT 4315  
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QY 1510 AlGlyValAspGlnGlnProLleMeTAsnHsAsnProTPMeLeuLeuTyRPhelLes 1530  
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QY 1580 --SerlySgluTySglMeAlAGluAlAGlnCySlySProTyRlyTySerAspTySera 1599  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 18, 2005, 18:10:57; Search time 721.312 Seconds  
(without alignments)  
5188.000 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028  
Sequence: 1 MLPHRVRPCVTRTPPLRGSGAR.....KKDTLSGLSSLDPTDMDPZ 2287

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cg2\_1/USPTO\_spool/US09611257/runat.15092005.134301.25201/app.query.fasta\_1.4878  
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Database : Issued Patents NA:\*

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- 2: /cg2\_6/prodata/1/ina/5B.COMB.seq:\*
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- 5: /cg2\_6/prodata/1/ina/PCTUS.COMB.seq:\*
- 6: /cg2\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11066.5	92.0	7741	3	US-09-426-998-4
2	10948.5	91.0	6822	3	US-09-426-998-3
3	10739	89.3	7405	4	US-09-949-016-3859
4	6241	51.9	7898	3	US-08-984-709A-49
5	6103	50.7	3993	4	US-09-398-522-51
6	5420	45.1	6816	3	US-09-404-650-1
7	5420	45.1	6816	4	US-09-935-541-1
8	5420	45.1	6855	4	US-09-404-650-3
9	5420	45.1	6855	3	US-09-935-541-3
10	5407	45.0	6503	4	US-09-404-650-12
11	5407	45.0	6503	4	US-09-935-541-12
12	2055	17.1	70308	4	US-09-949-016-15601

13	1974	16.4	1669	3	US-08-984-709A-51	Sequence 51, Appl1
14	1745.5	14.5	7362	1	US-08-455-543A-7	Sequence 7, Appl1
15	1745.5	14.5	7362	2	US-08-193-078B-7	Sequence 7, Appl1
16	1745.5	14.5	7362	2	US-08-223-305C-7	Sequence 7, Appl1
17	1745.5	14.5	7362	2	US-08-149-097D-7	Sequence 7, Appl1
18	1745.5	14.5	7362	3	US-08-949-386-7	Sequence 7, Appl1
19	1745.5	14.5	7362	3	US-08-450-562-7	Sequence 7, Appl1
20	1745.5	14.5	7362	3	US-08-984-709A-7	Sequence 7, Appl1
21	1745.5	14.5	7362	3	US-08-450-272-7	Sequence 7, Appl1
22	1745.5	14.5	7362	4	US-09-268-163-3	Sequence 7, Appl1
23	1743.5	14.5	7362	4	US-08-450-273-7	Sequence 7, Appl1
24	1740.5	14.5	7266	3	US-08-713-118-1	Sequence 1, Appl1
25	1740.5	14.5	7266	3	US-09-452-007-1	Sequence 1, Appl1
26	1739.5	14.5	7364	3	US-09-268-163-5	Sequence 5, Appl1
27	1727	14.4	7175	1	US-08-455-543A-8	Sequence 8, Appl1
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37	1703	14.2	5975	1	US-08-404-354B-1	Sequence 1, Appl1
38	1703	14.2	5975	1	US-08-314-083B-1	Sequence 1, Appl1
39	1703	14.2	5975	1	US-08-435-675B-1	Sequence 1, Appl1
40	1703	14.2	5975	3	US-08-884-599-1	Sequence 1, Appl1
41	1699.5	14.1	6114	4	US-09-495-714C-5	Sequence 5, Appl1
42	1693	14.1	7011	3	US-09-268-163-9	Sequence 9, Appl1
43	1693	14.1	5975	1	US-08-336-257A-3	Sequence 3, Appl1
44	1683.5	14.0	5962	6	5386025-5	Patent No. 5386025
45	1683.5	14.0	5962	6	5386025-5	Patent No. 5386025

ALIGNMENTS

RESULT 1  
US-09-426-998-4  
Sequence 4, Application US/09426998  
Patent No. 6358706  
GENERAL INFORMATION:  
APPLICANT: DUBIN, ADRIENNE E.  
APPLICANT: PYATT, JAYASHREE  
APPLICANT: ZHU, JESSICA Y  
APPLICANT: ERLANDER, MARK G  
APPLICANT: GALINDO, JOSE E  
TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM  
FILE REFERENCE: ORT-1057  
CURRENT APPLICATION NUMBER: US/09/426, 998  
CURRENT FILING DATE: 1999-10-26  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PATENTIN VER. 2.0  
SEQ ID NO 4  
LENGTH: 7741  
TYPE: DNA  
ORGANISM: HOMO SAPIENS  
US-09-426-998-4  
Alignment Scores:  
Pred. No.: 0  
Score: 11066.50  
Percent Similarity: 93.81%  
Best Local Similarity: 92.38%  
Query Match: 92.01%  
DB: 3  
Gaps: 5  
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Db 431 CCGCCGGGGCCCGGGGGTGGCGTGAAGGACACCTCCTCTAAGGGGCGCCCTTGCCTCT 490

QY 23 SerAspProGluYProArgIleuAlaArgIYTrpThrArgArgMetGluArgAla 42  
DB 491 CCGGATCCGCCGGGACCCCGGCTGGCCAGAGATGAAGAGAGAGATGAGCGGCG 550  
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DB 551 CCGAGAGATCGGAGACGCCCGGAGCTTCATGCGGCTCAACGACCTGTGCGGGGCGGG 610  
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QY 122 aIIleuIleuIleuAsnCysValIThrIleuGlyMetPheArgProCysGluAspIIeAlaCysA 142  
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QY 142 sPserGluArgCysArgIleIleuGluAlaPheAspAspPheIIepheAlaPhePheAlaV 162  
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QY 162 aGluMetValIleuIleuMetValIleuGlyIlePheGlyIleuIleuIleuIleuIleuIleu 182  
DB 911 TGGAGATGGTGGTGAAGATGGTGGCTTGGGCACTTTGGGAAAAAGTTAACTGGAG 970  
QY 182 sPThrTYrAsnArgIleuAspPhePheIIeAlaIleuGlyMetIleuGluTYrSerIleuA 202  
DB 971 ACACCTGGAAACCGGCTTCACTTTTCATGTCATGACGAGGATGCTGAAGATCTGCGTGG 1030  
QY 202 sPLeuGluAsnValSerPheSerAlaValArgThrValArgValIleuArgProIleuArgA 222  
DB 1031 ACTTCGAAAGCTCAAGCTTCTCAAGCTGCAGACAGTCCGTGTGCTGGACCGCTCAAGG 1090  
QY 222 IaIleAsnArgValProSerMetArgIleIleuValIThrIleuIleuAspThrIleuProM 242  
DB 1091 CCATTAAACCGGGTGGCCAGCATGCGCATCTTGTCACTGCTGTGATACGCTGCCCA 1150  
QY 242 eTleuGlyAsnValIleuIleuIleuCysPhePheValIlePheGlyIleValIleuIleu 262  
DB 1151 TGCTGGGCAACGTCGTGCTGCTGCTTCTTCTTCTTCACTTCCGCAATCGTCGGCG 1210  
QY 262 aGluIleuTrpAlaGlyIleuIleuArgAsnArgCysPheIleuProGluAsnPheSerIleuP 282  
DB 1211 TTCACCTGGGCAAGGCTGCTTCGAAACCGATGCTTCTTACTTGAATAATTCAGCTTCC 1270  
QY 282 roIleuSerValAspIleuGluProTYrTYrGluIleuIleuIleuIleuIleuIleuIleu 302  
DB 1271 CCTTGAAGGTGAGCTGAGGAGCTATTAACAAGACAGAGATGAGAGCCCTTCA 1330  
QY 302 leCysSerGluProArgGluAsnGlyMetArgSerCysArgSerValProThrIleuArg 322  
DB 1331 TCTGCTCCAGCAAGCGAGAACCGGATGCTTCGAGAAAGCGTGGCCAGCGCTCCG 1390  
QY 322 IYgluGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 342  
DB 1391 GGGAGCGGGGCGGTGGCCACCTTGGCTGGATGAGATGAGGCTTCAACAGCTCCACGA 1450  
QY 342 snThrThrCysValAsnTYrAsnGlnTYrTYrThrAsnCysSerAlaGlyIleuIleuIleuIleu 362  
DB 1451 ACACCAACCTGTGTCAACTGGAACCAAGTACTACCAACATGCTCAAGCGGGGAGCAAC 1510  
QY 362 roPheIleuGlyAlaIleuAsnPheAspAsnIleuGlyTYrAlaIleuIleuIleuIleuIleuIleu 382  
DB 1511 CTTTCAAGGGCGCATCAACTTTGACCAATTTGGCTATGCTGATCCGCATCTTCCAGG 1570

QY 382 aIIeThrIleuGluGlyTYrPValAspIIleMetTYrPheValMetAspAlaHisSerPheT 402  
DB 1571 TCATCAAGCTTGAAGGCTGGGTGCATCATGTAATCTTTGGATGAGATGCTCATCTTCT 1630  
QY 402 YrAsnPheIIeTYrPheIIeIleuIleuIleIleValIleGlySerPhePheMetIleAsnIleu 422  
DB 1631 ACAATTCATCATCTTCAATCTCTCTCAATCATCGGGCTCTCTTCTTCAATCAACCTGT 1690  
QY 422 YsIleuValIleIIeAlaThrGluIleuSerGluIleuIleuIleuIleuIleuIleuIleu 442  
DB 1691 GCTTGGTGTATGTCACAGGATTCACAGACACCAAGCGGAGAAAGCCAGCTGATGC 1750  
QY 442 rGluGluArgValArgPheIleuSerAsnAlaSerThrIleuAlaSerPheSerGluProG 462  
DB 1751 GGGAGCAGCGTGTCCGCTTCTGTCCAAACGCAACGCAACCTGGCTAGCTTCTTGAAGCCG 1810  
QY 462 IYserCysTYrGluGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 482  
DB 1811 GCACCTGCTATGAGAGACTGCTCAAGTACCTGGTGTACATCTTCTGTAGGCAACCCGCA 1870  
QY 482 rGluAlaGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 502  
DB 1871 GGCTGGCTCAGTCTTCGAGCAGCAGAGTGTGGGTTGGGCTGTCAAGCCACAGC 1930  
QY 502 laArgSerGlyGluIleuProGluProSerGlySerCysThrArgSerHisArgIleuS 522  
DB 1931 CCGTCGGGGGCGCAGAGAACCCAGCCAGCAGCAGCTCTCTCGTCCACCGCGGCTAT 1990  
QY 522 eValIleuIleuValIleuValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 542  
DB 1991 CCGTCCACCACTGTGTACACACACCAACCACTCAACCACTCACTGAGCAATG 2050  
QY 542 IYThrIleuArgValProArgAlaSerProGluIleuIleuIleuIleuIleuIleuIleuIleu 562  
DB 2051 GGAGGCTCAGGGCCCCCGGCGCAGCCGAGATCCAGAGAGGATGCAATGAGTCC 2110  
QY 562 rGArgIleuMetIleuProProSerThrProThrProSerGlyIleuProProArgIleuA 582  
DB 2111 GCAGGCTCATGCTCCACCAACCTCGACGCTGCTCCGCGGGGCCCCCTGCTGGCG 2170  
QY 582 IaGluSerValHisSerPheTYrHisAlaAspCysHisIleuGluProValArgCysGluA 602  
DB 2171 CAGAGCTGTGCACAGCTTTCATCATGCTCCAGCTGCCATTAGAACCACTGCGTCCAGG 2230  
QY 602 IaProProProArgCysProSerGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 622  
DB 2231 CGCCCTCCAGGTCCTCCATCTGAGGATCCGAGAGACTGTGGAGCGGGAAGGTGT 2290  
QY 622 YrProThrValHisThrSerProProProGluIleuIleuIleuIleuIleuIleuIleuIleu 642  
DB 2291 ATCCACCGTGCACACAGCCCTCCACCGAGAGCGTGAAGAGAGCACTAGTAGAGG 2350  
QY 642 AlaIleProSerProGlyProProThrIleuThrSerPheAsnIleProProGlyProPheS 662  
DB 2351 TGGTGGCAGGCTCGGGCCCCCAACCTTCAACAGCTTCAACATCCACCGGGGCTTACA 2410  
QY 662 eTleuMetHisIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 682  
DB 2411 GCTCATAGCACAACTCTGAGACACAGATACAGGTGCTGCAAGGCTTTCAGAGA 2470  
QY 682 leSerSerProCysSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 702  
DB 2471 TCTCAGCCCTTGTGTTGAAGACAGACAGTGAAGCTGTGTCCAGACAGTGGCCCTTACT 2530  
QY 702 YsAlaIleGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 722  
DB 2531 GTGCCCGGGCGGGGCGAGGAGGTGAGCTCGCGCAGCCGTGAATCTCGACTCAACACA 2590  
QY 722 eTleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 742  
DB 2591 GCGAGGCGATTATGAGTTCACACAGAGTCCAGCACAGGACCTCGGGAGCCCAACA 2650  
QY 742 eTArgArgArgIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 762

DB 2651 GC---CGGGGCAACGAGCCCTGGGCGCCAGATGCACAGCCCGCTGTGCTGGCCCTTCT 2707  
QY 762 rARgLeuIleCyAspThrPheArgLysIleValAspSerLysTyrPheGlyArgLysI 782  
DB 2708 GAGGCTAATCTGTACACCTTCCGAAAGATTGTGACAGCAAGTACTTTGGCCGGGGA 2767  
QY 782 lMeTlleAlaIleLeuValAsnThrLeuSerMetGlyIleGlyTyrHisGluGlnProG 802  
DB 2768 TCATGATCCCATCCCTGCTCAACACACTCAGCATGGGCAATGCACAGAGCCCG 2827  
QY 802 lGluLeuThrAsnAlaLeuGlnIleSerAsnIleValPheThrSerLeuPheAlaLeuG 822  
DB 2828 AGAGGCTTACCAACCGCTTGAAGTACAGAACATGCTTTCACACACCTCTTGGCCCTG 2887  
QY 822 lMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI 842  
DB 2888 AGATGCTGCTGAAGCTGCTTGTGTATGTCCTTGGCTACATCAAGAAATCCCTACACA 2947  
QY 842 lPheAspGlyValIleValIleSerValTrrpGlnIleValGlyGlnGlnGlyG 862  
DB 2948 TCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3007  
QY 862 lYLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP 882  
DB 3008 GCTTCGCGTGTGCTGGACCTTCGCTGATGCTGTGCTGAAGCTGTGCTTCCTG 3067  
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DB 3068 CGGCGCTGACGGGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3127  
QY 902 yMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC 922  
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QY 922 yAlaPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerI 942  
DB 3188 GCAGGTTTGCCTCTGAGCGGAGTGGGAGCACCTGCGACGCGGAAGATTGGACTCTCT 3247  
QY 942 euleuTrpAlaIleValIleThrValPheGlnIleLeuThrGlnGlnIleAspTrpAsnLysValI 962  
DB 3248 TGTCTTGGGCAATGTCATCTGTCTTTCATGATCTTCGACCGAGAGACTGGAAACAAGTCC 3307  
QY 962 eulYrAsnGlyMetAlaSerThrSerSerTrpAlaIleLeuTyrPheIleAlaLeuMet 982  
DB 3308 TCTACATGGTATGGCTTCACAGCTGCTGCGGCGGCTTATTTCATGATGCTCATGCA 3367  
QY 982 hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 1002  
DB 3368 CCTTCGGCAACTACGTGCTCTTCATATTGCTGTGCTGCATTCGTGTGAGAGGCTTCAGG 3427  
QY 1002 lAGlu----- 1003  
DB 3428 CGAGGAATACAGCAACGGAAGATCGAGTGCAGATTTAACTGATTCACCTGCTG 3487  
QY 1004 -----GlyAspAlaThrLysSerGlnSerGlnProAspPhePheSerProS 1019  
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QY 1019 erValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisA 1039  
DB 3548 GCTTCGATGTGTATGGGAGACAGAAAGATGCTTGGCTGTGTGCTTCGGAGAGAGACC 3607  
QY 1039 lAGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetS 1059  
DB 3608 CGAGGCTCGGAAGAGCTGCTGCTGCTTCATTCATCCACAGCCGCCACACCATGT 3667  
QY 1059 erHisProLysSerSerSerThrGlyValGlyGlnAlaLeuGlySerGlySerArgArgT 1079  
DB 3668 CGGTGCCCAAGAGACACAGACGGGCTGTGGGCGAGGCGCTGCGCTGCCGCGCGCA 3727  
QY 1079 hrSerSerSerGlySerAlaGluProGlyValAlaHisHisGluMetLysCysProProS 1099

DB 3728 CCAGCAGCAGGGGGCTGGCAGAGCTGGGCGGCC---CACGATGAATGATCACGCCCA 3784  
QY 1099 erAlaArgSerSerProHisSerProTrpSerAlaIleAspSerTrpThrSerArgAs 1119  
DB 3785 GGGCCCGAGGCTTCCGACAGCCCTTGAGCGCTGCAGAGAGCTGACACGAGGCCCT 3844  
QY 1119 erSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluA 1139  
DB 3845 CCAGCCGGAACAGCTTCGCGGTGACCCAGCTGACCGAGAGAGAGCCCAAGAGAGAGC 3904  
QY 1139 rGArgSerLeuLeuSerGlyGlnGlnGlnSerGlnAspGlnGlnGlnSerGlnG 1159  
DB 3905 GCGGCTTCCTGTGTGTGAGAGAGGCTCAGAGAGCTCAGATGAAAGAGAGCTCAGAA 3964  
QY 1159 lAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGlnArgGly 1179  
DB 3965 AGGACCGGCGCACCTCGGCGGCACTGACATCGCACAGGGGGTCTCTGGAGCGGGAG 4024  
QY 1179 lAlaSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAla 1199  
DB 4025 CCAGAGATTCCTTTAACCCTGCAGACACCTGCAAGTCCAGAGCTGCATGCACTGCCA 4084  
QY 1199 erGlyArgSerSerAlaSerGlnHisGlnAspCysAsnGlyLysSerAlaSerGlyArgL 1219  
DB 4085 GTGGCCGAGGGGTCTGCTTCTGACACCAAGACTGCATGCAATGGCAATCGGCTTCAGGGCGCC 4144  
QY 1219 eulAlaArgThrLeuArgThrAspProGlnLeuAspGlyAspAspAspAsnAspGlnG 1239  
DB 4145 TGGCCCGGCGCCCTGGCGCTGTATGACCCCACTGGAATGGGATATACCGCATGACGAG 4204  
QY 1239 lYAsnLeuSerLysGlyGlnArgGlnIleGlnAlaTrpValArgSerArgLeuProAlaCysC 1259  
DB 4205 GCACCTGAGCAAGAGGAGGAGCGGTCGGCGGTGATCCAGACCCGACCTCCCTGCTGCT 4264  
QY 1259 yArgGlnArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuL 1279  
DB 4265 GCTCGAGGAGATCTCTGTGACGCTACATCTTCCTTCAGTCCAGGATTCGGCTCC 4324  
QY 1279 euCysHisArgIleIleThrHisLysMetPheAspHisValIleLeuValIleIlePheL 1299  
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QY 1299 eulAsnGlyLeuThrIleAlaMetGlnArgProLysIleAspProHisSerAlaGlnArgI 1319  
DB 4385 TTTAACTGCATCAACATGCGCATGAGCGCCCAAAATGACCCCAACAGCGCTGAAACGA 4444  
QY 1319 lPheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValI 1339  
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QY 1359 AlLeuAspGlyLeuLeuValIleLeuSerValIleAspIleLeuValIleSerMetValSerA 1379  
DB 4565 TGTGTGACGGGCTGT 4624  
QY 1379 sPSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgTrpLeuArgP 1399  
DB 4625 ACNAGCGGACCAAGATCTCGGGCATGCTGAGGGTGTGCGGTGCGGAGACCTTCGCGC 4684  
QY 1399 rLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGlnThrLeuMetSerS 1419  
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QY 1419 erLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyI 1439  
DB 4745 CACTGAACCCATCGGCAATGTGTATCTGCTGTCCTTCTTCATCATTTTTCGGCA 4804  
QY 1439 lLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGlnAspThrArgA 1459  
DB 4805 TCTTGGGGGTGACGCTCTTCAAGGGAAGTTTTCGTGTGCCAGGGCGAGATACAGAGA 4864

QY 1459 snlleThrAsnLysSerAspCysAlaGluAsertyrArgTrpValArgHisLysTyrA 1479  
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Db 4925 ACTTTGACAACCTTGGCCAGGCCCTGATGTCCTCTTTCCTTTTGGCCCTCCAAAGATGGTT 4984  
QY 1499 TPValAspLleMetTyrAspGlyLeuAspAlaValGlyValAspGlnProIleMetA 1519  
Db 4985 GGGTGCACATCATGTACATGGCTGATGCTGTGGCGCTGGACCAAGCCCATCATAGA 5044  
QY 1519 snHisAsnProTrpMetLeuLeuTyrPheLleSerPheLeuLeuLeyAlaPhePheV 1539  
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QY 1539 alLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnG 1559  
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QY 1559 lvgGlnGlnGluAlaArgArgArgGlnGlnLysArgLeuArgArgLeuGlnLysLysArgA 1579  
Db 5165 AGGAAGAGAGGCGCGGCGCGGAGAGAGAGCGCTACGAAGACTGGAGAAAAAGAGAA 5224  
QY 1579 rGSerLysGlnLysArgLysMetAlaGlnGlnCysLysProTyrTyrSerAspTyrSera 1599  
Db 5225 GGAAGTAAAGAGAAAGATGGCTGAAGCCAGTGAACCTTACTACTCCGACTCC 5284  
QY 1599 rGPheArgLeuLeuValHisLysLeuCysThrSerHisTyrLeuAspLeuPheLleThrg 1619  
Db 5285 GCTTCGGCTCTCGTCCACCATCTGTGCACAGCACACTGAGACCTTCATCACAG 5344  
QY 1619 lYValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL 1639  
Db 5345 GTGTATCGGGCTGAACGTGTCAACATGGCCATGAGCATCAACAGAGCCCGCATTC 5404  
QY 1639 euAspGlnAlaLeuLysLleCysAsnTyrLlePheThrValLlePheValPheGlnSerV 1659  
Db 5405 TGGATGAGGCTCTGAAGATCTGAACCTACATCTTCACTGTCTTGTCTTGGAGTCAAG 5464  
QY 1659 alPheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeuA 1679  
Db 5465 TTTTCAACTGTGGCTTGGTTTGGTTCCGTCCGTCCAGAGAGGTGGAACCAAGCTGG 5524  
QY 1679 sPLeuAlaLleValLeuLeuSerLleMetGlyLleThrLeuGlnGlnLleGlnValAsnL 1699  
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QY 1719 alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA 1739  
Db 5645 TCTCTGAAGCTGTGAAGATGGCTGTGGGCAATGGCGGCTGTGACACAGGTGATGCAAG 5704  
QY 1739 lAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheLlePheAlaA 1759  
Db 5705 CCTCGCCCAAGGTGGGGAACCTGGGACTTCTCTCATGTGTGTTTTTCATCTTTGAG 5764  
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QY 1799 eTThrGlyAspAsnTrpAsnGlyLleMetLysAspProSerArgAspCysAspGlnGlnL 1819  
Db 5885 CCACAGGTGACAATTGGAATGGCATTTATGAAGACACCTTCGGGAGCTGTGACCGAGAGT 5944

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QY 1879 ePProGlnProHisSerProLeuGlySerProPheLeuTyrProGlyValGlnGlyValA 1899  
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Db 6185 ACAGCCCGGACAGCCCGCAAGCTGGGCTGTGCACCCAGCGGCCACGAGATCAAGCT 6244  
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QY 1939 euGlyProAspLeuLeuThrValArgLysSerGlyValaSerArgThrHisSerLeuProA 1959  
Db 6298 --GGAACAGACTTACTGATCTGTGCGAAGCTGTGGGTCAGCCGACCATCTTGTGCCA 6355  
QY 1959 snAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyT 1979  
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QY 1979 rPGlyLeuProLysAlaGlnSerGlySerLleLeuSerValHisSerGlnProAlaAspT 1999  
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QY 2019 roThrTrpGlyAlaLleProLysLeuProProGlyArgSerProLeuAlaGlnArgP 2039  
Db 6536 CAACCTGGGACCATCCCAACATGCTGCCCAACAGAGAGCTCCCTTGGCTCAGAGGC 6595  
QY 2039 roLeuArgArgGlnAlaAlaLleArgThrAspSerLeuAspValGlnGlyLeuGlySera 2059  
Db 6596 CACTAGGCGCAGAGCAATTAAGACTGACTCTTGTGAGCTTCAAGGCTGTGGGACGCC 6655  
QY 2059 rGluAspLeuLeuSerGlnValSerGlyProSerCysProLeuThrArgSerSerSerp 2079  
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QY 2079 heTTPGlyGlySerSerLleGlnValGlnGlnArgSerGlyLleGlnSerLysValSerL 2099  
Db 6716 TCTGGGGCACTGAAGTAAACCCAGGACAGCAGCACTCCGAGCCACAGCAAGATCTCCA 6775  
QY 2099 YHisAlaArgLeuProAlaProCysProGlyLeuGlnProSerTrpAlaLysAspProp 2119  
Db 6776 AGCAATGACCCCGCAGCCCTTGTCCCAAGGCCCAAGAACCAATGGGGCAAGGGCCCTC 6835  
QY 2119 roGlnThrArgSerSerLeuGlnLeuAspThrGlnLeuSerTrpLleSerGlyAspLeuL 2139  
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QY 2139 eu---ProSerSerGlnGlnGlnProLeuPheProArgAspLeuLysCysTyrSery 2158  
Db 6896 TGCCCCCTGGCGGCGCAGAGAGAGCCCATCCACAGCGGACTGMAAAGGTACTACAGCG 6955  
QY 2158 alGlnThrGlnSerCysArgArgArgProGlyPheTyrPheAspGlnGlnAlaArgArgHis 2178  
Db 6956 TGGAGGCCCAAGAGCTGCGCGGCTTACGTCTGCTGATGAGCAGAGGAGACCT 7015  
QY 2178 eTlleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSers 2198



Db 7016 CTATGCGCCCTGAGCTGCTGAGACGGGCTCCCAACCTCGGGCAGACACCCCTCTTA 7075  
Qy 2198 erLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProIlySylSleuSerProP 2218  
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Qy 2218 roSerLleSerLleaaPProProGlySerGlnGlySerArgProProCySerProGlyV 2238  
Db 7136 CTAGTATCAACCATAGACCCCCCGAAGACCAAGTCTCGGACCCCGCCAGCCCTGGTA 7195  
Qy 2238 aCySleuArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProL 2258  
Db 7196 TCTGCTCCGGAGAGAGGCTCGCTCCAGAGCATCCCAAGAGATCCCTTGGCCTCTGGCCCC 7255  
Qy 2258 euAspSerThrAlaAlaSerProSerProIlySylAspThrLleuSerLleuSerGlyLeuS 2278  
Db 7256 CTGACAGCATGGCTGCTGCTGCTCCCAAAAGAAAGATGCTGAGTCTCTCGGTTTAT 7315  
Qy 2278 erSerAspProThrAspMetAspPro 2286  
Db 7316 CCTGTACCCAGACAGCATGGACCCC 7341  
RESULT 2  
US-09-426-998-3 / Sequence 3, Application US/09426998  
/ Patent No. 6358706  
/ GENERAL INFORMATION:  
/ APPLICANT: DUBIN, ADRIENNE E.  
/ APPLICANT: PYATT, JAYASHREE  
/ APPLICANT: ZHU, JESSICA Y  
/ APPLICANT: ERLANDER, MARK G  
/ APPLICANT: GALINDO, JOSE E  
/ TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG-T-TYPE CALCIUM  
/ FILE REFERENCE: ORT-1057  
/ CURRENT APPLICATION NUMBER: US/09/426, 998  
/ NUMBER OF SEQ ID NOS: 5  
/ SOFTWARE: PATENTIN VER. 2.0  
/ SEQ ID NO 3  
/ LENGTH: 6822  
/ TYPE: DNA  
/ ORGANISM: HOMO SAPIENS  
US-09-426-998-3  
Alignment Scores:  
Pred. No.: 0 Length: 6822  
Score: 10948.50 Matches: 2111  
Percent Similarity: 94.03% Conservative: 32  
Best Local Similarity: 92.63% Mismatches: 105  
Query Match: 91.03% Indels: 31  
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Qy 34 TrpThrArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53  
Db 2 TGGACAGAGAGAGAGATGAGCGGGGCCCGAGAGATCGGAGACAGCCCGAGCTTCATGC 61  
Qy 54 SerSerThrThrCysArgProGlyProGlyAla-AlaGlyAla-GlySerThrGlnLysAsp 73  
Db 62 GGCTCAACGACCTGCGGGGGCCGGGGGCCGGGCCGGGGCTGAGCAGAAAGAGACC 121  
Qy 73 roGlySerAlaAspSerGluAlaGlnGlyLeuProTyrrProAlaAlaAlaProValAlaP 93  
Db 122 CGGGCAGCGGGGACTCGAGAGCGAGGGGCTGCGGTACCGGGGCTGGCCCGGTGGTTT 181  
Qy 93 hepPheTyrlLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsp 113  
Db 182 TCTTTCTACTTGAACGAGACAGCCCGCGGAGCTGTGTCTCCGACGGTCTGTAAAC 241  
Qy 113 roTrpPheGluArgValSerMetLeuValLleuLeuAsnCyValThrLeuGlyMetP 133

Db 242 CTTGCTTTGAGGCGCATGACGATGTTGGTATCTTCTCAATCGCGTGAACCTGGGCATGT 301  
Qy 133 hearGProCysGlnAspTrlAlaCysAspSerGlnArgCysArgTrlLeuGlnAlaPheA 153  
Db 302 TCCGGCCATGAGAGACATCCGCTGTGATCCAGCGCTGCGGGATCTCGCAGGGCTTTGG 361  
Qy 153 spAspPheLlePheAlaPhePheAlaValGlnMetValValLysMetValAlaLeuGlyI 173  
Db 362 ATGACTTCATCTTGGCTCTTCTTGGCTGGAGATGTGTGAAGATGGTGGGCGCA 421  
Qy 173 lePheGlyLysCysTyrlLeuGlyAspThrTrpAsnArgLeuAspPhePheLleValI 193  
Db 422 TCTTTGGAAAAAGTTCATCTCGGAGACACTTGAACCGCTTCATCTTTTCATGCTCA 481  
Qy 193 leAlaGlyMetLeuGlnTyrlSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213  
Db 482 TCGCAGGAGATGTGAGATGATCGCTGGAAGCTGCAGAAAGTCAGCTTCAGGTCAGGA 541  
Qy 213 hrValArgValLeuArgProLeuArgAlaLleAsnArgValProSerMetArgLleLeuV 233  
Db 542 CAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCTTG 601  
Qy 233 alThrLeuLeuLeuAspThrLleuProMetLeuGlyAsnValLeuLeuLeuCyPhePheV 253  
Db 602 TCACGTGCTGTGATACGCTGCGCCATGTGGGCAAGCTCTGCTGCTTCTGCTTCTG 661  
Qy 253 alPhePheLlePheGlyLleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273  
Db 662 TCTTCTTCACTTGGGATCGTCGGCGTCAGCTGTGGGCAAGGCTGCTTCCGAACCGAT 721  
Qy 273 yspPheLeuProGlnAsnPheSerLeuProLeuSerValAspLeuGlnProTyrrTyrlGlnT 293  
Db 722 GCTTCCTACTAGAAATTCACCTCCCTGAGGGTGAGCCTTGAGCGCTATTAACCA 781  
Qy 293 hrGluAsnGlnAspGlnSerProPheLleCysSerGlnProArgGlnAsnGlyMetArgS 313  
Db 782 CAGAGACAGAGATGAGACCCCTTCATCTGCTCCAGCAGCGAGAAAGGCATGCGGT 841  
Qy 313 erCyAspSerValProThrLeuArgGlyGlyGlyGlyProProCySerLeuA 333  
Db 842 CTTGACAGAGCGTGGCCACGCTCGCGGGGAGCGGGGGCGGTGCCCATCTGCGTCTG 901  
Qy 333 spTyrlGlnThrTyrlAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrrTyT 353  
Db 902 ACTATGAGGCTTACAAAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTACA 961  
Qy 353 hrAsnCySerAlaGlyGlnLysAsnProPheLysGlyValAlaLleAsnPheAspAsnLleG 373  
Db 962 CCAACTGCTCAGCGGGGAGACAAACCCCTTCAAGGGGCGCATCACTTTCACCACTTG 1021  
Qy 373 lYTrAlaTrpLleAlaLlePheGlnValLleThrLeuGlnGlyTyrrValAspLleMet 393  
Db 1022 GCTATGCCGTGATCCGCACTTCCTCAAGTATCAAGCTGAGAGGCTGGGTGCATCATGT 1081  
Qy 393 yrPheValMetAspAlaHisSerPheTyrrAsnPheLleTyrrPheLleLeuLeuLleIleV 413  
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Qy 413 alGlySerPhePheMetLleAsnLeuCySleuValValLleAlaThrGlnPheSerGlnT 433  
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Qy 433 hrLysGlnArgGlnSerGlnMetArgGlnArgValArgPheLeuSerAsnAlaS 453  
Db 1202 CCAAGAGCGGGAAGCCAGCTGATGCGGAGCAAGAGTGTGGTTCCGTCCAAGGCCA 1261  
Qy 453 erThrLeuAlaSerPheSerGlnProGlySerCysTyrlGlnGlnLeuLeuTyrrLeuV 473  
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Db 1382 GGGTTGGGCTGTGACGAGCCAGACACCTCGGGGGCCAGAGAAGCCAGCCAGCAGCA 1441  
Qy 513 eCyThArGSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHis 533  
Db 1442 GCTGCTCTCGCTCCACCGCCGCCCTTATCTGTCACACACTGTGTGACACACACACACC 1501  
Qy 533 iHisHisHisIstYrHisLeuGlyAenGlyYThrLeuArgValProArgAlaSerProGluI 553  
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Qy 553 legInAspArgAspAlaAenGlySerArgArgLeuMetLeuProProProSerThrProT 573  
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Qy 593 yHisHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGlyAlaSerG 613  
Db 1682 GCCACTTAGAGCAAGTCCGCTGGCCAGGGCCCCCTCCAGGTCCTCATGTAGGCGATCCG 1741  
Qy 613 lYArgThValAlGlySerGlyYLeuValYTrProThValHisHisSerProProProGluI 633  
Db 1742 GCAGAGCTGTGGGCGCGGAGAGGTATCCACCGTCACACACCGCTCCACCGGAGA 1801  
Qy 633 lLeuLyAspLyAspAlaLeuValGluValAlaProSerProGlyYProProThrLeuThrs 653  
Db 1802 CGCTGAGAGAGAGAGCACTAGTAAAGTGGCTGCCAGCTGTGGGCCCCCAACCTCACCA 1861  
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Db 1862 GCCTCAACATCTCCACCCGGGCTTCACGCTCATGCACAACTGCTGAGACACAGAGTA 1921  
Qy 673 hrGlyAlaCysHisSerSerCysLyHisIleSerSerProCysSerLyAspAlaSerGlyY 693  
Db 1922 CAGGCTCTGCMAAGCTCTTGCAAGATCTCCAGCCCTTGTAAGCAACAGCTGGAG 1981  
Qy 693 lAcSGlyProAspSerCysProLyYCysAlaArgThrGlyAlaGlyGluProGluSerA 713  
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Qy 713 lAsPHisValMetProAspSerAspSerGlyAlaValYTrGluPheThrGlnAspAlaG 733  
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Db 3476 GCCACAGGGGGTCCCTGAGAGCGGAGGCCAAAGATTCTTTGACCTGCGCAGACACACTGC 3535



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QY 2010 lSTYrLeuLeuGlnProHisGlyAlaProThrTyrGlyValAlaIleProLysLeuProProp 2030  
Db 5987 CTCATCTGCTCCAGCCCAACAGCCCACTGGGGGACCACTCCCAAACTGCCCCAC 6046  
QY 2030 roGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspS 2050  
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QY 2050 eRLeuAspValGlnGlyLeuGlySerArgGlnAspLeuSerGlnValSerGlyProS 2070  
Db 6107 CTTTGACCTTGAAGGTCTGGGACCGGAAAGCTGTGGCAAGGTGAGTGGCCCT 6166  
QY 2070 eCYsPProLeuThrArgSerSerPheTyrGlyGlySerSerIleGlnValGlnGlnA 2090  
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QY 2110 euGlnProSerTyrAlaLysAspProProGlnThrArgSerSerLeuGlnLeuAspThrG 2130  
Db 6287 CAGAACCCCACTGGGGCAGAGGCGCTCCAGAGACCAAGAGCTTGAAGTTGGACAGG 6346  
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QY 2209 eArgProLysLysLysLeuSerProProSerIleSerIleAspProProGlnSerGlnG 2229  
Db 6587 GCCGGCCCAAGAAAACCTCAGCCCGCTAGTATACCATAGACCCCGCCGAGAGCCAG 6646  
QY 2229 lYSerArgProProCysSerProGlyValCysLeuArgArgArgAlaProAlaSerAspS 2249  
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QY 2249 eRlyAspProSerValSerSerProLeuAspSerThrAlaIleAspProSerProLysL 2269  
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QY 2269 yAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetAspPro 2286  
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RESULT 3  
US-09-949-016-3859  
; Sequence 3859, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C0001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 3859  
; LENGTH: 7405  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-3859  
  
Alignment Scores:  
Pred. No.: 0 Length: 7405  
Score: 10739.00 Matches: 2077  
Percent Similarity: 92.09% Conservative: 29  
Best Local Similarity: 90.82% Mismatches: 95  
Query Match: 89.28% Indels: 86  
DB: 4 Gaps: 5  
  
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QY 23 SerAspProProGlyProAlaGlnAlaArgGlyTyrThrArgArgArgMetGlnArgAla 42  
Db 341 CCGGATCGCCCGGGGCCCCCGGCTGGCCAGAGATGACGAGAGAGATGAGACCGGGCG 400  
QY 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly 62  
Db 401 CCGAGAGTCCGGACAGCCCGGAGCTTACGCGCTCAACGACCTGTGGGGGCGGGG 460  
QY 63 Ala-AlaGlyAla-GlySerThrGlnLysAspProGlySerAlaAspSerGlnAlaGlnG 82  
Db 461 GCCGGCCGGGGCCGGGGTCAAGCAAGAAAGACCCGGGCAAGCGGAGCTCCGAGCGGAGG 520  
QY 82 lYLeuProTyrProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgP 102  
Db 521 GCGTCCGTACCCGCGCTGGCCCGCGGTGTCTTCTACTTGAAGCAGAGACGCGGC 580  
QY 102 roArgSerTyrCysLeuArgThrValCysAspPro--TyrPheGlnArgValSerMetL 121  
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Db 641 TGTGATCTCTTCTCACTGAGTGACCTTGGGCANTGTTCCGGCCATGGAGACATCGCCT 700  
QY 141 yAspSerGlnArgCysArgGlyLeuGlnAlaPheAspAspPheIlePheAlaPhePheA 161  
Db 701 GTGACTCCCAAGCGCTGCGGATCTCGCAGGCTTGTGATGACTTTCATCTTGGCTTCTTG 760  
QY 161 lAValGlnMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuG 181  
Db 761 CCGTGGAGATGTGTGTAAAGTGTGGCTTGGCACTTTTGGAAAAGTTTAACCTGG 820  
QY 181 lYAspThrThrAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlnTyrSerL 201

Db 821 GAGACACTGGAAACCGGCTTGACTTTTCATGTCATGCGAGAGATGCGGAGTACTGC 880  
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Qy 261 1uValG1naLeuThrPalaG1yleuLeuAArgAsnArgCysPheLeuProGlu1naAsnSer1 281  
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Qy 281 euProLeuSerValAspLeuGluProGlyTrpGlnThrGlu1naAsnGluSerProP 301  
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Qy 301 he1leCysSerGlnProArgGlu1naAsnGlyMetArgSerCysArgSerVal1ProThrLeuA 321  
Db 1181 TCATCTGCTCCAGACCGAGAACGGCATGCGCTTCGAGAAACGCTGCCACGCTTC 1240  
Qy 321 TGG1G1GluG1yG1yG1yProProCysSerLeuAspGlyTrpGluThr1TrpAsnSerSers 341  
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Qy 341 eArAsnThrThrCysValAsnTrpAsnGln1TrpThrAsnCysSerAlaG1yGlu1na 361  
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Qy 361 snProPhe1yseg1yAla1leAsnPheAspAsn1leG1yTrpAla1Trp1leAla1lePheG 381  
Db 1361 ACCCCTTCAAGGGCGGCATCACTTGAACAACATGGCTAGCTGATGCGCATCTTCC 1420  
Qy 381 1uVal1leThrLeuGluG1yTrpValAsp1leMetGlyPheVal1MetAspAla1na1SerP 401  
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Qy 401 he1TrpAsnPhe1le1yRhe1leLeuLeu1le1leValG1ySerPhePheMet1leAsn1 421  
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Db 1601 TGGGGAGAGCGGTGCGGCTTCTGTCAACGCCACGACCCCTGGCTAGCTTCTTGAGC 1660  
Qy 461 roG1ySerCysGlyTrpGluGlu1leuLeu1ySer1yLeuVal1Trp1leLeuA1yAla1a 481  
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Qy 481 TGA1yLeuAlaGlu1naValSerArgAla1leG1yAla1ArgAlaG1yLeuLeuSerSerProV 501  
Db 1721 GCAGGCTGTGCTCAGGCTCTCTCGGAGCAGAGTGTGGGTGGCTGCTCAGAGAGCCGAG 1780  
Qy 501 a1Ala1ArgSerGlyGlu1naGluProGlnProSerGlySerCysThrArgSerHis1ArgArg1 521  
Db 1781 CACCCCTCGGGGCGCAGAGAACCAAGCCGACGACGACTCTCTGCTCCACCGCGCC 1840  
Qy 521 euSerVal1na1shi1sleuVal1na1shi1shi1shi1shi1shi1shi1shi1shi1shi1 541  
Db 1841 TATCCGTCACCAACCTGTGTACACCAACCAACCAACCAACCAACCAACCAACCTGGGCA 1900  
Qy 541 snGly1ThrLeuArgVal1ProArg1leSerProGlu1leGlnAspAla1naAsnGlyS 561

Db 1901 ATGGAGCGCTCAAGGGCCCCCGGGCAGCCCGAGATTCAGAGACAGGAGTCCAATGGGT 1960  
Qy 561 eArArgArgLeuMetLeuProProSerThrProThrProSerG1yG1yProProArg 581  
Db 1961 CCGCGCGCTCATGTGTCACACCTTCAGAGCGCTTCGCGGCTTCGCGGCGCGCGCTGGT 2020  
Qy 581 1uValGluSerVal1HisSerPhe1yTrp1na1AspCysHis1leuGlu1naProValArgCysG 601  
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 RESULT 4  
 US-08-984-709A-49  
 ; Sequence 49, Application US/08984709A  
 ; Patent No. 6320032  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Williams, Mark E.  
 ; APPLICANT: Staederman, Kenneth A.  
 ; APPLICANT: Harpold, Michael M.  
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 ; NUMBER OF INVENTION: METHODS  
 ; NUMBER OF SEQUENCES: 52  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Heller Ehrman White & McAuliffe  
 ; STREET: 4250 Executive Square, Suite 700  
 ; CITY: La Jolla



STATE: California  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/984,709A  
FILING DATE: 02-DEC-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 450-8400  
TELEFAX: (619) 587-5360  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7898 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 249..7307  
OTHER INFORMATION:  
US-08-984-709A-49

Alignment Scores:  
Pred. No.: 0 Length: 7898  
Score: 6241.00 Matches: 1385  
Percent Similarity: 64.96% Conservative: 209  
Best Local Similarity: 56.44% Mismatches: 517  
Query Match: 51.89% Indels: 325  
DB: 3 Gaps: 64

US-09-611-257A-24 (1-2287) x US-08-984-709A-49 (1-7898)

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DB 1356 GCCATCTTCCAGGTGATCAGCGCTGGAAGCTGGGTGACATCATGATCACTACGTATGAGAC 1415  
QY 398 AlaHisSerPheTrrpAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417  
DB 1416 GCCACATCATTCACATCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1475  
QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluTrrpLysGlnArgGlu 437  
DB 1476 ATGATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1535  
QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457  
DB 1536 AGTCAGCTGATGCGGAGACGCGGACGCCACCTGTCCAAACGACACACACGCTGGCCAGC 1595  
QY 458 PheSerGluProGlySerCysTrrpGluGluLeuLeuLysTrrpLeuValTrrpIleLeuArg 477  
DB 1596 TTTCCTCAGGCTGGACCTGCTACGAAGAGCTGCTGAAGTACGTGGGACCATATTCCTCC 1655



Dh 3717 CGCGCCAGTGTGGGGAAGTGAAGTCCCTGTCTGTGGCGAGGGCAAGGACGACCGAC 3776  
Qy 1153 GluGluGluSerSerGluGluAspArgAlaSerProAla-----GlySerAspHisArg 1170  
Db 3777 GACGAA-----GCTGAGGACGGCGAGGCGCGGCCCGGCGCCGTGCACCACTGGCG 3830  
Qy 1171 HisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu--- 1189  
Db 3831 CGGGCCGAGTCTCTGGACCCACGAGCCCTGCGGCGCGGCCCTCCGCCCTACCAAGTGC 3890  
Qy 1190 -----GlnValProGlyLeuHis-----ArgThrAlaSer 1199  
Db 3891 CGCGATCCGACGGGCGAGTGTGGCTGTGGCCGACGACTTCTTCTCGCATCGACAGC 3950  
Qy 1200 GlyArgSerSerAlaSerGluHisGlnAspGlySerAsnGlyLysSerAlaSerGlyArgLeu 1219  
Db 3951 CACCGTGAAGATGACGCGGAGCTTGACGACGACTCGAGAGACAGTGTGCTGCGCTG 4010  
Qy 1220 AlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAspGluGly 1239  
Db 4011 CATAAAGTCTGGAGCCCTACAGCCCGAG----- 4040  
Qy 1240 AsnLeuSerLysGlyGluArgGlnAlaGlnAlaArgSerArgLeuProAlaCysCys 1259  
Db 4041 -----TGC-----TGC-----TGC-----TGC 4046  
Qy 1260 ArgGluArgAspSerTrpSerAlaTrpLeuPheProProGlnSerArgPheArgLeuLeu 1279  
Db 4047 CGGAGCCCGAGGCTGGAGCCCTTAACCTCTTCCCTCCACAGAACCGGCTCCGCTGCC 4106  
Qy 1280 CysHisArgIleIleThrHisLysMetPheAspHisValAlaLeuValIleIlePheLeu 1299  
Db 4107 TGGCAGAGAGTCATACACACAGATGTTTATCATCGTGCTCTGTTTCATCTTCTC 4166  
Qy 1300 AsnCysIleIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIle 1319  
Db 4167 AACTGCGTACCATGCGCTGGAGAGGCTGCATTTGACCCCGACAGCACCGAGCGGCTC 4226  
Qy 1330 PheLeuThrLeuSerAsnTrpIlePheThrAlaValPheLeuAlaGluMetThrValLys 1339  
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Qy 1340 ValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTrpLeuArgSerSerTrpAsnVal 1359  
Db 4287 GTGGTGGCCCTGGGCTGCTGTCGCGGACGACGCTACCTGACAGAGACGTGGAACCTG 4346  
Qy 1360 LeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAsp 1379  
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Qy 1380 SerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuAspPro 1399  
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Qy 1400 LeuArgValIleSerArgAlaGlnGlyLeuLysLeuValAlaGluThrLeuMetSerSer 1419  
Db 4467 CTAAAGGTCATAGCGGAGCCCGGCGCTCAAGCTGAGTGGTGGAGACCTGATATCGTGC 4526  
Qy 1420 LeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIle 1439  
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Qy 1460 IleThrAsnLysSerAspCysAlaGluAlaSerTrpArgTrpValArgHisLysTrpAsn 1479  
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Qy 1540 LeuAsnMetPheValGlyValValAlaGluAsnPheHisLysCysAlaArgGlnHisGlnGlu 1559  
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Qy 1600 PheArgLeuLeuValHisHisLysCysThrSerHisTrpLeuAspLeuPheIleThrGly 1619  
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Qy 1680 LeuAlaIleValIleLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeu 1699  
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Qy 1700 SerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgVal 1719  
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Qy 1720 LeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisSerThrValMetGlnAla 1739  
Db 5424 CTGAAGCTGTGAAGATGGCTACGAGGATGCGGCTGCTGAGACACTGTGTCAAGCT 5483  
Qy 1740 LeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAla 1759  
Db 5484 CTCGCCAGGTGGGGAACCTGGGCTTCTTTTCATGCTCTCGTTTATCTATGCTGCG 5543  
Qy 1760 LeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeu 1779  
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Qy 1780 GlyArgHisAlaThrPheAspPheGlyMetValaPheLeuThrLeuPheArgValSer 1799  
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Qy 1800 ThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys-----Asp 1816  
Db 5664 ACGGGGAGCAACTGGAACGGGATCATAGAGACACGCTGCCGAGTGTCTCCCGAGAGAC 5723  
Qy 1817 GlnGluSerThrCysTrpAsnThrValIleSerProIleTrpPheValSerPheValLeu 1836  
Db 5724 AAGCACTGCTGAAGCTACCTGCGGCGCTGTGCGCGCTTACTTCACTTCACTTGTGCTG 5783  
Qy 1837 ThrAlaGlnPheValIleValAlaAsnValValIleAlaValLeuMetLysHisLeuGluGlu 1856  
Db 5784 GTGGCCAGTTCTGCTGTGGAAGTGTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 5843



QY 63 Ala-AlaGlyAla-glySerThrGluIysAspProGlySerAlaaspSerGluAlaGluG 82  
Db 461 GCCGCCCGGGGGGGGGGCTCAGCAAGAAAGAGACCCGGGCAAGCCCGAGGCGAGG 520  
QY 82 IlyeupProTyTrProAlaAlaAlaProValIvalPhePheTyrieuSerGlnaaspSerArp 102  
Db 521 GGGTCCCGTACCCGGCGGCTGGGCGCGGGTGTCTTCTTACTTGAAGCAAGGACAGCCGCC 580  
QY 102 roArxSerTrpCysleuArghThrValCysAspProTrpPheGluuArgValSerMetLeuV 122  
Db 561 CGGGAGGCTGGGTGTCTCGCAAGGTGTGAACCCCTGGTTGAGCGCAATCAGCAAGTTGG 640  
QY 122 aAlIleIleuIeuAsnCysValThrIleuGlyMetPheArpProCysGluaspIleAlaCysA 142  
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QY 142 sPSeGlnArGcysArgIleIleuGlnAlaPheAspAspPheIlePheAlaPhePheAlav 162  
Db 701 ACTCCCAAGCGCTGCCGATCCCTGCAGGCGCTTGTGATGACTTCACTTTCCTTTCGCG 760  
QY 162 aGluMetValIValIyMetValAlaIeuGlyIlePheGlyIyIslyAcysTyrieuGlyA 182  
Db 761 TGGAGATGTGTGTGAAGATGTGTGGCTTGGGCACTTGTGGGAAAGTGTACCTGGAG 820  
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QY 202 sPLeuGlnaAsnValSerPheSerAlaValArgThrValArgValIleuArgProIleuArgA 222  
Db 881 ACCTGCACAACCTCAGCTTCTCAGCTGTCAAGGACAGTCCGTGTGTGCAGACGCGCTCA 940  
QY 222 IaIleAsnArGValProSerMetArgIleIeuValThrIleuIeuAsnAspThrIeuProM 242  
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QY 242 eCleuGlyAsnValIleuIeuIeuCysPhePheValPhePheIlePheGlyIleValGlyV 262  
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Db 1421 TCATCAACCTGAGGGCTGGGTGCAATCATGACTTGTGTGATGATGATCTCATTCCTTCT 1480  
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QY 442 rGluGlnArGValArgPheIeuSerAsnAlaSerThrIleuAlaSerPheSerGluProG 462  
Db 1601 GGGAGCAGCGGTGTGCGGTCTGTTCACACCGCACACCTGGGTAGGTTCTCTAGGCCG 1660  
QY 462 IySerCySTyTrGluGluIleuIeuIyTyTrIleIeuArgIyAlaIaArgA 482  
Db 1661 GCAGCTGTATGAGAGCTGTCAAGTACTGTGTGTACATCTTCTGTAGGACCCGCCA 1720  
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Db 1721 GGTGGCTCAGGTCTCTCGGGCAGCAGATGTGCGGGTGGCTGCTCAGACGCCACAC 1780  
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QY 522 eValIHisIleuValHisIleHisIleHisIleHisIleHisIleHisIleHisIleHis 542  
Db 1841 CCGTCCACACCTGTGTGACACCAACCAACCATCAACCACTTACACCTTGGGCAATG 1900  
QY 542 IyThrIeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySera 562  
Db 1901 GAGCGCTCAGGGGCCCGCGGGCCAGCCGGAGATCCAGACAGGAGATGCCAATGGTCCC 1960  
QY 562 rGArGleuMetIeuProProProSerThrProThrProSerGlyIyProProArgGlyA 582  
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QY 582 IaGluSerValHisSerPheTyTrHisAlaAspCysHisIleuGluProValArgCysGlnA 602  
Db 2021 CAGAGCTGTGTGACAGCTTCTTACATGCCAGTGTCCATTTAGAGCCAGTCCGCTGCCAG 2080  
QY 602 IaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyIySValT 622  
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QY 622 yTrProThrValHisThrSerProProProGluIleIeuIyAspIyAlaIeuValGluV 642  
Db 2141 ATCCACCGGTGCACACAGCCCTTCACCGGAGAGCTGAAAGAAAGCACTAGTAAAG 2200  
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QY 682 IeSerSerProCysSerIyAlaAspSerGlyAlaCysGlyIyProAspSerCysProTyTrC 702  
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QY 702 ySAlaArGThrGlyAlaGlyIyGluProGluSerAlaAspHisSValMetProAspSerAs 722  
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Qy 862 TLeuSerValLeuArgThrPheArgLeuMetArgValLeuYsLeuValATcPheLeuP 882  
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Qy 902 YMeLeuLeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuPheGlyC 922  
Db 2978 GCATGTGCTTATGCTTTCATCTTATCTTACGACATCCCTGGGACATGCACTCTTGCT 3037  
Qy 922 YLeuPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnAspSerL 942  
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Db 3278 CGGAGGGAATGTCACCAAGTCCGAATCAGAGCCCATTTCTTCAACCAGCTGAGT 3337  
Qy 1022 TAspGlyAspArgLysLysAspGluLeuValAlaLeuGlyGlnHisAlaGluLeuA 1042  
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Qy 1042 TgLySerLeuLeuProProLeuIleIleIleThrAlaAlaThrProMetSerHisProL 1062  
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Qy 1102 eSerProHisSerProTTPSerAlaAlaSerSerTrpThrSerArgArgSerSerArg 1122  
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Qy 1182 ePheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgS 1202  
Db 3815 CTTTGACCTGCGACACACTGTCAGAGTGCCAGGGCTGCAATCGCATCGCCAGTGGCCAG 3874  
Qy 1202 eSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyValGluAlaArgT 1222  
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Qy 1222 hLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAspGluGlyAsnLeu 1241  
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RESULT 6  
US-09-404-650-1  
; Sequence 1, Application US/09404650  
; Patent No. 6309858  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGivern, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; FILE REFERENCE: R0043B-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/404,650  
; CURRENT FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patencin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 6816  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (192)..(6716)  
US-09-404-650-1

Alignment Scores:  
Pred. No.: 0 Length: 6816  
Score: 5420.00 Matches: 1223  
Percent Similarity: 61.74% Conservative: 224  
Best Local Similarity: 51.82% Mismatches: 494  
Query Match: 45.06% Indels: 413  
DB: 3 Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-404-650-1 (1-6816)

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Db 207 TCCCGGCTCTCTCATCTGACAGACGCCGCTGAGCGAGTCAACGAGAGCAG 266  
Qy 26 ProGlyProArgLeuAlaArgGlyTTrpThrArgArgMetGluArgAlaProArgSer 45  
Db 267 CCCGAGCCCCGG----- 278  
Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65  
Db 279 -----AGCCCCCATCTCCCGCCAGGCTGAGAGACCTCTGGATGAGCT----- 326  
Qy 66 AlaglySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85  
Db 327 -----GATCCT-----CATGTCCACAC 344  
Qy 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105  
Db 345 CCAGACTTGGCGCATATTTCTTCTGCTGCGACACACACACAGCCCGGAACTGG 404  
Qy 106 CysLeuArgThrValCysAsnProTTPPheGluArgValSerMetLeuValIleLeuLeu 125  
Db 405 TGCATCAAGATGTGTGCAACCCGTGTGTTGAATGTGTACAGATGCTGTGATCTGCTG 464

QY 126 AsnCysVal1ThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145  
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QY 146 CysArg11LeuGlnAlaPheAspPhe11LeuAlaPhePheAlaValGlnMetVal 165  
DB TGCAAGATCCTGCGAGGCTTTGATGATCTTCACTTATCTTCTTTGCCATGGAGATGGTG 584  
QY 166 Val1ysMetValAlaLeuGly11LeuPheGly1ysGlyCysTyrLeuGlyAspThr1TrpAsn 185  
DB CTCAAGATGGTGGCCCTGGGATTTTGGCAAGAGTCTACCTCGGGGACACATGGAAAC 644  
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QY 286 AspleuGluProTyrTyrGln1ThrGlnAsnGluAspGlnUserProPhe11LeuSerGln 305  
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QY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGlnGly 325  
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Db      6179 -----TGCCTGGGGCGCCCGCCCTGCTCCAGAGCCCGGGC 6217
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RESULT 7
US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGovern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: R0043B-BEG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5420.00 Matches: 1223
Percent Similarity: 61.74% Conservative: 234
Best Local Similarity: 51.82% Mismatches: 494
Query Match: 45.06% Indels: 413
Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-935-541-1 (1-6816)
Qy      12 ThrProProLeuArgLysSerAlaArgProSerSerAspPro----- 25
Db      207 TCCCGCGCCCTCCTCATCTGCGAGAGCCCGCGCTGAGCCAGAGTACACCGAGAGCAG 286
Qy      26 ProGlyProArgLeuAlaArgLysTrpThrArgArgArgMetGluArgAlaProArgSer 45
Db      267 CCCGAGCCCCGG----- 278
Qy      46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db      279 -----AGCCCCCATCTCTCCCGCGAGCGCTGAGAGCTCGATGGAGCT----- 326
Qy      66 AlaGlySerThrLysLysAspProGlySerAlaAspSerGluAlaGlyLeuProTyr 85
Db      327 -----GATCCT-----CATGCCACAC 344
Qy      86 ProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db      345 CCGAGACTGGCGGCTATATGCTCTTCTGCTGCGAGACAGACACACAGCCCGGAACTGG 404
Qy      106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuVal11LeuLeu 125
Db      405 TGCATCAAGATGGTGCAACCGGTGGTTGAATGTGTCAAGATGCTGTGATCTGCTG 464
Qy      126 AsnCysValThrLeuGlyMetPheArgProCysGluAspLysLeuAlaCysAspSerGlnArg 145
Db      465 AACGCGTGACACTGGCATGTACAGCCGCGTGACGACATGCACTGCTGCGAGCCG 524

146 CysArg11LeuGlnAlaPheAspAspPhe11PheAlaPhePheAlaValAlaGluMetVal 165
Db      525 TGCAGATCTCTGCACAGTCTTTGATGATCACTTATCTTCTTTGCGCATGGAGATGGG 584
Qy      166 ValLysMetValAlaLeuGly11PheGlyLysCysTyrLeuGlyAspThrTrpAsn 185
Db      585 CTCAGATGATGGTGCGCTGGGAGTTTGTGGCAGAGAGTCTACTCTGGGGACACATGGAA 644
Qy      186 ArgLeuAspPhePhe11Val11Lea11GlyMetLeuGlyTyrSerLeuAspLeuGlnAsn 205
Db      645 CGCCTGATTTCTTATGCTGATGCGAGGAGATGTCGATGACTCCCTGACCTTCAGAAC 704
Qy      206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAla11AsnArg 225
Db      705 ATCAACCTGTACAGCATCCGACCGTGGCGCTCGAGGCCCTCAAGCCATCAACCGC 764
Qy      226 ValProSerMetArg11LeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db      765 GTGCCAGATGCGGATCTGTGTGAACCTGCTCTGACACACTGCCCATGCTGGGGAGAT 824
Qy      246 ValLeuLeuLeuCysPhePheValPhePhe11PheGly11ValGlyValGlnLeuTrp 265
Db      825 GTCTGCTGCTGCTGCTTCTTCTTCTTCTTCACTTGGCATATAGTGTCAGCTGG 884
Qy      266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerAla 285
Db      885 GCGGGCTGCTGCTGTAACCGCTCTTCTCGAGGAGAACTTACATCACTCAAGCGGATGG 944
Qy      286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPhe11LeuCysSerGln 305
Db      945 GCCTTGCCCGCATACTACAGCGGAGAGATGATGATGATGATGATGATGATGATGATGAT 1004
Qy      306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgLysGlyGly 325
Db      1005 TCGGGGACAAATGGGATATAGGCTGCCATGAGATCCCGCTCAAGAGAGAG----- 1058
Qy      326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrTrpAsnSer 339
Db      1059 ---GGCGGTGAGTGTGCTCTGTCGCAAGAGCAGCTGACGATTTGGGGCGGGCGCCAG 1115
Qy      340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
Db      1116 GACCTCAATGCCAGCGGCTCTGTGTCACTGMAACGTTTACTTCAATGATGTGCCAG 1175
Qy      358 GlyGluHisAsnProPheLysGlyAla11LeuAsnPheAspAsn11GlyTyrAlaTrp11 377
Db      1176 GCGAGGCGCAACCCCAAGAGGTGTCATCACTTGAACAACATGCGTTATGCTTGATT 1235
Qy      378 Ala11PheGlnVal11LeuLeuGlyTyrTrpValAsp11MetTyrPheValMetAsp 397
Db      1236 GTCATCTTCAGGTGATCACTCTGGAAGGCTGGGTGGATCATGTATCACTGAGATGAT 1295
Qy      398 AlaHisSerPheTyrAsnPhe11Leu11Phe11LeuLeu11LeuValGlySerPhePhe 417
Db      1296 GCTCACTCTTCTTACACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCTTC 1355
Qy      418 Met11LeuAsnLeuCysLeuValVal11Lea11Arg11PheSerGlnThrLysGlnArgGlu 437
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Qy      438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db      1416 CACCGGCTATGTGTGAGCAGCGGCGCTTCACTGCTCC---TCCAGCAGCGGTGGCCAC 1472
Qy      458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyr11LeuArg 477
Db      1473 TACGCGGAGCTGGGACACTGCTACAGAGATCTTCAATATGTCTGCCACATCTCGCC 1532
Qy      478 LysAlaAlaArgArgLeuAlaGlnValSerArgAla11GlyValArgAlaGlyLeu 497
Db      1533 AAGGCCAAGCGC-----CGGCGCTGGGCTTCAACAGGCGCTGAG 1574

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QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517  
DB 1575 ACC----- 1577  
QY 518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyr 537  
DB 1578 ---CGCGCGCAGGCCCTG----- 1592  
QY 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGlnIleGlnAspArgAsp 557  
DB 1593 -----GGCCCGGAG----- 1601  
QY 558 AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly 577  
DB 1602 -----GCCCGGCGCCCGCCCAACCTGGGGCC----- 1628  
QY 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597  
DB 1629 -----CACGCCAAG-----GAGCCC 1643  
QY 598 ValArgCysGlnAlaProProProArgCysProSerGlnAlaSerGlyArgThrValGly 617  
DB 1644 CGGCACTACCAAGCTGGCCCGCAACATAGACCCCTGGATGG----- 1685  
QY 618 SerGlyLysValTyrProThrValHisThrSerProProGluIleLeuLysAspLys 637  
DB 1666 -----ACGCCCAACAC----- 1697  
QY 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657  
DB 1698 ---CTGGTGCAG-----CCCATCCCGCCGACGCTGGCTTCC----- 1730  
QY 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676  
DB 1721 -----GATCCCGCCAGCTGCCCTTGGCTGGCAG 1757  
QY 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696  
DB 1758 CATGAGACGCGCGCGCGCCCTCGGGCCCTGGGACACACGACTCGGGCCAGAGGGCTCG 1817  
QY 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716  
DB 1818 GCGCTCC-----GGGAGCTCCGCTGGTGGCGAGAGAGAGCG----- 1853  
QY 717 MetProAspSerAspSerGlnAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736  
DB 1854 -----GATGGGGAGCGGGCC-----CGAGCAGCGAGAGAGAGAGCTCTCCAGAA 1898  
QY 737 LeuArgAspProHisSerArgArgArgGlnArgSerIleGlyProAspAlaGluProSer 756  
DB 1899 CTGGGGAGAGAGAGAGAGAGAGAGAG-----GCCGATGGGGCG 1940  
QY 757 SerValLeuAla-----PheTPrArgLeuIleCysAspThrPheArgLysIleValAsp 774  
DB 1941 GTCTGGCTGTGGCGGGAGTGTGGCGGGAGAGCGCAGCCAGCTCGCGGCACTCTGGAC 2000  
QY 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794  
DB 2001 AGCAAGTACTTAACCGGGGCACTCATGATGCCATCTGGTCAACACCGTGACATGGGC 2060  
QY 795 IleGluTyrHisGlnGluProGlnGluLeuThrAsnAlaLeuGlnIleSerAsnIleVal 814  
DB 2061 ATCGAGCAACAGACAGCGCGAGAGAGCTGACCAACATCTCGAATCGCAATGTGGTC 2120  
QY 815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGly 834  
DB 2121 TTCACGACGATGTTGGCCCTGAGATGATCTCGAAGCTGGCTGCAATTGGGCTCTTCAC 2180  
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DB 2181 TACCGCGTAAACCTTACAAACATCTTCGACAGCATCTTGTCATCATCTCGGAG 2240  
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QY 875 LeuLysLeuValAlaPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894  
DB 2301 CTGAACCTGGTGGCCCTTCATGCTCGCCCTCGGGGCGGAGCTGGTGGTCAAGAAACCC 2360  
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DB 2481 CCCGACAGGAAGAACTTCGACTCCCTGCTGGGCGCATTCGTCATGTTGTTCCAGATCTC 2540  
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QY 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023  
DB 2721 GACCAAGACTATCCAACTAGAAAGATTGATAGCTCCAGAAAGCCTGAGACAGAC 2780  
QY 1024 GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGlnHisAlaGluLeuArgLys 1043  
DB 2781 GGAATGCCAAG-----CTCGCCCAATCCCATGACCCCAATGGGCACTGGACCCC 2834  
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DB 2835 AGTCTC-----CCACGTGGTGGGACCTTAGCTCTGAGGTGGGACCTGCC-- 2885  
QY 1060 HisProLysSerSerSerThrGlyValGlyAlaLeuGlySerGlySerArgArgThr 1079  
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QY 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSer 1099  
DB 2943 AGTGTCAATGCTTA-----GGAGAGATGAGCTATGACCAAGCCTCCTCCAGC 2993  
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QY 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169  
DB 3156 GAGGGCGCGCGGCGCGGACCTTCGACACCCCAACGCCCAACATTCATCACGGG 3215  
QY 1170 -----ArgHisArgGlySerLeuGlnArgGlnAlaLysSer 1181  
DB 3216 CCCCATCTGGGCGACCGGCAACCGGCAACCGGCGGAGCGCTGTCTCCGCAAGAGGAC 3275  
QY 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201

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Qy 1202 SerSer-----AlaSerGIuH1aglnAapCyAsmglyLySerAlaSerGIuArgLeu 1219  
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Qy 1220 AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGIuAspAspAspAsnAspGIu 1238  
Db 3330 GCCAAAGACGCTTCCACCAAGATGGCGCAGCGGGGATCGCGGAGAGATAGAGAGAA 3449  
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Db 3450 ATGCATACACCTGCTGCTCCGCGTCCGCAAGATGATGACGCTCATTAAGCCCACTGG 3509  
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Qy 1299 LeuAsnCyAlleThrIleAlaMetGIuArgProIysIleAspProHisSerAlaGIuArg 1318  
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Qy 1319 IlePheLeuThrLeuSerAsnTrpIlePheThrAlaValPheLeuAlaGlnMetThrVal 1338  
Db 3690 ATCTTTCTCACCGCTGTCCAACTACATCTTCACGGGCATCTTCGTGGCGAGATGACATTG 3749  
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Qy 1355 ValIleuAspGIuLeuLeuValIleuIleSerValIleAspIleLeuValIleMetValSer 1378  
Db 3810 GTGCTGAGATGGCTTTTGTCTTCTGCTGCATCATGACATCGTGGTGTCCGCTGAGCTTA 3869  
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Db 3870 GCCGGGGAGCCAAAGATCTTTGGGGGTCTCCGAGTCTTGGGCTCGGACCCCTTAACC 3929  
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Qy 1419 SerLeuLeuProIleGIuAsnIleValIleCysCysAlaPhePheIleIlePheGIu 1438  
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Qy 1459 AsnIleThrAsnIysSerAspCyAlaGlnAlaSerTrpArgTrpValArgHisIleYsTrp 1478  
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Qy 1479 AsnPheAspAsnLeuGIuGlnAlaLeuMetSerLeuPheValIleuAlaSerIysAspGIu 1498  
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Qy 1499 TrpValAspIleMetTrpAspGIuLeuAspAlaValAlaGIuAspGlnGlnProIleMet 1518  
Db 4230 TGGGTGAACATCATGTAACATGACCTGCATGCTGTCTGTGACCAAGACGCTGTGACC 4289  
Qy 1519 AsnHisAsnProTrpMetLeuLeuTrpPheIleSerPheLeuLeuIleValAlaPhePhe 1538  
Db 4290 AACCAACAACCCCTGATGTGCTGTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4349  
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Db 4470 CGG-----AAGGCCAGCGCGCGCTTACTATGACCACTATTGT 4508  
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Qy 1639 LeuAspGIuAlaLeuLyelCysAsnTrpIlePheThrValIlePheValPheGlnSer 1658  
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Qy 1659 ValPheLySLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGIuLeu 1678  
Db 4689 GTGCTGAAGCTGTGGCATTTGTGTGAGAGCGCTTTCAAAGAACGATGAAACGAGCTG 4748  
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Qy 1818 GluSerThrCysTrpAsnThrVal-----IleSerProIleTrpPheValSerPheVal 1835  
Db 5169 GAGCGCAGCTGCTGAGCAGCTTCGAGATTGTGTGTGCGCTGTACTTGTGAGCTTCGTG 5228  
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Db 5229 CTCACCGGCACATTGCTGTCTATCAACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5288  
Qy 1856 GluSerAsnLyGIuAlaLySGlnGIuAlaGIuLeuGIuAlaGIuLeuGIuLeuGIuMet 1875  
Db 5289 GACAGCAACAAGAGCGCGAGAGCGCGGAGATGAGCCGAGCTCAGATGGAGATG 5348  
Qy 1876 ---LySPheLeuSerProGlnProHisSerProLeuGIuSerProPheLeuTrpProGIu 1894  
Db 5349 GCCCATGCTGGGCTTGGCCCGAGAGCTGCTTACCGGCTCC----- 5390  
Qy 1895 ValGIuGIuValAsnSerThrAspSerProLyAlaIlePheThrAlaHis 1914  
Db 5391 -----CCGGGCGCCCTTGGCCGAGAGGCGCG--- 5414

OY	1915	IleGlyAlaIAserGlyPheSerLeuIuHisProThrMetValPro-----	1930	
Db	5415	---GGAGGGGGGGGGCGCG--GGGCGAACCCAGAGGGCGGTGGTTCGCCGGCCTGTAATC	5470	
OY	1931	-----	-HisProGluIuValProValPro	1938
Db	5471	GCTGCCAGCACTCTTGAGGGGGAGCTACCATCAATGCACAACCTGTGGGTTCAT	5530	
OY	1939	LeuGIyProAePLeuThrValArgLysSerGIyAlaSerArgThrHisSerLeuPro	1958	
Db	5531	CTTCACACACTACTCTCGCTCGCGGTGCAGAAAGTGTA-----CCA	5575	
OY	1959	AsnAspSerTyrmetCysArgasnGlySerThrLaGluArgSerLeuGIyHisArgGIy	1978	
Db	5576	CGACAA-----GCMAAGGGTGAGCTGGCTGAGACGGA	5608	
OY	1979	TrpGIyLeuProLybAlaGlnSerGIySerIleLeuSerValHisSerGlnProAlaasp	1998	
Db	5609	GAGCTTCTCCCTGAATCAGACAGTCTCTGCATCTCTGGGTGTCAGACSTGAGTCT	5668	
OY	1999	ThrSerCysIleLeuGlnLeuProLysAspValHisTyrlauLeuGlnProHISglYala	2018	
Db	5669	CGAGA-----CCCCACAGCTG	5686	
OY	2019	ProthrTrpGIyAlaIleProLys-----	2026	
Db	5687	CCCACCTGG-----CCCGACAGACAGAGGGTAGCTGACCCACCTGAGCCAT	5737	
OY	2027	---LeuProProProGIyVArgSerProleuAlaGlnArgProLysArgArgGlnAlaIa	2045	
Db	5738	CGGTGTGGAGACCTGGGGCGAATGCTTTCCCTTGT-CCCTTACGGCCGTCTGGCCGG	5796	
OY	2046	IleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSerGIu	2065	
Db	5797	ATCCAGAAACTCTCCTG---GTAGAGTGAAGAGATCCAT-----TCAACC	5841	
OY	2066	ValSerGIyProSerCysProleuthrArgSerSerPheTrpGIyGIySerSerIle	2085	
Db	5842	CTGTCCGGTCTGGCTGAACATGCA-----	5868	
OY	2086	GlnValGlnGlnArgSerGIyIleGlnSerIyValSerIyHisIleArgLeuProAla	2105	
Db	5869	-----GCAGTCAAGCACCCCAAGTCCCTTCT	5895	
OY	2106	ProCysProGIyLeuGluProSerThrPalalysAspProProGluThrArgSerSerLeu	2125	
Db	5896	CCC-----CGATGCTCTCAAGC-----	5913	
OY	2126	GluLeuAspThrGluLeuSerTrpIleSerGIyAspLeuLeuProSerSerGlnGluGlu	2145	
Db	5914	-----CTCTCGCCCATCCAGCCGAGTTTCTTCACCTGT	5949	
OY	2146	ProleuPhePro-----ArgAspLeuLysIyScyTyrservalGluThnGlnSerCys	2163	
Db	5950	CAGTGTCTGCCAGCCAGAAAGCCCAAAAAGGCGACTGCATGGAACCTTCCCAAGA	6009	
OY	2164	ArgArgArgProGIyPheTrpLeuAspGlnArgArgHisSerIleAlaValSerCys	2183	
Db	6010	TTCGCGCTG-CAGGGCTCTGTGGCATCT-----CTGCGGTACCAAAGGTCACTGT	6055	
OY	2184	Leu-----AspSerGIySerGlnProArgLeuCysProSerProSerSerIeu	2199	
Db	6060	AACCTCTCCGGACGAGCCAGGGAGGACACAGTGCCTGAGACGCCAGGCCACAGNG-CTC	6118	
OY	2200	GlyGIyGlnProleuGlyGIyProGlySerArgProLybIySylbIyLeuSerProProser	2219	
Db	6119	CGCGGGCAGCTTGACAGACACAGCTTGACAGCTTGCCTGACGCAAGCCCGGCG	6178	
OY	2220	IleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----ProGIy	2237	
Db	6179	-----TGCCCTGGGGCGCCGCGGCTGTCTTCAGAACCCCGGCG	6217	
OY	2238	ValCysIeuArgArgArgAlaProAlaSerAspSerIyAspProSerValSerSerPro	2257	

Db	6218	CAGCCTGTCCCCCGCGCTCGCGCGCCTAGACCTGCGCGGCGCGGACCTTTCAGCTT	627
Qy	2258	LeuApSerThrAlaAlaSerProSerProTyrAlaSerThrLeuSerLeuSerGlyLeu	227
Db	6278	GCGGCGGCTCGCGGCGCATCAGCGGACGACGACGAGGCGGCGCTCCACGACGCGGCGT	633
RESULT 8			
	US-09-404-650-3		
	/ Sequence 3, Application US/09404650		
	/ Patent No. 6309858		
	GENERAL INFORMATION:		
	APPLICANT: Dietrich, Paul S.		
	APPLICANT: McGivern, Joseph G.		
	TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;		
	TITLE OF INVENTION: AND USES		
	FILE REFERENCE: R0043B-REG sequence listing		
	CURRENT APPLICATION NUMBER: US/09/404,650		
	CURRENT FILING DATE: 1999-09-23		
	NUMBER OF SEQ ID NOS: 12		
	SOFTWARE: PatentIn Ver. 2.0		
	SEO ID NO 3		
	LENGTH: 6855		
	TYPE: DNA		
	ORGANISM: Homo sapiens		
	FEATURE:		
	NAME/KEY: CDS		
	LOCATION: (192)..(6755)		
	US-09-404-650-3		
Alignment Scores:			
	Pred. No.:	0	Length: 6855
	Score:	5420.00	Matches: 1228
	Percent Similarity:	61.97%	Conservative: 235
	Best Local Similarity:	52.01%	Mismatches: 500
	Query Match:	45.06%	Indels: 402
	DB:	3	Gaps: 63
US-09-611-257A-24 (1-2287) x US-09-404-650-3 (1-6855)			
Qy	12	ThrProProLeuArgGlySerAlaArgProSerSerAPro-----	25
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Qy	26	ProGlyProArgLeuAlaArgGlyTyrThrArgArgMetGluArgAlaProArgSer	45
Db	267	CCCGACCCCG-----	278
Qy	46	ArgAspSerProValAlaSerArgSerSerThrTyrCysProGlyAlaAlaGly	65
Db	279	-----AGCCCCCATCTCTCCCGCCAGGCTGAGAGGAGTCTCGATGAGACT-----	326
Qy	66	AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr	85
Db	327	-----GATTCCT-----CATGTCCACAC	344
Qy	86	ProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgProArgSerTrp	105
Db	345	CCAGACCTGGCGGCTATTGCTCTTCTTGCTGCGACGACGACGACGACCGCCGGAAGTGG	404
Qy	106	CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu	125
Db	405	TGCATCAGATGAGTGTGCAACCCGGGTTTGAATGTGCAGCATCTGGTGTCTCGCTG	464
Qy	126	AsnGlyValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg	145
Db	465	AACGCGGACACCTTGGCATGTACACGCGGTGCGACGACATGAGACTGCTGTCCAGCCGC	524
Qy	146	CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal	165
Db	525	TGCAGATCTCGCAGGCTTGTGATACCTTATCTTCTTGCCATGAGATGGTG	584
Qy	166	ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn	185





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QY 934 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953  
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QY 954 ThrGlnGluAspTrpAsnLysValLeuTrpAsnGlyMetAlaSerThrSerSerTrpAla 973  
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QY 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993  
Db 2601 TCCCTCTACTTTGTGCCCCCTCATGACCTTCGGCAACTATGTGCTTCAACTGCTGGTG 2660  
QY 994 AlaIleLeuValGlyGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013  
Db 2661 GCCATCGTGTGGAGGCTTCACAGCGGAGGTGACGCCAATCGCTCTACTCGGACGAG 2720  
QY 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023  
Db 2721 GACCAAGACTCTATCCCAACTAGAAAGATTGATTAAGCTCCAGAAAGCTTGACAGCAC 2780  
QY 1024 GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGlnHisAlaGluLeuArgLys 1043  
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Db 3054 AGCTGGAAC-----AGCTCAAGCACAAGCCGCTCGCGGAGGACAT 3095  
QY 1140 ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGlu 1158  
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Db 3156 GAGGGCGCGCGGCGCGCACCTTGCAACCCCAACGCGCCACACATTCATCATCGGAG 3215  
QY 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181  
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QY 1299 LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg 1318  
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QY 1339 LysValValAlaLeuGlyLysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn 1358  
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QY 1359 ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer 1378  
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Db 4170 AACTTCACAACCTGGGCGAGGCTCTGATGTCCCTTTGCTCGGATCCAAAGATGT 4229  
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Qy 1918 AlaSerGlyPheSerLeuGluHisIleProThrMetValProHisProGluGluValProVal 1937

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Db 5567 CATCTTCCACCACTACTCTCTCGCGGCTGCAAGAGTGTCA----- 5611  
Qy 1958 ProAsnAspSerTyrlMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg 1977  
Db 5612 CCAGCAACA-----GCAAGAGTGCAGCTGGCTGAGAC 5644  
Qy 1978 GlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla 1997  
Db 5645 GGAAGGCTTCTCCCTGAACTGACAGAGTCCGTCATCTCGTGGGAGACCTGAG 5704  
Qy 1998 AspThrSerCysIleLeuGluLeuProLysAspValHisTyrlLeuLeuGlnProHisGly 2017  
Db 5705 TCTCGAGA-----CCCCACAGC 5722  
Qy 2018 AlaProThrTrpGlyAlaIleProLysLeuProPro----- 2029  
Db 5723 CTGCCCACTG-----CCGCAAGAAGCAAGGCTGAGCTGACCCACTGAGCC 5773  
Qy 2030 -----ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAla 2044  
Db 5774 CATGGCTGGAGAGACTGGGCGGAATGCTTCTTCCCTTGT-CTCTACGGCGCTGCG 5832  
Qy 2045 AlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSer 2064  
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Db 5878 ACCGTGCGGTCTCGGTGGAACATGACA----- 5907  
Qy 2085 IleGlnValGlnGluArgSerGlyIleGlnSerValSerGlyHisIleArgLeuPro 2104  
Db 5908 -----GCAGTCAACGACCCCAAGTCCCT 5931  
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Db 6096 TGTACCTCTCTCCGAGGCGCAACCGGAGCGACACGTCGCTGAGCGCCAGCCACAG- 6154  
Qy 2199 LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPro 2218  
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Qy 2237 GlyValCysLeuArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSer 2256  
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Qy 2257 ProLeuAspSerThrAlaIleSerProSerProLysLysAspThrLeuSerLeuSerGly 2276  
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QY 2277 leu 2277  
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RESULT 9  
US-09-935-541-3  
Sequence 3, Application US/09935541  
Patent No. 6589787  
GENERAL INFORMATION:  
APPLICANT: Dietrich, Paul S.  
APPLICANT: McGivern, Joseph G.  
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
TITLE OF INVENTION: AND USES  
FILE REFERENCE: R0043B-REG sequence listing  
CURRENT APPLICATION NUMBER: US/09/935,541  
CURRENT FILING DATE: 2001-08-23  
PRIOR APPLICATION NUMBER: 09/404,650  
PRIOR FILING DATE: 1999-09-23  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 6855  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (192)..(6755)  
US-09-935-541-3

Alignment Scores:  
Pred. No.: 0 Length: 6855  
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Query Match: 45.06% Indels: 402  
Gaps: 63

US-09-611-257a-24 (1-2287) x US-09-935-541-3 (1-6855)

QY 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25  
Db 207 TCCCGCGCCCTCTCATCTGCAGACAGCCCGCTGCAGAGTCACGACGAGAG 266  
QY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgAlaGArgMetGluArgAlaProArgSer 45  
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QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85  
Db 327 -----GATCCT-----CATGTCCACAC 344  
QY 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105  
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Db 585 CTCAAGATGGTGGCCCTGGGATTTTGGCAAGAGTCACTCGGAGACATGGAGAC 644  
QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGlyTyrSerLeuAspLeuGlnAsn 205  
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QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285  
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QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339  
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QY 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357  
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QY 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAsnIleGlyTyrAlaIleTrpIle 377  
Db 1176 GCGACGCGCAACCCCAACAGGATGTCATCACTTCAACATCGGTATGATCTTGGATTT 1235  
QY 378 AlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetCysPheValMetAsp 397  
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QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417  
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QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477  
Db 1473 TACCGCGAGCTGGCGACTGCTGACGAGAGATCTTCCAGATGTCTGCCATCCTGCGC 1532  
QY 478 LysAlaIleArgAlaGluAlaGlnValSerArgAlaIleGlyValAlaArgAlaGlyLeuLeu 497  
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 Qy 538 HisLeuGlYAsnGlYThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557  
 Db 1593 -----GAGCCGGAG----- 1601  
 Qy 558 AlaAsnGlySerArgAlaGlyLeuMetLeuProProProSerThrProThrProSerGlyGly 577  
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 Db 1629 -----CACGCCAAG-----GAGCCC 1643  
 Qy 598 ValArgCysGlnAlaProProProArgCysArgProSerGlyAlaSerGlyArgThrValGly 617  
 Db 1644 CGGACATACCAAGCTGTGCCGCAACATAGCCCTGGATGCG----- 1685  
 Qy 618 SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys 637  
 Db 1686 -----ACGCCCCACACC----- 1697  
 Qy 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657  
 Db 1698 ----CTGGTGGAG-----CCCATCCCCCGCCAGCTGGCTTCC----- 1730  
 Qy 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676  
 Db 1731 -----GATCCCGCCAGCTGCGCTTGTGCAG 1757  
 Qy 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696  
 Db 1758 CATAGGACGCGCCCGGCGCTCGGCGCGAGCAACCGACTGGCGAGAGAGGCTCG 1817  
 Qy 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716  
 Db 1818 GGGCTCC-----GGAGCTCGCTGTGGCGAGAGAGGCG----- 1853  
 Qy 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736  
 Db 1854 -----GATGGGAGCGGGGCC-----CGAGACGAGAGAGAGAGGCTCTCTCAGAA 1898  
 Qy 737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756  
 Db 1899 CTGGCGAAGAGAGAGAGAGAGAGAGAGAG-----GCCGATGGGCGC 1940  
 Qy 757 SerValLeuAla-----PheThrArgLeuIleCysAspThrPheArgLysIleValAsp 774  
 Db 1941 GTCTGGCTGTGCGGGAGATGTGTGGCGGAGACGCGCAAGCTGGCGGCGATGTGGAC 2000  
 Qy 775 SerIleTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794  
 Db 2001 AGCAAGTACTTTCACCGCGGGCATCATGATGCGCATCTCGTCAACCCGTGAGCATGGCGC 2060  
 Qy 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814  
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 Qy 815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPheGly 834  
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 Qy 835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyrGlu 854  
 Db 2181 TACCTGCCTAACCTTACATCATCTTGACAGACATCTGTCAATCATCAGCATCGGAG 2240  
 Qy 855 IleValGlyGlnGlnGlyGlyLysSerValLeuArgThrPheArgLeuMetArgVal 874  
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 Qy 875 LeuLysValLeuValArgPheLeuProAlaLeuGlnArgGluValLeuValValLeuMetLysThr 894  
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Qy 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIle 914  
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 Qy 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGlyLysArgAsp---GlyAspThrLeu 933  
 Db 2421 CTGGGATGATATTTTGGCTGCAAGTTCAAGCTCCGACGAGACACTGGAGACAGGTG 2480  
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 Db 2601 TCCCTTACTTGTGCGCTCATGACCTTGGCACTATGTGCTTTCACCTGTGTG 2660  
 Qy 994 AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerPro 1013  
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 Qy 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023  
 Db 2721 GACCCAGACTCACAACATGAAGATTGATAGCTCCAGAGAGGCTGAGACAGAC 2780  
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 Db 2835 AGTCTC-----CCACTGGGTGGGACCTAGCTCTGTGGGCTGGCGGAGCTGCC--- 2885  
 Qy 1060 HisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr 1079  
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 Qy 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSer 1099  
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 Qy 1140 ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerGlu 1158  
 Db 3096 GAGTCTGCTGCTCTGGAGAGCGGCGGCGGCGCGCGGCTGTGCGAGCTTCCCGCGGAC 3155  
 Qy 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169  
 Db 3156 GAGGGCGCGCGGCGCGGCGGACCCCTGACACCCCAACCCCAACCATTCATCAGGG 3215  
 Qy 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181  
 Db 3216 CCCCATCTGGCGCACCGGACCGGACCGGCGGAGCTGTCTCTGCAACACAGGAGAC 3275  
 Qy 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201  
 Db 3276 TCGGTGAACCTTGGCGGAGCTGTGCTCCGCGGTGGGCGGACCCCGGCGCGCTGGAG 3335  
 Qy 1202 SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219  
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Db      5525 CTGGAGG---GGAGCTAACAT-----CATGACAACTGTGGGCTC 5566
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Db      5567 CATCTTCACACACACTCTCTGCTGCGGCTGCAGAAAGTGCA----- 5611
Qy      1958 ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg 1977
Db      5612 CCACGACAA-----GCAAGAGGTGACGCTGCTGAGAC 5644
Qy      1978 GlyTyrProLysProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla 1997
Db      5645 GGAAGGCTTCTCCCTGAACTCAGACAGAGTCTCTCATCTCTGCTGAGTACAGCTGAG 5704
Qy      1998 AspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGly 2017
Db      5705 TCTCGAGAA-----CCCCACAGC 5722
Qy      2018 AlaProThrTyrGlyAlaIleProLysLeuProPro----- 2029
Db      5723 CTGCCACACTGG-----CCGCAAGACAGCAGAGGTGAGCTGAGCCACCTGAGCC 5773
Qy      2030 -----ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAla 2044
Db      5774 CAGCGGTGGAGAGACCTGGCGAATGCTTCTCCCTTGT-CTCTACGGCGCTTCGC 5832
Qy      2045 AlaIleArgThrAspSerLeuAspValGlnGlyLysSerArgGlnAspLeuLeuSer 2064
Db      5833 CGGATTCAGAGAACTTCTGT---GTGAGATGAGAGAGATCCAT-----TCA 5877
Qy      2065 GluValSerGlyProSerCysProLeuThrArgSerSerPheTyrGlyGlySerSer 2084
Db      5878 ACCCTGTCCGGTCTGCTGCTGAACATGACA----- 5907
Qy      2085 IleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuPro 2104
Db      5908 -----GCATCAAGCAACCCCAAGTCCCT 5931
Qy      2105 AlaProCysProGlyLeuGlnProSerTyrAlaLysAspProGluThrArgSerSer 2124
Db      5932 TCTTCC-----CGAGTCCCTCAGCC----- 5952
Qy      2125 LeuGlnLeuAspThrGlnLeuSerTyrIleSerGlyAspLeuLeuProSerSerGlnGlu 2144
Db      5953 -----CTCTCTGCCCATGCCAGCCGAGTTCTTCCACC 5985
Qy      2145 GluProLeuPhePro-----ArgAspLeuLysLysCysTyrSerValGluThrGlnSer 2162
Db      5986 CTGCAGTGTCTGCCAGCAGAAAGGCCAGAAAGGAGCATGGGCACTGGAAACCTCCCA 6045
Qy      2163 CysArgArgArgProGlyPheTyrLeuAspGlnGlnArgHisSerIleAlaValSer 2182
Db      6046 AGATTGGGCTG-CAGGGCTCTGGGCACT-----CTGCGGTCCCAAGGTGAC 6095
Qy      2183 CysLeu-----AspSerGlySerGlnProArgLeuCysProSerProSerSer 2198
Db      6096 TGTACCTCTCTCCGAGCAGCAGCGGAGCAGACACTGCTGAGACGCGGCCAGCAG- 6154
Qy      2199 LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysValSerLeuPro 2218
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Qy      2219 SerIleSerIleAspProProGlySerGlnLysSerArgProProCysSer-----Pro 2236
Db      6215 GCG-----TGCCCTGGGGCGCGCGCGCGCTGTCTCAGACAGCCCG 6253
Qy      2237 GlyValCysLeuArgArgArgAlaProLysAspSerLysAspProSerValSerSer 2256
Db      6254 GGGCGGCTGTCCCGCGCGCTGCGCGCTGAGCTGCGGCGCGCGGCTCTTTCAG 6313
Qy      2257 ProLeuAspSerThrAlaLysSerProSerProLysLysAspThrLeuSerLeuSerGly 2276
Db      6314 CCTGGGGGGGCTGCGGCGCATCAGCGCAGCGAGCGGGGGCTTCACCAAGCCCGG 6373

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Qy      2277 Leu 2277
Db      6374 CTG 6376

RESULT 10
US-09-404-650-12
; Sequence 12, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; NUMBER OF SEQ. ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-404-650-12

Alignment Scores:
Pred. No.: 0 Length: 6503
Score: 5407.00 Matches: 1234
Percent Similarity: 61.05% Conservative: 241
Best Local Similarity: 51.08% Mismatches: 502
Query Match: 44.95% Indels: 444
Gaps: 60

US-09-611-257a-24 (1-2287) x US-09-404-650-12 (1-6503)
Qy      3 ProHisArgValProArgCysValArgThrProProLeuArgLysSerAlaArgProSer 22
Db      64 CCCCCGGGGCCCCCGCGCTGATGCGCCCTGCTGCGCCCGGGGGCGCA----- 114
Qy      23 SerAspPro-----ProGlyProArgLeuAlaArgGlyTyrThrArgArgArg 38
Db      115 GGTGATCCGGGAATCCGAGGCGTGGGGCCGGCGGG--GCGGGGGTCCCTCCACGCCGG 173
Qy      39 Met-----Glu-ArgAlaProArg-----SerArgAspSerProValAla----- 51
Db      174 CTTCGGGAGACCGCGTCAACCCGCGCTGTGCGCGGAGACCCGCTCGCGGCCACG 233
Qy      52 -----SerArgSerSerThr 57
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Qy      57 rCysProGlyProGly-----AlaAlaGlyAla-GlySerThrG 70
Db      294 CTGCAGAGAGCCCGGCGCCCTGAGCGCGGGAATCACTGAGCAGCGGGGCCCGGATCCCC 353
Qy      70 IuLysAspProGlySerAlaAspSerGluAlaGly-----LeuProTyrP 86
Db      354 CTCATCCCTCCAGCGCTGAGGAGCATTGAGAGGAAACCAACCTGAGCTCCACATC 413
Qy      86 roAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgProArgSerTyrP 106
Db      414 CAGACCTGGGCTCGGTGCTTCTTCTGCGCGCCAGACCAAGACCGCAAGAACTGCT 473
Qy      106 ySLeuArgThrValCysAsnProTyrPheGlnArgValSerMetLeuValIleLeuLeu 126
Db      474 GCATCAAGAGGTGTGTAACCGGTGTTGAGAGTGTGACATGCTGTTATTCTGCTGA 533
Qy      126 snCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 146
Db      534 ACTGTGTACCTCGGCGATGTACAGCAGCATGTATGACATGAGAGTGTCTGGAACGTT 593
Qy      146 ysaGlyLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 166

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Db 594 GCAAGATCTCGAGGCTTCGTGATGACTTCATCTTCACTCTTGGCCATGAGATGATGCG 653  
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Db 654 TTAAAGATGGTGGCCCTGGGCAATTTTGGCAAGAGTGTACTCTCGAGACACATGGAACCC 713  
Qy 186 rglLeuAspPhePheIleValIleAlaGlyMetLeuGlyTyrSerLeuAspLeuGlyAsnY 206  
Db 714 GCGTGAATTTCTTCACTTGTATGACGAGGATGGTGAAGTACTCTCTGCACTTACAGAAC 773  
Qy 206 alserPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgY 226  
Db 774 TCAACCTGACGCATCCGACATGTGGTGTCTTGAGGCTCTCAAGCCATCAACCGT 833  
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Db 834 TACCCAGACGACGGAATCTGTGTAACTGTCTCGACACGCTGCCATCTGGGGAACG 893  
Qy 246 alLeuLeuLeuCysePhePheValPhePheIlePheGlyIleAlaGlyValGlnLeuTyrP 266  
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Db 954 CAGGCTGTACGGAACCGCTGCTTCTTGAGAGAACTTCACCATVACAAGGGGATGTGG 1013  
Qy 286 sPheuGluProGlyTyrGlnThrGluAsnGluAspGlySerProPheIleCyseSerGlnP 306  
Db 1014 CCGTGCCCTTATTTACCAACAGAGAGATACGAGATGCCCTTATATCTGCTCCCTGA 1073  
Qy 306 roArgGluAsnGlyMetArgSerCyseArgSerAlaProThrLeuArgGlyGlyGlyG 326  
Db 1074 CTGGGACATGGCATATGAGGCTGCCACAGATCCCCCACTGAGAGAGACAG----- 1126  
Qy 326 lyGlyProProCyseSerLeu-----AspTyrGlyuThrTyrAsnSers 340  
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Qy 378 laIlePheGlnValIleThrLeuGlnGlyTyrTyrValAspIleMetTyrPheValMetAspA 398  
Db 1305 TGAATTTCCAGTGATCACTCTGGAGGCTGGGGTGGAGATCATGTACTATGTATGTAGCG 1364  
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Qy 438 erGlnLeuMetArgGlnGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerP 458  
Db 1485 ACCGGCTGATGCTGGACCAACGCGGCTACCTGTCC---TCCAGACACGGTGGCCAGTT 1541  
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Db 1542 ACCGTGAGCCCGGTGATGTGATGAGAGATCTTCCAAATATGTGTCAACATCTTGCA 1601  
Qy 478 ysaIalaIaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuS 498  
Db 1602 AAGCCAGAGCC-----CGTGCCCTAAGGCTCTTACAGAGCCCTG----- 1639  
Qy 498 erSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCyseThrArgSerH 518  
Db 1640 -----CAGA 1643

Qy 518 laArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisTyrH 538  
Db 1644 ACCGGCGCCAGGCC----- 1657  
Qy 538 laLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspA 558  
Db 1658 --ATGGGCCCGGGAGCA----- 1672  
Qy 558 laAsnGlySerArgLeuMetLeuProProProSerThrProThrProSerGlyGlyP 578  
Db 1673 -----CCAGCCCTGGCCAAAGCTTGGGCC----- 1696  
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Db 1697 -----CATGCCAAG-----GAGCCCA 1712  
Qy 598 aArgCyseGlnAlaProProProArgCyseProSerGluAlaSerGlyArgThrValGlys 618  
Db 1713 GGCACGTGCAAGCTGTGCGCCACAGACAGACGCCCTGAGC----- 1750  
Qy 618 erGlyIlyValTyrProThrValHisThrSerProProProGluIleLeuIlysaPlysa 638  
Db 1751 -----CCCACTCCCAACAC----- 1765  
Qy 638 laLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProP 658  
Db 1766 --CTGGTGAC----- 1774  
Qy 658 roGlyProPheSerSerMetHisIlysaLeuLeuGluThrGlnSerThrGlyAlaCyseHis 678  
Db 1775 -----CCCATCTCTGCATCTG----- 1792  
Qy 678 erSerCyseIlyHisSerSerProCyseSerIlysaIaAspSerGlyAlaCyseGlyProAsp 698  
Db 1793 -----GCCTGTGACCCAGCA 1808  
Qy 698 erCyseProTyrCyseAlaArg-----ThrGlyAlaGlyGluProGluS 712  
Db 1809 GCTGCCCTCAGCTGCCAGACAGAGGACGAGGCGGCCCTGTGGCCGTGGCCAGACAGTACT 1868  
Qy 712 erAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspA 732  
Db 1869 CAGGCGAGAGAGGCTCAGGTTCTGTGGCTGTGACAGAGGCCCAAGCCATAGGGATGAGC 1928  
Qy 732 laGlnHisSerAsp-LeuArgAspProHisSer-----ArgArgArgGlnArgSerLeu 749  
Db 1929 TCCAGAGCAGTAGAGATGGGGTCTCTCGAGCCTGGGAGAGAGAGGACAGAGAGAGC 1988  
Qy 750 GlyProAspAlaGluProSerSerValLeuAlaPheTyrArgLeuIleCyseAspThrPhe 769  
Db 1989 GGG-----CAGCCGACGCTGTGGG-GATGTGTGGCGGAGACAGAAAAAGCTG 2038  
Qy 770 ArgIlyIleValaAspSerIlyTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn 789  
Db 2039 CCGGGCATGTGAGACAGCAAGTACTTCAACAGAGATCATATGATGCTTCTGTGGTGAAC 2098  
Qy 790 ThrLeuSerMetGlyIleGlyTyrHisGlnGluInProGluGluLeuThrAsnAlaLeuGlu 809  
Db 2099 ACAGTAGAGAGGACATCGACACACAGACAGCCGAGAGACTGACCAACATCTGGAG 2158  
Qy 810 IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuIlysaLeuVal 829  
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Qy 850 IleSerValTyrGlnIleValaGlyGlnGlnGlyGlyIlyLeuSerValLeuArgThrPhe 869  
Db 2279 ATCAGATCTGGGAATCTGTGGGACGCGAGCGGTGCTGTGTGTGGCGCACCTTC 2338



[illegible]

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Db	3443	---ATACCCAAGAGATGCTTTCACCAAGATGATGACCGCGCACCGCGGGAGAGACGAG	3499
Qy	1237	AspGlnGlyAsnIleuSerLySgIyGluArgIleGlnAlaTrpValArgSerArgIleuPro	1256
Db	3500	GAGAGAGATCGCATTTACCTGCTGTGTTTCCGGGATCGGCAAGATGATGATGTCACCAAGCG	3559
Qy	1257	AlaCysGlyAspArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPhe	1276
Db	3560	GACTGGTGCAGAGTCCCGAGAGACTGGTCCGCTACTCTTCTTCCCGGAGAACAAATTC	3619
Qy	1277	ArgLeuIleuCysHisArgIleIleThrHisIlySerMetPheAspHisValIleuValIle	1296
Db	3620	CGAATCCTGTGTGACAGACATCATTTGCTCACAAAGCTTTTGATCTACGTGATCTTGACCTTT	3679
Qy	1297	IlePheIleuAsnCysIleThrIleAlaMetGluArgProLySleAspProHisSerAla	1316
Db	3680	ATCTTCTCTCAACTGTATACCATTTGCTCTGAGAGACCAGATTTGAAGCTGTAGACT	3739
Qy	1317	GluArgIlePheIleuThrIleuSerAsnTyrIlePheThrAlaValPheIleuAlaGlnMet	1336
Db	3740	GAGGCGAATCTTCTCAGCGGTCTTACTACTACTTTCACAGCCATCTTCTGTGGCGAAGTG	3799
Qy	1337	ThrValIlyValAlaIleAlaIleuGlyTyrCysPheGlyGlnGlnAlaTyrIleuArgSerSer	1356
Db	3800	ACACTGAAAGTGCTTCTCTGCGGCTGTACTCTTGATGGAGCGGCTACGTGCTGACAGC	3859
Qy	1357	TrpAsnValIleuAspGlyIleuIleuValIleuIleSerValIleAspIleIleuValSerMet	1376
Db	3860	TGGAATGATCACTGATGGTTCCTGCTCTGTTCCTCATCTCATCTGATTCGATGTCGTG	3919
Qy	1377	ValSerAspSerGlyTyrThrIlyIleGlnMetIleuArgValIleuArgLeuIleuArgThr	1396
Db	3920	GCCCTGTGCGGGAGCCAGAAATTCGTGGGGTCTCCGGAGTCTTGGCGATCTTCGTAAC	3979
Qy	1397	LeuArgProIleuArgValIleSerArgAlaGlnGlyIleuIlySleuValIleGluThrIleu	1416
Db	3980	TTAGCTCTTTGAGGGTTATCAGCGGGCCCTGGCGTGAAGCTGGTGTGAGACCGCTC	4039
Qy	1417	MetSerSerIleuIlyProIleGlyAsnIleValIleCysGlyAlaPhePheIleIle	1436
Db	4040	ATTCCTCTCCCTCAAGCCCATTTGGGAAACATCGTCTCATCTGCTGTGCTTCTTCATATC	4099
Qy	1437	PheGlyIleIleuGlyValGlnIleuPheIlySgIyIlyPhePheValCysGlnGlyIleuAsp	1456
Db	4100	TTCCGCATCTCCGGGGGTGCACCTTTTCAAGGCAAGTTTCAACATTTGTTGGAGTGCAC	4159
Qy	1457	ThrArgAsnIleThrAsnIlySerAspCysAlaGlnIleuAspTyrArgTrpValArgHis	1476
Db	4160	ACCAGAAACATCACCAACCATCTGACCTGCGCGCGGCGCACTACCGTGGGTGCATCAC	4219
Qy	1477	LysTyrAsnPheAspAsnIleuGlyGlnAlaIleuMetSerIleuPheValIleuAlaSerIlyS	1496
Db	4220	AAATACCACTTTGACCACTGGGCGAGGCACTGTATGTCCCTCTTGTGCTTGGCTCCCAAG	4279
Qy	1497	AspGlyTrpValAspIleMetTyrAspGlyIleuAspAlaValGlyValAspGlnIlePro	1516
Db	4280	GACGGCTGGGGAACATCATGTATTAATGATTAATGCTGTGTGCTGTGGACAGACGCA	4339
Qy	1517	IleMetAsnHisAsnProTrpMetIleuIlyPheIleSerPheIleuIleIleValAla	1536
Db	4340	GTCAGAACACCAACCCCTGATGCTACTGACTTCAATTCGTTCTGCTCATGTGTACG	4399
Qy	1537	PhePheValIleuAsnMetPheValGlyValIleValIleGluAsnPheHisIlySlyCysArgGln	1556
Db	4400	TTCTTTTGCTCAACATGTGTGTGGGCGGTGCTGTGGAGAACTTCCACAAATGCGCGAG	4459
Qy	1557	HisGlnGluGlnGluIleAlaArgArgGlnGluIlySargIleuArgArgIleuGlnIlyS	1576

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Dh 4460 CACCAGAGGCTGAGAGGCGCGAGCGCTGAGAGAAACGCTGCGGCGCTGAGAAAG 4519
Qy 1577 LysArgArgserIysgluIysgluMetAlaGluAlaGlnCysIysProTyrTyrSerAsp 1596
Dh 4520 AACGCGCGT-----AAGGCTCAGAGGCTGCTCACTATGCTAC 4558
Qy 1597 TyrSerArgPheArgLeuValHisHisIleuCysThrSerHisTyrIleuAspLeuPhe 1616
Dh 4559 TACTGTCGCCAAGAGCGCTGCATCTCATCTGCATGTGCACGCCACTACCTGCAGATCTTC 4618
Qy 1617 IleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnPro 1636
Dh 4619 ATTACCTTCATCTGCTCCCAATGTGTGCACCATGTCCCTGAGAGACTCAACCGAGCT 4678
Qy 1637 GlnIleuAspGlnAlaIleuIysIleCysAsnTyrIlePheThrValIlePheValPhe 1656
Dh 4679 ACATCCCTAGACAGCGCTTAAGTACTGCACCTACATGTTCACCACTGCTTGTGCTG 4738
Qy 1657 GluSerValPheIysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTyrAsn 1676
Dh 4739 GAGGCTGTGCTGAAGCTGTGTGCATTTGGCTGAGGCTTCTTCAAGAGCCGATGGAAC 4798
Qy 1677 GlnIleuAspLeuAlaIleValIleuLeuSerIleMetGlyIleThrLeuGlnGluIleGln 1696
Dh 4799 CAGCTGGACCTGGACCATTTGTGTGCTGTCCGTATGGGCATCACACTGAGAGATCGAG 4858
Qy 1697 ValAsnLeuSerIleuProIleAsnProThrIleIleAlaArgIleMetArgValIleuArgIle 1716
Dh 4859 ATCAATGCCCGCTTCCCATCAACCCACCATCATCTCGTATCATGCGTGTTCGCGTATC 4918
Qy 1717 AlaArgValIleuIysLeuIleuIysMetAlaValAlaGlyMetArgAlaIleuIleuHisThrVal 1736
Dh 4919 GCCCGGGTGTGAAGCATTTGAAGATGGCCACAGAGATGGCGGCCCTGCGTGCAGACAGTG 4978
Qy 1737 MetGlnAlaIleuProGlnValAlaIysAsnLeuGlyIleuLeuPheMetLeuIleuPheIle 1756
Dh 4979 GTACAGGCTCTGCGCCCGAGTGGGCAACTGGGCTGCTCTTCATGCTGCTCTTCTTCATC 5038
Qy 1757 PheAlaAlaIleuGlyValAlaIleuIleuPheGlyIysAspLeuGluCysAspGlnThrHisProCys 1776
Dh 5039 TATGCTGCTGTGGAGAGAGCTCTTGGAAAGCTGTCTGCATATGACGAACCCGCTGT 5098
Qy 1777 GluGlyIleuGlyIysArgHisAlaIleuPheArgAsnPheGlyMetAlaPheLeuThrIleuPhe 1796
Dh 5099 GAGGGGATAGACCGGCGACCGCCACTTTGAAACACTTGGGATGGCTTCTTCACAGCTCTTC 5158
Qy 1797 ArgValSerThrGlyIysAspAsnTyrAsnGlyIleMetIysAspProSerArgAspCys--- 1815
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Qy 1816 AspGlnGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSer 1833
Dh 5219 CATGATGAGCGCACGAGCTTAAGAGCTTCAGAGTTGTGTACCGGCTTACTTGTGAGC 5278
Qy 1834 PheValLeuThrAlaGlnPheValIleuValAsnValValIleAlaValIleuMetIysHis 1853
Dh 5279 TTGTGTGTACAGCTCACTGTTGCTCATCACTGAGTGTGGCCGCGTGCATGAAACAT 5338
Qy 1854 LeuGluGluSerAsnIysGluAlaIysGluGluAlaGluLeuGluAlaGluLeuGluLeu 1873
Dh 5339 CTGAGATCAGCAACAAGAGGCGCCAGAGAGATGAGATGCTGATGATCGAGCTG 5398
Qy 1874 GluMetIysThrIleuSerProGlnProHisSerProIleuGlySerProPheLeuThrPro 1893
Dh 5399 GAGATG----- 5404
Qy 1894 GlyValGluGlyValAsnSerThrAspSerProIysProGlyValaProHisThrThrAla 1913
Dh 5405 ----GCCCATGGCTCGGCGCCCTGCGCTGCGCCGCTGGT----- 5443
Qy 1914 HisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGln 1933
Dh 5444 -----CCCTGCGCCCTGCG 5455

Qy 1934 GluValProValPro---LeuGlyProAspLeuLeuThrVal----- 1946
Dh 5456 CCCTGCGCCCTGCGCCCTGTGCTGTGAGGAGGCTGCCACTGATTCACCTGGGCTCCGGG 5515
Qy 1947 ArgIysSerGlyValSerArgThrHisSerIleuProAsnAspSerTyrMetCysArgAsn 1966
Dh 5516 CGAGGATCGGAGGGGAGAGTGTCTGGAGG---GACACCGAGAGTCACTGTGCGGCGAC 5572
Qy 1967 ---GlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProIysAlaGln 1985
Dh 5573 TGTATTTCTCCAGCCGAGAGACCTG-----TGG-----CTGAGC 5608
Qy 1986 SerGlySerIleuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeu 2005
Dh 5609 AGCGTCTTTATATATCAAGAGCTCTTGGAGGGGAGACTGATCATCATCAACACTG 5668
Qy 2006 ProIysAspVal---HisTyrIleuLeuGlnProHisGlyAla----- 2018
Dh 5669 TCTGGGTCCGTCTCCACACATAGCGCTCACCTGACGCGCTGTGGCAAGTGCACCATGAC 5728
Qy 2019 -----ProThrTyrGlyAlaIleProIysIleuProPro 2030
Dh 5729 AAGCAAGACAGCTTTCATTCATCTGCTGAGGAGATGACTGAGTCTTGAAGACCTCA 5788
Qy 2031 GlyArgSerProIleuAlaGlnArgProIleuArgArgGlnAlaAlaIleArgThrAspSer 2050
Dh 5789 CGGCTGCCCAAGAGGCCCAAGAGAGAGAGAGAGTGAAGTAAAGCTCCGAGGCCCATGC 5848
Qy 2051 LeuAspValGlnGlyIleuGlySerArgIysAspLeuLeuSerGlu-----ValSerGly 2068
Dh 5849 AGGCTGAGACCTGATGATGATCTTTTGCCCTTGGCCMAAGAGAGCAAGTGTCCACAGCG 5908
Qy 2069 ProSerCysProIleuThrArgSerSerSerPheThrGlyGlySerSerIleGlnValGln 2088
Dh 5909 CCAAGAG-CTGTGCTGTGGAAT-----GGGGGCAATTCATCAAC-CTG 5954
Qy 2089 GlnArgSerGlyIleGlnSerIysValSerIysHisIleArg----- 2102
Dh 5955 TCCAGTCTGTGCTCAACACAGAGAGAGCAAGCACCAGAGCCCTTCTCCCGGATG 6014
Qy 2103 -----LeuProAla 2105
Dh 6015 GCTCCAGCCTCTCGTATGATGCTGTGATGTTCTTCCACCCTGTGTGTGCCAGCG 6074
Qy 2106 -----ProCysProGly-----LeuGluPro 2112
Dh 6075 AGAAGGGCAGAAACGGGCAATGATGACGAACCTGCCCCAAG-ATTGCACCTTCAGGG 6133
Qy 2113 SerTyrAlaIys---AspProGluThrArgSerSerLeuGluIleuAspThrGluLeu 2131
Dh 6134 TCTGTGGCATGCTGAGAGTCAACAGAGTCAACCTGACCTCTTGGCCAGGCTACTGTG 6193
Qy 2132 SerTyrIleSerGlyIysAspLeuLeuProSerSerGlnGluIleuProIleuPheProArgAsp 2151
Dh 6194 AGTGAACACCTCTTGGATCCAGTCTTACCACTCA----- 6229
Qy 2152 LeuIysIysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheThrLeu 2171
Dh 6229 ----- 6229
Qy 2172 AspGluGlnArgArgHisSerIleAlaValSerCysIleuAspSerGlySerGlnProArg 2191
Dh 6230 -----GCGGCGAGCTTACAGACACACAGAGAACAGTCTGACT----- 6268
Qy 2192 LeuCysProSerProSerSerLeuGlyGlyIleProIleuGlyIleProGlySerArgPro 2211
Dh 6269 CTGAGTGAACAGTCCCGAGCTGCTCGGGGCGCGGATCCAGATGCTGG-----CCA 6322
Qy 2212 LysIysIysLeuSerProProSerIleSerIleAspProProGluSerGlnIysSerArg 2231
Dh 6323 CGGGCTAGCTGTACCGGCGACCGCGG-----CGGCTGAGCTGCGGGCGCGTGG 6376
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QY 2232 ProProCySerPro-GlyValCysLeuArgArgAlaProAlaSer----- 2247
DB 6377 CCTGTTTAGTCTGCGTGGCGGCCCAACCGTAGCCAGAGTGGCGCTCCAC 6436
QY 2248 -----AppSerLysAspProSer 2253
DB 6437 CAGCCCTGGCTGCACCTACCAACGACTCATGACCCCTCT 6476

RESULT 11
US-09-935-541-12
; Sequence 12, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGiven, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCULUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence 11etctg
; CURRENT APPLICATION NUMBER: US/09/935,541
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-935-541-12

Alignment Scores:
Pred. No.: 0 Length: 6503
Score: 5407.00 Matches: 1234
Percent Similarity: 61.05% Conservative: 241
Best Local Similarity: 51.08% Mismatches: 502
Query Match: 44.95% Indels: 444
DB: 4 Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-935-541-12 (1-6503)
QY 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
DB 64 CCCCCGGGGCGCGCCCTGCATGCGCGCTCCCTCCGCCCGGGGGCGCA----- 114
QY 23 SerAspPro-----ProGlyProArgLeuAlaArgGlyTyrThrArgArgArg 38
DB 115 GCTGATCCCGGAATCCGAGGGGTGGGGCGGG-GGCGGGGGTCCCTCCACGCCGG 173
QY 39 Met-----Glu-ArgAlaProArg-----SerArgAspSerProValAla----- 51
DB 174 CTTGGGGGACACGGGTCAACCCCGGCTCTGCGCGGAGACACCCCGCTGCCCGGCCACG 233
QY 52 -----SerArgSerSerThrTh 57
DB 234 TCCATGCCAAGGGCTCCCTGCTCCACGCTGACAGCTGACAGCAACTTACCGCCCTCAT 293
QY 57 rCySProGlyProGly-----AlaAlaGlyAla-GlySerThrG 70
DB 294 CTGCAGACGCCCGCCCTGAGCGCGGAATCATGACAGACGCGGGGCCCGGAGTCCCC 353
QY 70 LuLysAspProGlySerAlaAspSerGluAlaGlyLys-----LeuProTyrP 86
DB 354 CTCATCCCTCCAGGCGCTGAGAGCCATTGGAAGAACCAACCTGACGTCCACATC 413
QY 86 roAlaLeuAlaProValAlaPhePheTyrLeuSerSerGlnAspSerArgProArgSerTrpC 106
DB 414 CAGACCTGCTCTCTGCTCTTCTCTGCTGCGCCAGACCAACGAGCCCAAGAACTGAT 473
QY 106 ySLeuArgThrValCysAspProTyrPheGluArgValSerMetLeuValIleLeuLeuA 126
DB 474 GCATCAAGATGTTTGTAAACCGGTGTTGAGTGTAGAGCATGCTGTTATTCTGCTGA 533
QY 126 snCySValThrLeuGlyMetPheArgProCySGLuAspIleAlaCysAspSerGlnArgC 146

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DB 534 ACTGTGTACCTGGGCGATGTACACGCATGTATGATGAGTGCCTGTGGACCGTT 593
QY 146 ySArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetValY 166
DB 594 GCAAGATCTCGACAGGCTTGTGATGATCTTCACTTCTTCTTGTGCGATGAGATGATGC 653
QY 166 allySmetValAlaLeuGlyIlePheGlyLysArgCysTyrLeuGlyAspThrTrpAsnA 186
DB 654 TTAAAGATGGTGGCGCTGGGCAATTTTGGCAAGAGTCTACCTCGGAGACACATGAAAC 713
QY 186 rgleuAspPhePheIleValIleAlaGlyMetLeuGlyTyrSerLeuAspLeuGlnAsnY 206
DB 714 GCCTGATTTCTTCTATGTATGATGACGAGGATGTTGATGATCTCTGAGACTTACAGACA 773
QY 206 alSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgY 226
DB 774 TCAACCTGTCAGCATCCGACATGTGGTGTCTGAGAGCTCTCAAGCCATCAACCGTG 833
QY 226 alProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnY 246
DB 834 TACCACAGCATGCGGATCTGTGTAACCTGTGCTGCACACGCTGCCATCTGGGGAGAC 893
QY 246 alLeuLeuLeuCySPhPheValPhePheIlePheGlyIleValGlyValGlnLeuTrpA 266
DB 894 TGCTCTGCTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 953
QY 266 laGlyLeuLeuArgAsnArgCySPhLeuProGluAsnPheSerLeuProLeuSerValA 286
DB 954 CAGGCTGCTACCGAACCCTGCTCTTCTGGAAGAACTTCAACATCAAGAGGATGTGG 1013
QY 286 sPLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnP 306
DB 1014 CCTGCGCCCTTATTTCACCAACAGAGAGATGACGAGATCCCTTATGCTGCTCTGA 1073
QY 306 roArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGlyG 326
DB 1074 CTGGGCAAGATGGCATATGGGCTGCCACAGATCCCCACATCAAGAGACAG----- 1126
QY 326 lyGlyProProCySerLeu-----AppTyrGluThrTyrAsnSerS 340
DB 1127 --GGCGGGAATGCTGCTGCTGCCAAGATGATGATGATGATGATGATGATGATGATG 1184
QY 340 erSerAsnThrTrm-----CyValAsnTrpAsnGlnTyrTyrThrAsnCySerAlaG 358
DB 1185 ACCTCACAGCGCAGGCTGTGCTGCTCAACGGAACCGCTACTCAACGCTGCGCACGG 1244
QY 358 lyGluHisAsnProPheLysGlyValAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleA 378
DB 1245 GCAACGCCAACCCTCACAGAGGCGCCATCACTTTGACACATTTGGCTATGCGGGATTG 1304
QY 378 laIlePheGlnValIleThrLeuGluGlyTyrValAlaPheIleMetTyrPheValMetAspA 398
DB 1305 TGATTTTCAGATGATCATCTGTGAAGCTGGGGAGATCATGTATCATGTATGTATGAGC 1364
QY 398 laHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheM 418
DB 1365 CACATCTCTTCAACATTCATCTACTTCACTTCTGCTCATCATAGTGGGCTCTTCTTCA 1424
QY 418 etIleAsnLeuCySLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluS 438
DB 1425 TGATCAACTGTGCTGCTGTTGATGATACCAACCGATCTCTGACACCAAGACGGAGAC 1484
QY 438 erGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerP 458
DB 1485 ACCGGCTGATGCTGGAACAACGCGGCTACCTGCTC--TCACAGCAGGTGGCCAGTT 1541
QY 458 heSerGluProGlySerCySArgGluGluLeuLeuLysTyrLeuValTyrIleLeuArgL 478
DB 1542 ACGCTGAGCCCGGATGCTGATGAGAGATCTTCAATATGCTGTACATCTTGTGCA 1601
QY 478 ySAlaIaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuS 498

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QY	1180	lysSerSerPheAerPLeuProAerThrLeuGlnValProGlyLeuHisAArgThrAlaSer	1199
Db	3326	AGGCACTCTGTGACCTGGAGAGACTGGTGGCCCTGGTGGGTGGCACTACAGGGCCGT	3385
QY	1200	-----GlyAgsSerSerAlaSerGlnHisGlnAerPsyAenGlyLysSerAlaSerGly	1217
Db	3386	TGAGAGGGGGGGGCGGTCAAGGCCCTGGGACAGAGACTGGCAATGGCAAGATGCCAAC--	3442
QY	1218	ArgLeuAlaArgThrLeuAerGThrAerP---AerProGlnLeuAerGlyAerAerAerAer	1236
Db	3443	---ATAGCGCAAGAGATGTCTTACCAACAAGTGAATGACCGCGCGACCGCGGGAGAGACGAG	3499
QY	1237	AerGlnGlyAenLeuSerSerLeuGlyGlnAerGLeuGlnAlaTrpValAerSerAerGLeuPro	1256
Db	3500	GAGGAGATCGACTATACCTGTGTGTTTCCGGGTCCGCAAGATGATGTATGTATCAACCG	3559
QY	1257	AlaCysPsyAerGlnAerAerSerTrpSerAlaTrpLeuPheProGlnSerAerPhe	1276
Db	3560	GACTGGTCCGAAGTCCGGAGAGACTGGTGGCTTACCTCTTCCCGGAGAACAGATTC	3619
QY	1277	ArgLeuLeuCysHisAerGLeuLeuLeuHisLeuSerPheAerHisValAlaLeuValAlaLeu	1296
Db	3620	CGGATCTCTGTGTCAAGCATCATTTGCTCACAGCTTTTGACTAAGTGGTCTTGCGCTT	3679
QY	1297	LeuPheLeuAenCysLeuLeuThrLeuAlaMetGlnAerProLysLeuAerProHisSerAla	1316
Db	3680	ATCTTCTCAACTGATATACATCATTTGCTGGAGAGACCCAGATGGAAGCTGTATGACCT	3739
QY	1317	GlnAerGLeuPheLeuThrLeuSerAerHisTrpLeuPheThrAlaValPheLeuAlaGlnMet	1336
Db	3740	GAGCCCATCTTCTCTCACGGGTGTCTAATCAATCTTCACAGCCATCTTGATGGCGAATG	3799
QY	1337	ThrValLysValAlaValAlaLeuGlnYTrpCysPheGlnGlnAlaTrpLeuAerSerSer	1356
Db	3800	ACACTGGAAGTGGTTCCTCTCTGGCGCTGTACTTGGTAGCAGGGGTACTCTGTAAGACGC	3859
QY	1357	TrpAenValLeuAerGlyLeuLeuValLeuLeuSerValLeuAerLeuValSerMet	1376
Db	3860	TGGATGTACTGGAGTGGTTCCTGGTCTTGTGTCCATCATCGATATCGTATGTCCTGGT	3919
QY	1377	ValSerAerSerGlyThrLeuGlnLeuGlnMetLeuAerGValLeuAerGLeuAerGThr	1396
Db	3920	GCCCTGTGCTGGGGAGCCAGAAATTTGGAGGCTCTCGGGGCTCTGGGCTCTCGTAC	3979
QY	1397	LeuAerProLeuAerValLeuSerAerGlnGlnGlyLeuLysLeuValAlaGlnThrLeu	1416
Db	3980	TTACGCTCTTTGAGGGTTATACAGCGGGGCCCTGGGCTGGAAGCTGGTGTAGAACGCTC	4039
QY	1417	MetSerSerLeuLysProLeuGlnAenLeuValAlaCysValAerPheLeuLeu	1436
Db	4040	ATCTCTCCCTCAAGCCCATTTGGAGAAATCGHCTCATCTGTGCGCTTCTTCATCATC	4099
QY	1437	PheGlnLeuGlnValGlnLeuPheGlnGlyLysPhePheValCysGlnGlyLysPro	1456
Db	4100	TTCCGCATCTCGGGGTGCAGCTTTTCAAGGCAAGTTCACATTTGTTGGAGTGCAC	4159
QY	1457	ThrAerAenLeuLeuHisLysSerAerCysAlaGlnAlaSerTrpAerGTrpValAerGHis	1476
Db	4160	ACCAGAAACATACCAACCGATCTACCTGGCGGGCGCAATACCGCTGGGTGCATCAC	4219
QY	1477	LysTrpAaenPheAerAerLeuGlnAlaLeuMetSerLeuPheValLeuAlaSerLys	1496
Db	4220	AAATCAACTTGTGACAACTGGGGCAGGCAATGATGATGCTCTTGTGTGGCTCCCAAG	4279
QY	1497	AerGlnTrpValAerPLeuMetTrpAerGlyLeuAerAlaValGlnValAerGlnPro	1516
Db	4280	GACGCTGGGTAAACAATCATGTATATAGATTATGATGCTGTGCTGTGAGACAGACGCA	4339
QY	1517	LeuMetAenHisAerProTrpMetLeuLeuTrpPheLeuSerPheLeuLeuLeuAla	1536
Db	4340	GTGACGAAACACAAACCCCTGGATGCTACTGTAATCTTCTGCTTCTGCTCATGCTGACG	4399
QY	1537	PhePheValLeuAenMetPheValGlnValValAlaGlnAenPheHisLysCysAerGln	1556

Db	4400	TTCTTTGTGCTCAACATGTTTGTGGCGTGGTGTGTGGAGAACTTCCACAAGTCCCGCAG	44459
Qy	1557	HiSGInGIuGIuGIuGIuLaIaArGaTgArGInGIuLyArGLeuAArgArGLeuGIuLyS	1576
Db	4460	CACACAGAGGCTGAGAGGCGCGGAGCGCGTGAAGAAACGGCTGGCGCCCTTGGAAMAAG	44519
Qy	1577	LyArGArGserLySGLuLySGImeAlaGIuLaIGInCybLySProTyTyTyTySerAsp	1596
Db	4520	AAAGGCGGT-----AAAGCTCAAGGCGTCCCTCACTAGTCTACC	4558
Qy	1597	TyTserArGpHeArGLeuLeuValHiShiLeuCyethrSerHiSTyTLeuAspLeuPhe	1616
Db	4559	TACTGTCCCAACAGGCTGCTCATCTCACTCCATGTGCACAGCCACACTACCTGGACATCTTC	4618
Qy	1617	IllethrgLyValIlleGIyLeuAsnValValThrMeAlaMeTGluHiSTyTgInGIuPro	1636
Db	4619	ATTACCTTCATCATCTGCTCCATAGTTGTGTACACCATGTCCTCGAGACACTCAACACGCTT	4678
Qy	1637	GlnIlleLeuAspGIuLaLeuLySIlleCyAsnTyTIllePheThrValIllePheValPhe	1656
Db	4679	ACATCCCTCAAGACAGCGCTTAAAGTACTGTGCACACTACATGTTCACTGCTTTGTGCTG	4738
Qy	1657	GluserValPheLySLeuValAlaPheAlaPheArGArGpPhePheGlnAspArGTpAsn	1676
Db	4739	GAGGCTGTGTGAGACTGTGTGGCAATTGGCTGTAGGCGTTTCTTCAAGACCCATGGAAC	4798
Qy	1677	GInleuAspLeuAlaIlleValIlleuLeuSerIlleMeGlyIlleThrLeuGIuIlleGIu	1696
Db	4799	CAGCTGGAACCTGGCACTGTGTGCTGTCTGCTCATATGGGATCACTACGTGAGAGATCGAG	4858
Qy	1697	ValAsnLeuSerLeuProIlleAsnProThrIlleIlleArGIIlleMeArGValIlleArGIle	1716
Db	4859	ATCATATCCCGCTTCCATCAACCCCAACATATCCGTATCATGCGTGTGTTCGCGTATC	4918
Qy	1717	AlaArGValleuLySLeuLeuLySMeAlaValGIyMeArGAlaLeuLeuHiSThVal	1736
Db	4919	GCCGGGAGTTTGAGACTATTGAAAGATGGCCACAGAAATGGCGGCCCTGCTGGACACAGTG	4978
Qy	1737	MeGIuAlaLeuProGIuValGIyAsnLeuGIyLeuLeuPheMeLeuLeuPhePheIlle	1756
Db	4979	GTAACAGGCTCGCCCAAGGGGCAACTGGGCGTCTCTTCACTGCTGCTCTTCTTCATC	5038
Qy	1757	PheAlaAlaLeuGIyValGIuLeuPheGIyAspLeuGIySaAspGIuThrHisProCyS	1776
Db	5039	TATCTGCTCTGGAGATGGAGCTCTTGGAAAGCTGTCTGTGCATGTACGAGAACCCTGT	5098
Qy	1777	GluGIyLeuGIyArGHiSaIaThrPheArGAspPheGIyMeAlaPheLeuThrLeuPhe	1796
Db	5099	GAGGCAATGAGCCGCGCACGCCACTTGGAAAACCTTGCGAATGGCCTTCTTCACGCTTTC	5158
Qy	1797	ArgValSerThrGIyAspAsnTyTpdAsnGIyIlleMeLySaSPProSerArGAspCyS---	1815
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Qy	1816	AspGIuGIuSerThrCySTyArAsnThVal-----IlleSerProIlleTyTPhrPheValSer	1833
Db	5219	CATGATAGGCGCAAGCTGCTCAAGACGCGCTGAGTTTGTGTCAACGCGCTTACTTGTGTACG	5278
Qy	1834	PheValleuThrAlaGlnPheValLeuValAsnValValIlleAlaValIlleMeLyHis	1853
Db	5279	TTTCGTGTCCACAGCTCAGTTGTGTCTCATCAACCTGGTGGTGGCGCGATGATAAACAT	5338
Qy	1854	LeuGIuGIuSerAsnLySGluAlaLySGluGIuLaIaGIuLeuGIuLaIaGIuLeuGIuLeu	1873
Db	5339	CTGATATGACAGCAACAAGAGGCCACAGAGAGATGACAGATGTGATGTGATGACGCTG	5398
Qy	1874	GluMeLySThrLeuSerProGlnProHisSerProLeuGIySerProPheLeuTyTPro	1893
Db	5399	GAGATG-----GAGATG-----	5404
Qy	1894	GIyValGIuGIyValaAsnSerThrAspSerProLySProGIyAlaProHiSThThAla	1913

Db 5405 ---GCCCATGGCGCTCGGCGCCCTGCGCCCTGCGCCCTGCTGCT----- 5443  
Qy 1914 HisIIeGIYAlaIaIaSerGIYpHeSerLeuGIHISerProThMetValProHISerProGIu 1933  
Db 5444 -----CCCTGCCCTTGC 5455  
Qy 1934 GluIValProValPro---LeuGIYProAspLeuLeuThVal----- 1946  
Db 5456 CCGTGGCCCTGCGCCCTGCTGCGCCGAGGCTGCCCATGTTACCTGGGGGCTCCGGGG 5515  
Qy 1947 ArgIYSerGIYValSerArgThHISerLeuProHISerGIYMetCysArgAsn 1966  
Db 5516 CGAGATCGGAGGAGGAGGTGCTGAGAGC---GACACCGAGATCAGCTGCGCGGAC 5572  
Qy 1967 ---GlySerThrAlaGluArgSerLeuGIYHISerGIYProGIYLeuProIYsAlaGlu 1985  
Db 5573 TGCTATTCTCCAGCCCGAGAGACCTG-----TGG-----CTGAGC 5608  
Qy 1986 SerGIYSerLeuSerValHISerGIYProAlaSerPheSerCysIleLeuGIu 2005  
Db 5609 AGCGTCTCTTAACTCAAGAGACTCTTGGAGGGGAGCTGACCATTTGACAACTG 5668  
Qy 2006 ProIYSerVal---HisTYrLeuLeuGIYProHISerGIYAla----- 2018  
Db 5669 TCGGGTCCGCTTCCACCACTAGCGCTCACTGAGCGGTGGAGAGTGCACATGAC 5728  
Qy 2019 -----ProThTrpGIYAlaIleProIYsLeuProPro 2030  
Db 5729 AAGCAGAGACAGGTCTTCACTCACTCTGCGGGAGTGAAGCTGAGTCTTGAAGACCCA 5788  
Qy 2031 GIYArgSerProLeuAlaGluArgProLeuArgArgIuAlaIleArgThAspSer 2050  
Db 5789 CGGCTGCCCAAGAGGCCCAAGAGAGCAAGGTGAACCTAGAGCTCCGAGGCCATGC 5848  
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Qy 2069 ProSerGIYProLeuThrArgSerSerPheTrpGIYGIYSerIleGIYAlaGlu 2088  
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Qy 2212 LysIYsIleLeuSerProProSerIleAspProProGIYSerGIYArg 2231  
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Qy 2232 ProProCysSerPro-GIYValCysLeuArgArgAlaProAlaSer----- 2247  
Db 6377 CCGTTTAACTGTCGCGGGCTGCGGGCCATCAGCGCTACACAGCAGTGGCGCTCCAC 6436  
Qy 2248 -----AspSerIYsAspProSer 2253  
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US-09-949-016-15601  
; Sequence 15601, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15601  
; LENGTH: 70308  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15601  
Alignment Scores:  
Pred. No.: 9 78e-114 Length: 70308  
Score: 2055.00 Matches: 697  
Percent Similarity: 21.05% Conservative: 35  
Best Local Similarity: 20.04% Mismatches: 108  
Query Match: 17.09% Indels: 2640  
DB: 4 Gaps: 21  
US-09-611-257A-24 (1-2287) x US-09-949-016-15601 (1-70308)  
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Db 9539 TTGCTTCTCTTAAACATATAGAAAGCTGGGTCCAGAGAGTGATGACCAAGTGG--- 9595  
Qy 36 ArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArgSer--- 54  
Db 9596 -----GACTCCCTTCTGTGATGAGGAGTCTG 9622  
Qy 55 -----SerThrThrCysProGIYProGIYAlaIaIaGIYSerThr 69  
Db 9623 GGGCTGGGGGCTGTGCTGGGTGATGTCAAGGCGCTGGCAGCACCACTGCT---TAGCCT 9679  
Qy 70 GluIYsAspProGIY-----SerAlaAspSerGIuAla 80  
Db 9680 CAGATGAGGACAGAGAGTAAACAGAGAGAGGTGTAGGCGGGGCTCGGGGCGGCGCT 9739  
Qy 81 GluGIYLeuProThrProAlaLeuAlaProValAlaPhePheTYrLeuSerGIuAspSer 100  
Db 9740 CAGCTCAAGCTTGGCAGCTGTTCC----- 9766  
Qy 101 ArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGIuArgValSerMet 120

Db	9767	-----TTGACTGCCAGTACCTGGTTTGAAGCCATCAGATG	9802
OY	121	LeuValIleLeuLeuAanCyValThrLeuGlyMetPheArgProCysGluAspIleAla	140
Db	9803	TTGGTATCTCTTCTCAACTGCTGACCCCTGGGCATGTTCCGGCCATCGAGACATCGCC	9862
OY	141	CysAspSerGlnArgCyValGlyIleLeu-----	149
Db	9863	TGTGACTCCACGGCGCTCGCGGATCTCGAGGTAGTGTGTGTGTGTGTGTGTGTGT	9922
OY	149	-----	149
Db	9923	GTTGTGTGTGTGTGGGGGTGGCCCTCTTAATCTTAATACCTCTACTCTCTGCAAG	9982
OY	149	-----	149
Db	9983	AGGCCCTGACCCAACTGTTGGGGGACTAGGGTGGACTAGAGGGTATTCCTCACCCACGT	10042
OY	150	-----GlnAlaPheAspAspPheIlePheAlaPhe	159
Db	10043	CTCAGTTTCAGCCACTCTTGTCTCCCACTCAGGCGCTTTGATGATCTTCACTTGGCTTC	10102
OY	160	PheAlaValGlyMetValValIleMetValAlaLeuGlyIlePheGlyIleValCysTyr	179
Db	10103	TTTCCCGTGGAGATGT	10162
OY	180	LeuGlyAspThrTTPAanArgLeuAspPhePheIleValIle-----	193
Db	10163	CTGGAGACACTTGTGAACCGGCTTGACTTGTTCATGTCGACGAGGTGTAGACACTGGG	10222
OY	193	-----	193
Db	10223	CTGGGGTGGAGAGACATGATCAGATCGTCCCTTCCCGGGGCGAGGGTTCGGGCT	10282
OY	193	-----	193
Db	10283	GTCACCTCTCAGCTCCAGCCAGTTTACAGCACACTTCTCCCTGGCTATCTCTGAGGG	10342
OY	193	-----	193
Db	10343	TCTGAGGCTGCCTGCCTCTAGCACTGTAGCCTTAATCTTAATTCAGAGCCCTAATTC	10402
OY	193	-----	193
Db	10403	TAAATCTGCCCTTCTCTGTATGGGCAATCTGTCTGTCTCGGGGTAGCTTGCCCCC	10462
OY	193	-----	193
Db	10463	AGACAGAGCCGAGATCTTCAGGGTCCCTGTGTGAAGAAAGAGAGTCAAGTTCAT	10522
OY	193	-----	193
Db	10523	CCTGCTGCCCTTAAGCAGATTCCTCAATTGACCTTGTGACCCCACTGTGGCCTGAGA	10582
OY	194	-----AlaGlyMetLeuGlyTyrSerLeuAspLeu	203
Db	10583	CTCAAGGGGCTCCCTTTGGGCCCCCTCCCTGAGAGATG-CTGAGTACTGCTGGAACCTG	10641
OY	204	GlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIle	223
Db	10642	CAGAAAGTCACTTCTCACTGCTGACGACAGATCCGTGTGTGTGTGTGTGTGTGTGT	10701
OY	224	AsnArgValProSer-----	228
Db	10702	AACCGGTGCCCCAGTGAAGTGAACCTCAGCCCTCAGCCCTGAAGAGAGCCCGCAGAGA	10761
OY	228	-----	228
Db	10762	AATGTGAATCTCTCAGACCCCACTCTAATCTGTGTCTTCACTGACCCCTCACAGGCC	10821
OY	228	-----	228
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OY	228	-----	228
Db	10882	GTTGACATATGGAGATTACTGTGGAAAAACCCACTCAATTTTATGCTGTGTGTGTGTG	10941
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Db	10942	AGTCTCAGAAACATCTCAGATGACCTCTTCTTCTTGTAGCTAGTATGACACTCCCCCAGA	11001
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Db	11002	GGATTAGGGGTGTGGGACTGAGAGGCTTACAGGCAAGSAGTGTGAACGAAATGTGAATG	11061
OY	228	-----	228
Db	11062	GCCTTTTTCAGCAGAACAGCCTCTCATGATCTGTGTTCTTGTGTGTGTGTGTGTGTGT	11121
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Db	11122	CCAGCTGAACGTGACTTCTCTCAAGACAAAGGCCACTCATGTCTCACCTCCGCTCTG	11181
OY	228	-----	228
Db	11182	TCCCTTCTCTCTTCCCGCCCCCTTCCAAACCATTTGACGTAACTGCCGGGCCATTATCT	11241
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Db	11242	AATTAACATGATGTGTTTCTGAGCCAGAGGCTTGGAGCTTATGTTCTCCCTAC	11301
OY	228	-----	228
Db	11302	ATACTGCCCCCTCCCTTGTCTGAGGCCCCCTTGTGAATCCCAACTACACAGCTGCA	11361
OY	228	-----	228
Db	11362	GATGTCCCTGCTGTGTGTCTTAGAGTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT	11421
OY	228	-----	228
Db	11422	CTCAGTCCCTGTTGTGTACTGATGTATGACAGAGCCCTCGCTGTGTGTGTGTGTGT	11481
OY	228	-----	228
Db	11482	GTTGT	11541
OY	228	-----	228
Db	11542	GCAGACTGTGAATGTGTCTCTGGGGCTCGGGGTGTGTGTGTGTGTGTGTGTGTGTGT	11601
OY	228	-----	228
Db	11602	GAAGAGGGGATGCTCGCTCTCTCCGCCCAAGTATGTGTCAGATTTAATAGGC	11661
OY	228	-----	228
Db	11662	CTGTGTCTAACACCGGTGAATTCCTTAATGCAAAACCTGAGAAATGATCTCAGTTG	11721
OY	228	-----	228
Db	11722	GACACAGAAAGCTGAAAGGGGATGGGTAGAGAGAGGGAGAGAGACTAGTGAGAA	11781
OY	228	-----	228
Db	11782	AATCGGCTGGCAGGGGCGAGGCTGTGGCGCTGCATGACCAAGAGGTTAATTAAGTGTCT	11841
OY	228	-----	228
Db	11842	GCTTAGAGCTTTTGGCCTGAGAGGGCGAGGGGCAATGATGTGCACTTTGGGGGTGAAG	11901
OY	228	-----	228
Db	11902	CCAGCAATTAGAGATCTGTCTTGTACGAGGGCTTGGCGGACTGGGGGCTGTCTCAGAC	11961



[illegible]

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Db 14181 AGTAGAGGAGCACCAAGTGCAGAGTCAAGAGAAATCCAAAGTCAAGCGGCACTTAAC 14240  
QY 412 ----- 412  
Db 14241 TGCTATTGGACCTTGGGCAAGTCAATCTCATGAGGCTCCAGCACTGCTGCGGCTC 14300  
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QY 673 ----- 673



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QY 161 AlaValGluMetValValIysMetValAlaLeuGlyIlePheGlyIyValysCysTyrLeu 180  
Db 62 GCGGTGAGATGGTTCATCAAGATGATGGCTTGGGCTGTTCGGGAGAGTTCATCG 121  
QY 181 GlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer 200  
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QY 201 LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeu 220  
Db 182 TTGAGACGACACACGAGCTCTCGGCTATCAGACCGTGGGGTGGCGGCTTC 241  
QY 221 ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAspThrLeu 240  
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QY 261 GlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGlnAsnPheSer 280  
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QY 281 LeuProLeuSerValAsp---LeuGluProTyrTyrGlnThrGluAsnGluAspGluSer 299  
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Db 713 GGCTACCGCTGGATTGGCATCTTCCAGATGATCACGCTGGAGGCTGGGATCATCATG 772  
QY 393 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 412  
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QY 473 ValTyrIleLeuArgGlyAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVal 492  
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Db 1000 ----- 1000  
QY 533 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGlu 552  
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QY 613 GlyArgThrValGlySerGlyValTyrProThrValHisThrSerProProProGlu 632  
Db 1001 -----CCGTACTGCAC----- 1012  
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QY 672 rThrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGly 692  
Db 1032 -----GAGGTGACTCAGCGGCTCGGAAGAATGG 1060  
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 QY 2071 sProLeuThrArgSerSerSerPheTrrpGlyLysSer11LeuValGlnGlnArgse 2091  
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Qy	2111	----gluprosertrpalalyaspproglu-Thirgarserleuglnuapt	2129
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Qy	2129	hrgluleuSertrp11eserelyaspleu-----leuProserSerindluGlupol	2147
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Qy	2158	alg1uthrglnSerCysharghargArpProglyphetrpleuapb1nglnargh1as	2170
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Qy	2247	erAap-----SerlyAspProserValserSerProleuA	2259
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Qy	2259	apSerThrAla1aSerProserProlysllyAspThrleuSerleu-----	2274
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RESULT 15  
US-08-193-078B-7  
; Sequence 7, Application US/08193078B  
; Patent No. 5846757  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael  
; APPLICANT: Ellis, Steven  
; APPLICANT: Williams, Mark  
; APPLICANT: Feldman, Daniel  
; APPLICANT: McCue, Ann  
; APPLICANT: Brenner, Robert  
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN  
; STREET: 1660 UNION STREET

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CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193.078B
FILING DATE: 07-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..7163
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 7161..7362
US-08-193-078B-7

Alignment Scores:
Pred. No.: 2,92e-96 Length: 7362
Score: 1745.50 Matches: 662
Percent Similarity: 37.80% Conservative: 356
Best Local Similarity: 24.58% Mismatches: 879
Query Match: 14.51% Indels: 798
DB: 2 Gaps: 84

US-09-611-257A-24 (1-2287) x US-08-193-078B-7 (1-7362)
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QY 34 TrpThrArg-ArcArgMetGluArgAlaProArgSerArgAspSerProValAlaSerAr 53
Db 123 TGCACCGGGGGCCCGGAGACCAATGATCCGCTTCGGGGAGACAGCTGGCGCGCGCTATGGA 182
QY 53 gSerSerThrThrCysProGlyProGlyAlaAlaGly---AlaGlySerThrGluYAs 72
Db 183 GCGCCCGGCGGCGAGAGCGGGCCCGGGGCGGGCGGGCGGGCGGGCGGGCGGCGGCT 242
QY 72 pProGlySerAlaAspSerGluAlaGluGlyLeu----- 83
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QY 84 -----ProLYrProAlaLeuAlaProVal----- 91
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 QY 130 uGlyMetPheArgProCysGlnAspIleAlaCysAspSerGlnArgCysArgIleLeuG 150  
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 QY 167 smetValAlaLeuGly----IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnR 186  
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 DB 1356 -----AGAAATGCAGAGAGAAAGTCCCTTTGGACGTCTGAAGG 1396  
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Qy 931 pThrLeuProAspArgLysAsnPheAspSerIleuLeuTyrAlaIleValThrAlaPheG1 951  
Db 2069 CACA-----ACCACTTGCACACCTTCCCTCGCCCATCTCATCTCTCTCA 2116  
Qy 951 nIleLeuThrGlnGluAspTyrAsnLysValLeuTyrAsnGlyMet----- 966  
Db 2117 GATCTGACGAGAGAGAGCTGAATGATGATGATGATGATGATGATGATGATGATGAT 2176  
Qy 967 -AlaSerThrSerSerTrrAlaIleLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyr 986  
Db 2177 CGTCAAGCAAGAGATGTTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2236  
Qy 986 rValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnIleGluGlyAspAl 1006  
Db 2237 CACTCTGCTGAATGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2296  
Qy 1006 aThrLysSerGluSerGluProAsp----- 1014  
Db 2297 GACCAAGATGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2356  
Qy 1015 -----Phe-PheSerProSerValAspGlyA 1023  
Db 2357 CAAGAAGCTGCTGAATGATGAGCCCATGTCGCGCAACATCTCATCTCGCGCA 2416  
Qy 1023 spGlyAspArgLysLysArg-LeuAlaLeuValAlaLeuGlyGlnHisAla----- 1039  
Db 2417 GCAGAACTCGGCAAGCGCGCTCGGTGTGGAGAGAGCGGCGCAGCTACGCTGCA 2476  
Qy 1040 -----GluLeuArgLysSerLeuLeu-----ProProLeu 1049  
Db 2477 GAACCTGGGGGACACTGAGAGCGCTGTACAGAGATGAGACCCGAGAGCGGCTGCG 2536  
Qy 1050 lIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1069  
Db 2537 CTTCGCCACTACGCGCCCACTGCGCGCGAGCATGAGAGAGAGAGAGAGAGAGAGAG 2596  
Qy 1070 GluAla-LeuGlySerGlySerArgArgThrSerSerSerSerSerSerSerSerSer 1089  
Db 2597 GGTGAGCTGGGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2656  
Qy 1089 aAla-----HisHis-----GluWe 1094  
Db 2657 TCGGAGAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2716  
Qy 1094 cLysCybPro----- 1097

Db 2717 CAAGACCCCGCGCGCGCGCGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2776  
Qy 1098 -ProSerAlaArgSer-----ProHisSerProTrrSerAlaIleSerTr 1114  
Db 2777 GCGCGGTGCGCGGAGAGAGAGCGCGCGCGCGCACCGGACGAGAGAGAGAGAGAGAG 2834  
Qy 1114 pThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSe 1134  
Db 2835 ----GGCGCGCGGAGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2875  
Qy 1134 rProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlyGlnGlnSerGlnAspGluG1 1154  
Db 2876 CCGGAGAGGCGCGCGGAG 2935  
Qy 1154 u-----GluSerSerGlnLysAspArgAlaSerPr 1164  
Db 2936 GCGCGGAGCGCGAGCGCGCGAGCGCGAGATCCAGAGAGAGAGAGAGAGAGAGAGAG 2995  
Qy 1164 oAlaGlySerAspHisArgHisArgGlySerLeuGlu-----ArgGluAlaLysSe 1181  
Db 2996 GGGCGAGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3055  
Qy 1181 rSerPheAspLeuProAspThrLeuGlnValProGly---LeuHisArgThrAlaSerG1 1200  
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Qy 1200 yArgSerSerAlaSerGlu-----HisGlnAspCysAsnGlyLysSerAlaSerGlyAr 1218  
Db 3095 GCGCGACCGCTGTCAG 3154  
Qy 1218 gLeuAla-----ArgThrLeuArgThrAspArgProGlnLe 1230  
Db 3155 GAGAGCTGAGATGAG 3214  
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Db 3215 GCCACACTGTGACTGTGAG 3260  
Qy 1250 pValArgSerArgLeuProAlaCysArgGluArg----- 1262  
Db 3261 ----ATGCACACACTGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3316  
Qy 1263 -AspSerTrp----- 1265  
Db 3317 AGACAATCAAGCGAG 3376  
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Db 3377 ACATATCCAGATGATGCTGACGGGCGCTTGGGGAAGCAGCGTCCGTCCAGTGTAA 3436  
Qy 1265 ----- 1265  
Db 3437 CGTGAAGCTGGAAG 3496  
Qy 1266 -----SerAlaTyrIlePheProProGlnSerAr 1275  
Db 3497 GAGCGCGCGCGCGCTATGCTCCATACAGCTCATGTTCTGTTAAAGCCCAACCACT 3556  
Qy 1275 gPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValIleuVa 1295  
Db 3557 GCTCGCGCGCTTCTGCACTCATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3616  
Qy 1295 lIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSe 1315  
Db 3617 GGTATGCGCTTGAAGAGAGATCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3673  
Qy 1315 rAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValIleuAlaG1 1335  
Db 3674 GCCAGAGAAACCGCTCGAAATACCTGAGATTAATTTCACTGTGTCTTACCTTTGA 3733  
Qy 1335 uMetThrValLysValAlaIleuGlyTrrCysPheGlyGluGlnAlaIleuArgSe 1355  
Db 3734 GATGTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3793

Oy	1355	rSerTrpAsnValIleuAspGlyLeuLeuValIleuIleSerValIleAspIleLeuValIle	1375
Db	3794	CTTGGAACATTTCTTGAGC-----TTCAATGTGTGTCAGGGCCCTGGTGGC	3841
Oy	1375	MetVal---SerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuIle	1394
Db	3842	GTTTGCTTCTTCAGAGATCCAAAGGMAAGATCAATACATTCAGTGTCTGAGAGTCT	3901
Oy	1394	uArgThrLeuArgProLeuArgValIleSerArgIaGlnGlyLeuLysLeuValIaGln	1414
Db	3902	TCGTGTCCCTGGGGCCCTCAAGACCATCAACCGGTGCCCAAGCTCAAGCGTGTGTGGA	3961
Oy	1414	uThrLeuMetSerSerLeuLysProIleGlyAsnIleValIaLysCysSalIaPhePh	1434
Db	3962	CTGTGTGTGAACCTCCCTGAAGAATGTCTCAACATCTTGATGTGTCAATGCTCTTCAT	4021
Oy	1434	eIleIlePheGlyIleLeuGlyValaGlnLeuPheLysGlyLysPhePheValCysGlnGln	1454
Db	4022	GTTCAATATTTGCCCGCATTTGGCGGTGCAGCTCTTCAAGAGGAATTTTCTACTGCACAGA	4081
Oy	1454	YGLu-----AspThrArgAsn-----IleThrAsnLysSerAspCys	1466
Db	4082	TGAATCCCAAGAGCTGAGAGCGACCTGACAGGGGTCAATATTGATTAATGAGAAAGAGA	4141
Oy	1466	sAlaGluIlaSerTyrArg--TrpValArgHisLysTyrAsnPheAspAsnLeuGlyGln	1485
Db	4142	AGTGGAACTCAGCCCAAGCAGTGGAAATAATACACTTTCACATACGACATGTGTCTGTG	4201
Oy	1485	nAlaLeuMetSerLeuPheValIleuAlaSerLysAspGlyTrpValAspIleMetTyrAs	1505
Db	4202	GGCTTCGTGTCAGCGCTGTTCAACAGTGTCCACGGAGAGCGTGGCCATGTGTGGAAACA	4261
Oy	1505	pGlyLeuAspAlaValaGlyValaAspGlnGlnProIleMetAsnHisAsnProTyrMetLe	1525
Db	4262	CTCCGTGATGTCACACTTATGAGAGACGAGGTTCACAGCCCTGGATACCGCATGAGACTGTC	4321
Oy	1525	uLeuTyrPheIleSerPheLeuLeuIleValaIaPhePheValLeuAsnMetPheValGln	1545
Db	4322	CATCTTCAAGCGTGTCACTTGTGTGTGTCTTCCCTTCTTCTGCAACATCTTGTGTGC	4381
Oy	1545	yValValValaGlnAsnPheHisLysCysArgGlnHisGlnGlnGlnGlnIaIaAspArg	1565
Db	4382	TTTGATTCATCACTTC-----CAGAGCAAGGGGCAAGAGTGAT	4423
Oy	1565	gArgGluGlnLysArgLeuArgArgLeuGlnLysLysArgArgSerLysGlnLysGlnMe	1585
Db	4424	GTCTGAA-----TGCAGCTGTGAAGAAGACGAGGGTTCATTAAGCTTGC	4471
Oy	1585	CalAGluIaGlnCysLysProTyrTyrSerAspTyrSerArg-----PheArgLeuLe	1603
Db	4472	CATCAGCCCAAAACCCCTGACACGGTACATGCCCAAAACCGGCAAGTGTTCAGATATA	4531
Oy	1603	uValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLe	1623
Db	4532	GACGTGACATTTGTGTCTCCCGCCCTTGAATATCTTCATCAAGCCATGATAGCCCT	4591
Oy	1623	uAsnValValThrMetAlaMetGlnHisTyrGlnGlnProGlnIleLeuAspGlnAlaLe	1643
Db	4592	CAACACTGTGTGTGATGATGAAGTTCTAATGATGACCCCTATGAGTACGACGTAGTACT	4651
Oy	1643	uLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheLysLeuVal	1663
Db	4652	GAAATGCTGAACATGTGTCACTTCATGTCTTCCATGGAATGCGTGGTGAAGATAT	4711
Oy	1663	lAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleVal	1683
Db	4712	CGCTTTGGGGGTGCGAAGTATTTCAAGAGATGCGCGAATGTCTTTGACTTTGCACAGCT	4771
Oy	1683	lLeuLeuSerIleMetGlyIleThrLeuGlnGlnIleGlu-----ValAs	1699
Db	4772	GTTGGGAAGTATTAATGATATTTTGAACAGAGATTTCCGGAACGAATTCATCA	4831

OY	1698	nLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr	1718
Db	4832	CCTCAGC-----TTCTCCGGCCTCTTTGGAGCTGGCG	4864
OY	1718	gValLeuIleValLeuLeuMetAlaValIleMetArgAlaLeuLeuIleThrValMetG	1738
Db	4865	GCTGATCAAGCTGTCTCCGACAGGGGCTACACCAATCCGATCTGTGTGGACCTTTGTCCA	4924
OY	1738	nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAl	1758
Db	4925	GTCTTCAAGGCCCTGGCCTACAGTGTCGTGCTCATTTGCATGGCATGGTGTCTTTCATCTACGC	4984
OY	1758	aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG	1778
Db	4985	CATCATCGGATGAGGCTGTTGGGATATATGGCCCTGGATGAAC-----ACCAG	5035
OY	1778	ylLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa	1798
Db	5036	CATACACCGCACACAACACTTCGGACGTTTGGCAAGCCCTGATGCTGTCTTTCAGAG	5095
OY	1798	lSerThrGlyAspAsnTrpAsnGlyIleMetCysAsp-----ProSerArgAspCysAs	1816
Db	5096	CGCCACGGGGGAGGCGCTGCACAGAGATCATGCTGCTGCTGACGAAACAGCGCTGTGA	5155
OY	1816	pGlnGlu-----SerThrCysTrpAsnThrValIleSerProIleTrpPheValSerph	1834
Db	5156	TGACACAGGCCAATGCCACGAGTGTGGAAATGACTTGGCTTCACTTCACTTCGCTCTT	5215
OY	1834	eValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet-----	1851
Db	5216	CATCTTCCTGTGCTCTTCTTGATGTGAACCTTGTGTGGCTGTATCATGGCAATT	5275
OY	1852	-----LysHisLeuGluGlu-SerAsnL	1859
Db	5276	TGATTAACCTACGCGGGAGCTTCCATCCATCGATCGTCAACACACTGGATGATTCATCCG	5335
OY	1859	ysGluAlaIysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeu-	1878
Db	5336	GGTCTGGCGTGAATATACACCGCGGTGGTGGCGCATCATTAACATATCATGTGTTGA	5395
OY	1878	SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyVal	1898
Db	5396	GATGCTAAACACATGTGTCCCGGCTCTGGG-----GCTGGGGAAGAAATCCCC	5443
OY	1899	AsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAla	1918
Db	5444	TGCTCGAGTTCCTTACAAGCGCCTGTTCG---CATGAACATGCCATCTCCAAACAGAGA	5500
OY	1918	SerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProValPro	1938
Db	5501	CATGACTGTTCATCTTCACTGACGCTCAAGCTGATGGCCCTCATCCGACGGCAGCTGGAGATCAA	5560
OY	1938	LeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro	1958
Db	5561	GCTGGCCCCAGCTGG-----GACAAAGCACATCAAGTGAACGGGAGATTGAG	5608
OY	1959	AsnAspSerTrpMetCysArgAsnGlySerThrAlaGluArgSerLeuGly-----	1975
Db	5609	GAAAGAGATTTCCCTTGT---GTGGGCAATCTGCCCAAGAAGCTTTGGACTTGTCTGT	5665
OY	1976	-----HisArgGlyTrpGlyLeuProLysAlaGlnSerGly	1987
Db	5666	ACCACCCCATTAAGCCTGATGATGATGACAGTGGGGAAGTTTATGCACTGTGATGATATT	5725
OY	1988	SerIleLeuSerVal-----HisSerGlnPro-----	1996
Db	5726	TGACTTTTACAAGACGAACAAACACACAGAGACCAATGSCAGACAGGCTCTTGAGGCTT	5785
OY	1997	---AlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTrpLeuLeuGlnPro	2015
Db	5786	CTCCCAAGTGGTCTCTGTGTCCTGTTCCACCTCTGAAGGCCAC-----	5830
OY	2016	HisGlyAlaProThrTrpGlyAlaIleProLysLeuPro-----	2028

Db 5831 CTTGAGACAGACAGCCGCTGTGCTCTCGAGAGCCCGGGTTTCTTTCAGACAGAGAG 5890  
QY 2028 ----- 2028  
Db 5891 TTCCACCTCCTCAGCAATGGCGGGCCATACAAACCAAGAGATGGCATCAAGATC 5950  
QY 2029 -----ProProGly 2031  
Db 5951 TGTCTCTGGGGCACTCAAGAGACCAGATGACCCCATGAGGCGAGGCCACCCCTGGA 6010  
QY 2032 ArgSerProLeu-AAlaGlnArgProLeuArgGlnAlaAlaIleArgThrAsp----- 2049  
Db 6011 GCGTGGCCACTCCACAGAGATCCCTGTGGCGGTGAGAGACACTGCTGTGACAGCTTCA 6070  
QY 2050 -----SerLeuAspValG1 2054  
Db 6071 GATGCAAGCATTAACCCGAGGGCCCTGATGGGAGCCCAAGCTTGGGCTGAGAGCCA 6130  
QY 2054 nglyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyPro-----SerCy 2071  
Db 6131 GGGTCGAGCGGCTTCATGACCCCGCTTGGCGGCGAGACTCAGCCCTCACAGATGCCAG 6190  
QY 2071 sProLeuThrArgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSe 2091  
Db 6191 CCCCATGAAGGCTCCATCTCC-----ACGCTGGCCCAAGCGGCC 6229  
QY 2091 rGlyIleGlnSerLeuValSerLeuHisIleArgLeuProAlaProCyProGlyLeu-- 2110  
Db 6230 CCGTGG-GACTCATTTTTCAGACACACCCGAGACCCCAAGCCCTAGCCAGGCTGT 6288  
QY 2111 ----GluProSerTrpAlaLeuAspProProGlu-ThrArgSerSerLeuGluLeuAspT 2129  
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QY 2147 euphePro-----ArgAspLeuLeuValSerCyTyrserv 2158  
Db 6406 GGCTGCCCGCGGAGAGGGGCTTACAGGCTGCCGCGGAGACAGAGCGCCGCGAGAGC 6465  
QY 2158 alGluThrGlnSerCyAlaArgArgArgProGlyPheTrpLeuAspGlnGlnArgHis 2178  
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QY 2224 roProGluSer-----GlnGlySerArgProProCySerP 2236  
Db 6757 CGGCCAACTCTCACCCATCTTCGCGGGGGCTCAAGCAGCTCTCTGCTTCTCC 6816  
QY 2236 roGly-----ValCysLeuArgArgAlaProAlas 2247  
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QY 2247 erAsp-----SerLyAspProSerValSerSerProLeuA 2259

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QY 2259 sSerThrAlaAlaSerProSerProLyblybAspThrIleuSerLeu----- 2274  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 18, 2005, 18:24:02 ; Search time 2796.34 Seconds  
(without alignments)  
5449.019 Million cell updates/sec

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Searched: 7389322 seqs, 333128559 residues

Total number of hits satisfying chosen parameters: 1478644

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11980	99.6	6942	19 US-10-377-139-7	Sequence 7, Appl
2	11829	98.3	7285	10 US-09-383-894-3	Sequence 3, Appl
3	11673	97.0	7129	10 US-09-383-894-3	Sequence 1, Appl
4	10963.5	91.1	7825	22 US-10-756-149-31	Sequence 31, Appl
5	10963.5	91.1	7825	22 US-10-786-148-120	Sequence 120, Appl
6	10845.5	90.2	7648	19 US-10-377-139-10	Sequence 10, Appl
7	10845.5	90.2	7648	19 US-10-757-126-15	Sequence 15, Appl
8	10707	89.0	8116	17 US-10-062-674-2011	Sequence 2011, Ap
9	6242	51.9	7898	22 US-10-483-467-3	Sequence 3, Appl
10	6103	50.7	3993	21 US-10-930-301-51	Sequence 51, Appl
11	5432.5	45.2	6990	19 US-10-377-139-8	Sequence 8, Appl
12	5420	45.1	6816	9 US-09-935-541-1	Sequence 1, Appl
13	5420	45.1	6816	16 US-10-425-800-1	Sequence 1, Appl
14	5420	45.1	6855	9 US-09-935-541-3	Sequence 3, Appl
15	5420	45.1	6855	16 US-10-425-800-3	Sequence 12, Appl
16	5407	45.0	6503	9 US-09-935-541-12	Sequence 12, Appl
17	5407	45.0	6503	16 US-10-425-800-12	Sequence 12, Appl
18	3950	32.8	5562	9 US-09-030-482B-18	Sequence 18, Appl
19	3861.5	32.1	6073	19 US-10-377-139-11	Sequence 11, Appl
20	3399.5	28.3	6933	22 US-10-450-763-10945	Sequence 10945, A
21	1745.5	14.5	7362	17 US-10-375-251-11	Sequence 11, Appl
22	1743.5	14.5	7376	13 US-10-033-026-3	Sequence 3, Appl
23	1739.5	14.5	7364	9 US-09-954-456-1179	Sequence 1179, Ap
24	1739.5	14.5	7364	13 US-10-033-026-5	Sequence 5, Appl
25	1739.5	14.5	7364	20 US-10-736-883-31	Sequence 31, Appl
26	1739.5	14.5	7364	21 US-10-843-641A-4206	Sequence 4206, Ap
27	1739.5	14.5	7364	22 US-10-483-467-5	Sequence 5, Appl
28	1732.5	14.4	6984	20 US-10-736-883-37	Sequence 37, Appl
29	1727	14.4	7175	17 US-10-375-253-13	Sequence 13, Appl
30	1726.5	14.4	7121	20 US-10-736-883-43	Sequence 43, Appl
31	1725	14.3	7185	20 US-10-736-883-39	Sequence 39, Appl
32	1721	14.3	7177	13 US-10-033-026-7	Sequence 7, Appl
33	1721	14.3	7177	20 US-10-736-883-33	Sequence 33, Appl
34	1721	14.3	7177	22 US-10-483-467-7	Sequence 7, Appl
35	1720.5	14.3	6792	18 US-10-627-370-1	Sequence 1, Appl
36	1720	14.3	6695	20 US-10-736-883-27	Sequence 27, Appl
37	1720	14.3	6695	21 US-10-486-706-207	Sequence 207, App
38	1717.5	14.3	6083	22 US-10-029-413A-21	Sequence 21, Appl
39	1717.5	14.3	6083	13 US-10-726-216-21	Sequence 21, Appl
40	1716.5	14.3	7713	20 US-10-736-883-41	Sequence 41, Appl
41	1693	14.1	7011	13 US-10-033-026-9	Sequence 9, Appl
42	1693	14.1	7011	20 US-10-736-883-29	Sequence 29, Appl
43	1686	14.0	7348	19 US-10-322-696-175	Sequence 175, App
44	1685.5	14.0	7291	19 US-10-322-696-83	Sequence 83, Appl
45	1685.5	14.0	7477	19 US-10-322-696-177	Sequence 177, App

ALIGNMENTS

RESULT 1  
US-10-377-139-7  
; Sequence 7, Application US/10377139  
; Publication No. US20040175761A1  
; GENERAL INFORMATION:  
; APPLICANT: Mackinnon, Roderick  
; APPLICANT: Jjiang, Youxing  
; APPLICANT: Lee Mackinnon, Alice  
; APPLICANT: Ruta, Vanessa  
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins  
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9  
; CURRENT APPLICATION NUMBER: US/10/377,139  
; CURRENT FILING DATE: 2003-03-01  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 7
; LENGTH: 6942
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-377-139-7

Alignment Scores:
Pred. No.: 0 Length: 6942
Score: 11980.00 Matches: 2283
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 3
Query Match: 99.60% Indels: 2
DB: 19 Gaps: 0

US-09-611-257a-24 (1-2287) x US-10-377-139-7 (1-6942)
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QY 21 ProSerSerAspProProGlyProArgGluAlaArgGlyTTPThrArgArgMetGlu 40
Db 76 CCTCTTCGAGACCCCGGGGCCCCGGCTGGCCAGAGATGACGAGAGAGAGATGAG 135
QY 41 ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGly 60
Db 136 CGGGCGCCGAGAGACTGGGACAGCCCGGTAGCTTCACGCACTCAACGACTCTCCGGG 195
QY 61 ProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGlu 80
Db 196 CCGGGGGCCGAGGGGCGGGGGTCGACGAGAAAGACCCGGGACGCGGACTCCGAGG 255
QY 80 IagLugLylLeuProTyrProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAsp 100
Db 256 CGAGGGGCGCGGTACCCGCGCTAGCCCGGGGTTCCTTCTACTTGAAGCCAGGACA 315
QY 100 eArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgValSerM 120
Db 316 GCCGCCCGCGAGCTGTGTCTCCGACGGTCTGTAAACCGTGGTTGAGCGAGTCACTA 375
QY 120 etLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleA 140
Db 376 TGCCTGATCTTCTCTCACTGATGTGACTCTGGGTATGTTCAAGCCGTTGAGGACATTG 435
QY 140 IacYsaAspSerGlnArgCysArgGlyLeuGlnAlaPheAspAspPheIlePheAlaPhe 160
Db 436 CCGTGTACTCCCGCGCTGCGGATCTCTGCAAGGCTTCGATGACTTCATCTTTGGCTTCT 495
QY 160 heAlaValGluMetValValIleMetValAlaLeuGlyIlePheGlyLysLysCysTyrL 180
Db 496 TTGCTGTGGAATGTGTGTAAAGATGTGGCTTTGGGCATCTTTGGGAAGAAATGTTACC 555
QY 180 eugLysAspThrTyrPAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrS 200
Db 556 TGGAGACACATGTGAAACCGGCTTGACTTTTCATTGTCATTGCAAGGATCTCGAATAT 615
QY 200 etLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProL 220
Db 616 CGCTGAGCTGCGAAGAGTGCAGCTTCTCCGACAGCAGAGACAGTCCGTTGCTCGACCGC 675
QY 220 euaArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrL 240
Db 676 TCAAGGCGCATTTAACCGGGTCCCGACATGCGCATTCCTCGACATTTACTCTGGACACT 735
QY 240 euaProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyTylev 260
Db 736 TGCCTATGCTGGGCAACGTCTGCTGTGTTCTTCGCTTTTTCATCTTTTGAGCATCG 795
QY 260 alGlyValGlnLeuTTPAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPhes 280
Db 796 TGGCCGTCGACGTGTGGGACGAGACTGTCTTGCAACCGGTGTCTTCCCGAGAACTTCA 855
QY 280 etLeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerP 300
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QY 300 roPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrL 320
Db 916 CTTTCATCTGTCTCTGAGCTCCGGGAAATGAGCATGAGATCTCGACAGATGTGGCCACAC 975
QY 320 euaArgGlyGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerS 340
Db 976 TGGTGTGGGAAGCGGTGTGGCCACTGACGTCTGAGCTGTGAGACTTAAACAGTT 1035
QY 340 eSerAsnThrThrCysValAsnTyrPAsnGlnTyrTyrThrAsnCysSerAlaGlyGluH 360
Db 1036 CCAAGAACACCACTGTGTCACTGGAAACAGATGATACCAATGCAATGCTGTGCGGGGAGAC 1095
QY 360 IeAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTyrPheIleAlaIleP 380
Db 1096 ACAACCCCTTCAAAAGCGGCATCAACTTTGACAAACATGTGCTATGCTGGATCGCCATCT 1155
QY 380 heGlnValIleThrLeuGluGlyTTPValAspIleMetTyrPheValMetAspAlaHis 400
Db 1156 TCCAGGTCACTCACTGAGAGGCTGGGTGACATCATGTACTTCGTAAATGACGCTCACT 1215
QY 400 ePheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleA 420
Db 1216 CTTTACAACTTCATCTCACTTCACTTCTTCATCATCATGAGGCTCTTCATGATACA 1275
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QY 460 IuProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgValAla 480
Db 1396 AGCCAGGACGCTGCTATGAGAGTCACTCAAGTACTGTGTATCACTCCGAAAGACAG 1455
QY 480 IArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerP 500
Db 1456 CCGGAAGGTGGCCAGGTCTCTAGGGCTATAGGCGTGGGGCTGGGCTGTCAAGAGCC 1515
QY 500 roValAlaArgSerGlyGlnGluProGlnProSerGlySerCysPheArgSerHisArgA 520
Db 1516 CAGTGGCCCTGATGTGGACGAGAGCCCAAGTGGACGTGCATCTCCCTACACCGCT 1575
QY 520 rgluSerValHisHisLeuValHisHisHisHisHisHisHisTyrHisSLeuG 540
Db 1576 GTCTGTCTGCCAACCACTGTGTCAACCAATCACCAACCATCACCACTACCACTGG 1635
QY 540 IyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnG 560
Db 1636 GTAATGGACGCTCAAGATTTCCCGGGCCAGCCCAAGATCCAGGACAGAGATGCCAAAG 1695
QY 560 IySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProA 580
Db 1696 GGTCTGGCGGCTCATGTCAACCAACCTCTTACACCACTCCCTCTGGGGGCCCTCCCA 1755
QY 580 rglYAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgC 600
Db 1756 GGGGTGCGAGTGTGTAACAAGCTTCTCAATGCTAAGTGCACACTTGAGGCCAGTCCGTT 1815
QY 600 yseGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyL 620
Db 1816 GCCAGGACACCCCTCCCAATGCCCATTCGAGGCACTGTGTAGCATGTGGGTAGTGGGA 1875
QY 620 yseValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuY 640
Db 1876 AGGTGTAACCCACTGTGTATCAAGCCCTCCACAGAGTATCTGAAGATTAAGCACTAG 1935
QY 640 alGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyP 660
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Db 1936 TGAAGTGGCCCCAGAGCCCTGGGGCCCCCACCCTCACCAAGCTTCAACATCCCACTGGGC 1995  
Qy 660 ropheSerSerMetuHleuyleuLeuGluThrgInSerThrgIvalaCyshiSerSerC 680  
Db 1996 CCTTCACTCCATGACACAAAGCTCTCTGGAGACACAGAGTACGGGAGCCTGCATAGTCTCT 2055  
Qy 680 yelyleSerSerProCySerSerIyvalaAapSerGlyvalaCyGlyProaapSerCySp 700  
Db 2056 GCAAAATCTCCAGCCTTGCTCCCAAGGACACAGTGGAGCCTGGGGCCGGACAGTTGTCTC 2115  
Qy 700 roTyrCybaAargThrgIvalaGlyGluProGluSerIaAapHiAvalMetProaapS 720  
Db 2116 CTTACTGTGCCCCGACAGAGACAGAGACAGAGTCCGCTGACCACTGCTACTGCTACT 2175  
Qy 720 eAapSerSerGluAvalaTyrgIupheThrgInaapAagInhiSerAapIeuaArgaap 740  
Db 2176 CAGACAGAGAGGCTGTGTATGATTCACACAGACGCTCAGACACAGTACCTCCGGGATC 2235  
Qy 740 rohiSerAargArgArgInaArgSerleuGlyProaapAagIupProSerSerValleua 760  
Db 2236 CCCACACCGCGCGGACAGCGGAGCCTGGGCCAGATGCAGAGCCTAGTTCTGTGCTGG 2295  
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Qy 780 rGgIyIleMerIlealaleuValaAnthrLeuSerMetGlyIleGluTyrhiSglug 800  
Db 2356 GGGGAATCATGATGCCATCTCTGGTCAATACATCAGCATGGGATGGATGACACAGAC 2415  
Qy 800 lnpProGluGluLeuThraAnaIleuGluIleSerAnaIlevalPheThSerleuPhea 820  
Db 2416 AGCCCGAGAGCTCACCAACCCCTGGAAATCAGCAACATGCTCTTCCACGCGCTTTCG 2475  
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Db 2476 CCTTGGAGATGCTGTAACCTGCTGTCTACGGTCCCTTGGCTACATTAGATCCCT 2535  
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Qy 860 lyGlyGlyLeuSerValleuAargThrPheAargLeuMetAryvalleuIySleuValaArg 880  
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Db 2776 TTGGTTGCAAGTTGCGCATCTAACCGGAGTGGGGAACACGTTGCCAGACCGGAAGAATTTCCG 2835  
Qy 940 spSerleuLeuTTPAlaIleValaThrValaPheGlnIleuThGlngInuapSPTPaenL 960  
Db 2836 ACTCCCTGCTCTGGGCGCATGCTGATGCTTTCATATCTGATCTCAGGAAGATGGAAAT 2895  
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Db 2896 AAGTCTCTTACAAGCGGACATGGCTCCACATGCTTGGGCTGCTCTTACTTCAATCGCCC 2955  
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Db 2956 TCATGACTTTTGGCAACTATGTGCTCTTAACTGCTGTGGCCATTTCTTGGGAAGGAT 3015  
Qy 1000 heGlnAlaGlyGluIyAapAlaThrIySserGluSerGluProaapPhePheSerProSerV 1020  
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Qy 1020 aIaapGlyAapGlyAapAargIyAargIyAargIyAargIyAargIyAargIyAargIyAarg 1040  
Db 3076 TGAATGATGATGGGACAGAAAGAGCGCTTGGCCCTGATGGCTTTGGGAGAACCGCG 3135  
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Db 3136 AACTACGAAGAAGCCTTTTCCACCCCTCATATCATACAGGTGGGACACCAATGTCA 3195  
Qy 1060 lAProIySerSerSerThrgIyvalaGlyGluAlaIleuGlySerGlySerAargThrs 1080  
Db 3196 ACCCAAGAGCTCCAGACACAGTGTGGGGAACACATGGGCTGTGCTCTGACATCA 3255  
Qy 1080 erSerSerGlySerAagIupProGlyAlaAlaIlehiSngIuMetIyCyAProProSerA 1100  
Db 3256 GTAGCAGTGGTCCGCTGAGAGCTGAGAGTCCCACTAGATGAATAATGTCGCAAGTG 3315  
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Qy 1140 rGserleuLeuSerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 1160  
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Db 3796 GAGAGCAAGATTCCTGTGCGGCTTATTCCTTCTCTCAAGTTCAGAGGTTTCGTCTCGT 3855  
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Db 3856 GTACCGGATATACCAACAAAGATGTTTACCATAGTGGTCTCTGTCATATCTTCTCA 3915  
Qy 1300 snCySIIleThriIleAlaMetGluAargProIySIIleAapProhiSserAlaGluAargIleP 1320  
Db 3916 ACTGTATCACATGCTATGAGAGCGCCCAAAATTTGACCCCAACAGCGCTGAGCGCATCT 3975  
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Qy 1340 aIvalAlaIleuGlyTTPCyPheGlyGlyGlnAlaTyrrLeuAargSerSerTTPAnaVal 1360  
Db 4036 TGGTGGCACTGGGCTGTGTCTTTGGGAGAGAGCTTACCTGCGAGACAGCTGGAATGTC 4095  
Qy 1360 euaAapGlyLeuLeuValleuIleSerValIleAapIleuValaIleuValaSerMetValSerAps 1380  
Db 4096 TGAAGGCTTGCTGTGCTCATCTCCGTATTCAGCATCTGAGTCTCATAGGTCTCCGACA 4155

QY	1380	ERG1YTHRYEIIIEENG1YMEIEUARYVALLEUAIGLEUEAIXTHLEUAIRPROL	1400
DB	4156	GCGGCACCAATGCTTGCGCATGCTGAGGGTGCTGCGGCTGCTGCGGACCTTGCTGCAC	4215
QY	1400	EUAARGVALIIIESERARGAIIAGINGLYEUYSLEUVALVALGIUTHLEUMETSERL	1420
DB	4216	TCAGGGATATACGCGGGCCGAGGADCTGAAGCTGTGGTGAAGACTTGATGTCATCCC	4275
QY	1420	EULYSPROIIIEGLYASNIILEVALIIECYSCYSAIAPHENIIIEPHEGIYIIEL	1440
DB	4276	TCAAACCATGGGCAACATTGCGCATTTGCTGCTTGCCTTTCATCATTTTGGAAATTC	4335
QY	1440	EUGIYVALIIGINLEUPHEIYSGIYLYSPHEPHEVALCYSGINGIYLIASPTHARGANI	1460
DB	4336	TCGGGGTGCACCTCTTCAAGGGAAGTTCTTCTGTGTCAAGGGTGAAGACCCGGAACA	4395
QY	1460	IETHRANLYSSERAPRCYEAIIAGIULASERTYRATGTTPVALARGHIELYERTANP	1480
DB	4396	TCACCTAAACAAATCCGACCTGCGCTGAGGCGACCTACCGATGGGTCCGACAAAGTCAACT	4455
QY	1480	HEAPASLEUGIYGINIALEUMETSERLEUPHEVALLEUALASERTLYASPGIYTRPV	1500
DB	4456	TTGACACACCTGGGCGCAGGCTTGATGTCTCCCTGTTGTGTGCTTGCTCCAGAGATGGTTGGG	4515
QY	1500	ALASPIIEMETTYRASPGLYLEUAPRALVALGIYVALASPGINGINPROIIEMETASNI	1520
DB	4516	TTGACATCATGTATGATGGCTGATGCTGTGGGTGTGATCCAGACCCCATCATCTGAACC	4575
QY	1520	ISANPRTOTMETLEUETRYRPHETIIIESERPHETLEUIIEVALIAPHENIIVALL	1540
DB	4576	ACMACCCCTGGATGCTGTATATCTTCATCTCTCTCTCATGTGACCTCTTCTTGTCC	4635
QY	1540	EUAENMETPHEVALIGIYVALIIVALIUISANPHENISLYSCYARGIINHISGLINGUG	1560
DB	4636	TGAACATGTTTGTGGGCGCTGGTGGTGAAGAACTTCCATMACTGCAGACAGACCAAGGAGG	4695
QY	1560	IUGIUGIUALIARGHARGRIGIUGIULYSAIGLEUAARGARGLEUGIULYLSYARGHARGS	1580
DB	4696	AGGAGGAGGCGAGGCGCGCTGAGGAGGAAGCGACTACGGAGGCTGGAAGAAAGAGAGGA	4755
QY	1580	ERYSGIULYEGIMETLAIAGIULIAGINCYBLYSPROTYYTYRSEARSPTYRSEARXP	1600
DB	4756	GTAAGGAACACAGATGGCGCCAGCCGAGTCAAGCCCTACTACTGTGACTACTCGAGAT	4815
QY	1600	HEARGLEUVALHISHISEUCYTHRSERHISRYRLEUASPLEUPHEIIETHRISYV	1620
DB	4816	TCCGGCTCTTGTCACACCACTGTGTACCAAGCCACTACCTGGACCTTCTTCACTACCTGGT	4875
QY	1620	ALIEGLYLEUASNVAVAIITHMETALIMETGIUHSITYRGINGINPROGINIIIELEUA	1640
DB	4876	TCATCGGGCTGAACGTGTGCTCATGTAGCCATGGAACATTACACAGACCCAGATCTCTGG	4935
QY	1640	SPGIUALIIEULYSIIIECYASANTYRIIEPHETRIVALIIEPHEVALIIPHEGUSERVALP	1660
DB	4936	ACGAGGCTCTGAAGATTCGCAATTACACTTTACCTTCATCTTGTCTTTGAGTCAGATTT	4995
QY	1660	HELYSLEUVALIAPHENIAPHARGARGPHEPHEGINASPARXTTPASGIIIEUASPL	1680
DB	4996	TCAAACTGTGGCTTTGGCTTCGCGGCTTCTTCCAGAGAGGGAAGCAAGCTTGAGACC	5055
QY	1680	EUALAIIEVALIIEUUSEERIIEMETGIYIIEHRIEUGIUGIUIEGIULVALASNIENS	1700
DB	5056	TGCGATTTGTGTTCTGTCCATCANGGGCACTACACTGGAGAGATTTGAGGTCAATCTGT	5115
QY	1700	ERTLEUPROIIEASNPROTHRIIEIIEARGIIEMETARGVALLEUAIGTIIIEALARGYVALI	1720
DB	5116	CGCTGCCCATCAACCCCAACATCACTCCATATCAGAGGGTGCCTCCGATGTGCTGCAATTC	5175
QY	1720	EULYSLEUULEYMERALIVAGIYMETARGALIEULEUHIETHYVALMETGINIAL	1740
DB	5176	TGAACCTGTTGAAGATGGCTGTGGGCATGCGGGCACTGCTGCACACGCGTATGCAAGGCC	5235
QY	1740	EUPROGINIVALIYASNIENGIIYLEUUPHEMETLEUUPHEMETLEUPHEIIEPHEALAIATL	1760
DB	5236	TGCCCCAGGTGGGGAACCTGGGACTTCTTTCATGATTATTTTTCATCTTTGCAAGCTC	5295
QY	1760	EUGIYVALIIGIUEUPHEGIYASPLEUGIUCYASAPGIUTHRHISPROCYSGIUGIYLEUG	1780
DB	5296	TGGGCGTGAAGCTCTTTTGGAGACCTCGAGGTGTGATGAGACACCCTTGTGTGAGGGCTTGG	5355
QY	1780	IYARGHIEALATHRPHARGANPHEGIYMETALAPHLEUTHRIEUPHEARGVALISERT	1800
DB	5356	GTCGGCATGCCACCTTTATGGAACCTTGGTATAGGCTTTTCTACACCTCTTCCGAATCTTCCA	5415
QY	1800	HRCGIYASAPASPTTPASNGIYIIEMETLYSAPPROSERARGASPCYASAPGINIUSERT	1820
DB	5416	CTGTGTGACAACTGGAGATGATATTATGAAAGACACCTTCGGGACTGTGACAGAGATCCA	5475
QY	1820	HRCYSTYRASNTHRIVALIIIESERPROIIETRYRPHENIISERPHENIIVALLIAGINP	1840
DB	5476	CCTGCTACACACTGTGATCTCCCTATCTACTTTGTGTCTTGTGTGTGTCAGGCCCAAGT	5535
QY	1840	HEVALIIEUVALASNVAVAIIIIEALIVALEUMETLYSHISLEUGIUGIUSERANLYSG	1860
DB	5536	TTGTGTGTTGTCACAGCTGGCATATGCTGTGATGAACACTTGGAAGAAAGCAACAAAG	5595
QY	1860	IUALIYSGIUGIULIAGIULIENGULIAGIULIENGULIENGULIMETLYRTHRIEUSERP	1880
DB	5596	AGGCCAAGAGGAGGCGCAGCTCGAGGCGCGAGCTGGAAGTGAAGTAAGACGCTCAGCC	5655
QY	1880	ROGINPROHISERPROLEUGIYSEPRPHETLEUTRPROGIYVALIGIUGIYVALIANS	1900
DB	5656	CGCAGCCCACTCCCGCTGGGCAAGCCCTTCTGTGCGCGGGGTGAGGGGTGTCAACA	5715
QY	1900	ERTHRSASERPROLYSPROGIYVALIAPHROHISRTHRIALHISIIIEGIYVALIIASERG	1920
DB	5716	GTACTGACAGCCCTTAAGCCTGGGGCTCCACACACCACTGCCACATTGGACACAGCTTCGG	5775
QY	1920	IYPHESERLEUGIINHISPROTHMETVALIIPHROHISPROGINIULIVALIIPROLEUG	1940
DB	5776	GCTTCTCCCTTAGAGACCCACGATGTRACCCCAACCCGAGAGAGGTGCAGTCCCTCAG	5835
QY	1940	IYPROASPLEUETHRIVALIARGIYLSERGIYVALISERARGTHRHISSEURPROASNA	1960
DB	5836	GACACACCTGTGACTGTGAGGAAGTCTGGTGTGACGCGGACGCACTCTTGCCCAATG	5895
QY	1960	SPSERIYMETCYARGHANGIYSERTHRIALAGIUAJRSERLEUGIYHISARGIYTPG	1980
DB	5896	ACAGCTACATGTGGCGCAATGGAGACACTGCTGAGAGATCTCCTAGACACAGGGGCTGGG	5955
QY	1980	IYLEUPROLYALAGINSERGIIIELEUSERVALHISSEGINPROHIALAPRTHRS	2000
DB	5956	GGCTCCCAACCCCAAGTCAAGGCTCACTTGTGCTGCTCACTCCCAACACACAGACACA	6015
QY	2000	ERCYSEIIIELEUGIINEUPROLYSASPVALHISITYRLEUENGINPROHISGIYALAPROT	2020
DB	6016	GCTGATCTTACAGCTTCCCAANAGTGTGACATTACTCTCTCAAGCTTATAGGGCTCCA	6075
QY	2020	HRTSPGIYALIIIEPROLYSEUPROPROPOGIYARGSERPROLEUAIIAGINARGPROL	2040
DB	6076	CTGGGGGCGCATCCCTTAAACATACCCCAACAGCGGCGGCTCCCTCTGGCTCAGAGGCTTC	6135
QY	2040	EUAJARGGINALAIIEARGHTRASPSEURLEUASPVAGIINGIYLEUGIYSEARAGG	2060
DB	6136	TCAGGCGCGAGCACCAATTAAGACTGACTCCTCTGAGTGTCAAGGCGCTGGGTAGCCGGG	6195
QY	2060	IJASPLEUUSEERGIVALISERGIIYPROSERCYSPROLEUTHRARGSESERSEPHET	2080
DB	6196	AAAGCTGTTGTCAAGAGTGAATGGGCTCTGCTGCTTGAACCCGATCTCACTCACTCTTCT	6255
QY	2080	IRPGIYGIYSESERIIIEGINVALIINGINARGSEGIYIIIEGINSEIRIYVALSEIRIYSH	2100
DB	6256	GGGGGGGGTGCAGCATCCAGGTGCAGAGCGGTTCGGGATCCAGAGCAAGGTCTTCAAGC	6315
QY	2100	ISIIIEARGLEUPROALAPROCYSPPROGIYLEUGIUPROSETRTPALIALYASPPROPROG	2120

Db 6316 ACATCCGCGCTGCCACCCCTTGGCCAGGCTCGAACCAGCTGGGCCAAGSACCTTCAG 6375  
Qy 2120 luthrArgSerSerLeuGluLeuaspThrGluLeuSerTrpIleSerGlyAspLeuLeup 2140  
Db 6376 AGACCAAGAGAGAGCTTAGAGCTGGAACAAGAGCTGAGCTGATTTTCAGAGACCTCTTC 6435  
Qy 2140 roserSerGlnGluGluProleuPheProArgAspLeuValSerCysThrSerPalaGluT 2160  
Db 6436 CCAGCACCAGGAAGAACCTCTGTTCACCGAGCTGAGAGAGTGTACAGTATAGAGA 6495  
Qy 2160 hrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgIleSerIleA 2180  
Db 6496 CCCAGAGCTGAGAGCGAGGCTGGGTTCTGGCTAGATGAACACGAGACACTCCATTG 6555  
Qy 2180 lavalSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuG 2200  
Db 6556 CTGTACAGCTGTCTGAGACAGCGGCTCCCAACCCCGCTATGTCCAAGCCCTCAAGCCTCG 6615  
Qy 2200 lylGlyGlnProLeuGlyGlyProGlySerArgProGlyValSerGlyLeuSerProSerI 2220  
Db 6616 GGGGACCAACCTCTGGGGGCTCTGGAGCGCGCTTAAGAAAAAACTCAGCCACCAGTA 6675  
Qy 2220 laseSerLeuAspProGluSerGlnGlySerArgProProCysSerProGlyValCysL 2240  
Db 6676 TCTCTATAGACCCCGGAGAGCCAGGCTCTCGGCCCATGCACTGCTGTCTGCC 6735  
Qy 2240 euArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAspS 2260  
Db 6736 TCAGAGAGAGGGCGCGGCGAGTGACTTAAGATCCCTCGGCTCCAGCCCTTGACA 6795  
Qy 2260 erThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSera 2280  
Db 6796 GCAGGGCTGCTCAACCTCCCAAGAAAGACAGCTGAGTCTCTGGTTGTCTCTG 6855  
Qy 2280 sPProThrAspMetAspPro 2286  
Db 6856 ACCCAACAGACATGACCC 6875

RESULT 2  
US-09-383-894-3  
; Sequence 3, Application US/09383894  
; Publication No. US20030125269A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Ming  
; TITLE OF INVENTION: T-Type Calcium Channel  
; FILE REFERENCE: 004.00191  
; CURRENT APPLICATION NUMBER: US/09/383,894  
; CURRENT FILING DATE: 1999-08-26  
; EARLIER APPLICATION NUMBER: US 60/098,004  
; EARLIER FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: US 60/117,399  
; EARLIER FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 7285  
; TYPE: DNA  
; ORGANISM: Rattus sp.  
US-09-383-894-3

Alignment Scores:  
Pred. No.: 0 Length: 7285  
Score: 11829.00 Matches: 2270  
Percent Similarity: 97.72% Conservative: 1  
Best Local Similarity: 97.68% Mismatches: 15  
Query Match: 98.35% Indels: 38  
DB: 10 Gaps: 2

US-09-611-257a-24 (1-2287) x US-09-383-894-3 (1-7285)

Qy 1 MetLeuProHisArg-ValProArg-CysValArgThrProProLeuArgGlySerAlaA 20  
Db 57 ATGCTCCCAACCGGGGTCCTCCCGGTTGGGTGAGAGACACTCTCTTGAAGGGGCTCCGCTC 116

Qy 20 rGProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetG 40  
Db 117 GCCCTCTTGGACCCCCCGGGGCCCGGCTGGCCAGAGAGTGAAGAGAGAGATGG 176  
Qy 40 lualArgAlaProArgSerArgAspSerProValAlaSerArgSerThrThrCysProG 60  
Db 177 AGCGGGCGCGAGAGAGTCCGGGACAGCCCGTACTTCAAGCACTCAACGACCTGTCCG 236  
Qy 60 lylProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerG 79  
Db 237 GCGCGGGGCGCGCAGGGCGCGGGGTGACGAGAAAGAGACCCCGGAGCCCGGACTCCGA 296  
Qy 79 uAlaGluGlyLeuProLysProAlaLeuAlaProValAlaPhePheThrLeuSerGlnAs 99  
Db 297 GCGGAGAGGGCTCCGTAACCGGCGCTAGCCCGGTGGTTTCTTCTACTTGAACCAAGA 356  
Qy 99 pSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSe 119  
Db 357 CAGCCGCGCGCGAGCTGAGTGTCTCCGACGCTGTGAACCGGTGGTTGAGGAGTCAAG 416  
Qy 119 rMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspI 139  
Db 417 TATGCTGTATCTTCTCAACTGTGTGACTGTGGTATGTTCAGGCGGTGAGACAT 476  
Qy 139 eAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPh 159  
Db 477 TGCTGTGACTCCAGAGGCTGCGGAGTCTGCAAGGCTTGAGATTCATCTTGGCTT 536  
Qy 159 ePheAlaValAlaGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTr 179  
Db 537 CTTTGCTGTGGAATGTTGTTGTAAGATGTTGGCTTGGGATCTTTGGGAATGTTA 596  
Qy 179 rLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTr 199  
Db 597 CTTGGAGAGACACTTGAAACCGGCTTGACTTTTTCATTGTATGTCAGGGATGCTGAGTA 656  
Qy 199 rSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuAspGr 219  
Db 657 TTGCTGTGACCTCGAGAACCTCAAGCTTCTCGGACAGACAGTCCGTGGTGCACAC 716  
Qy 219 oLeuArgAlaIleAsnArgValProSerMetCArgIleLeuValThrLeuLeuAspThr 239  
Db 717 GCTAGAGGCCATTACCGGGGTGCCAGCATGCCGATCTGTCACTTACGTGGACAC 776  
Qy 239 rLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyI 259  
Db 777 CTTCCTATGCTGGGCAACGTCCTGCTGTCTGTCTTCTTTCATCTTTGGCAT 836  
Qy 259 eValGlyValGluLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPh 279  
Db 837 CGTGGGGGTCAAGCTGTGGGAGAGAGCTTCGACACCGATGCTTCCCGGAACTT 896  
Qy 279 eSerLeuProLeuSerValAspLeuGluProGlyTrpGlyThrGluAsnGluAspGluSe 299  
Db 897 CAGCTCCCGCTGAGCTGAGCTGAGCTTATTTACCAACAGAGATAGAGACGAGAG 956  
Qy 299 rProPheIleCysSerGlnProArgGluAsnGlyMetCysSerCysArgSerValProTh 319  
Db 957 CCCTTCATGCTGCTCAGGCTCGGAGAAATGGCATGATCCGAGAGATGGCCAC 1016  
Qy 319 rLeuArgGlyGlyGlyGlyGlyGlyProProCysSerLeuAspTrpGluThrTrpAsnSe 339  
Db 1017 ACTGCGTGGGAGAGCGGTGTGGCCCACTGAGTGTGACATATAGACTATTAACG 1076  
Qy 339 rSerSerAsnThrThrCysValAsnTrpAsnGlnTrpThrAsnCysSerAlaGlyI 359  
Db 1077 TTCCAGACACCACTGTGTCAACTGGAACAGATCATATACCACTGCTGTGGGGCGA 1136  
Qy 359 uHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTrpAlaTrpIleAlaI 379  
Db 1137 GCACACCCCTTCAAGAGCGGCATCACTTGAACAATGGGTATCCGTGATCCGCAT 1196

QY 379 ePheGlnValIleThrLeuGlnGlyTrpValAspIleMetTrpPheValMetAspAlaH 399  
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Db 1197 CTTCCAGGTATATACATCGAGGGCTGGTGCATCATCTACTTGTATATGACGCTCA 1256  
QY 399 sSerPheTrpAsnPheIleTrpPheIleLeuLeuIleIleValGlySerPhePheMetII 419  
| | | | |  
Db 1257 CTCCTTCAACAATCTCACTTCACTTCTTCATCATCGTGGGCTCCTTCTTCATGAT 1316  
QY 419 eAanLeuCyLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerG 439  
| | | | |  
Db 1317 CAACCTGTGCTGTGTGTGTATGCCAGCATCTTCGAGACCAACAGGGAGATGTC 1376  
QY 439 nLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrIleuAlaSerPheS 459  
| | | | |  
Db 1377 GCTGATGCGGAGACAGGCTTACGATTCCTGTCCAATGCTAGACCCCTGGCAAGCTTCTC 1436  
QY 459 rGluProGlySerCysTrpGlnGluLeuLeuLysTrpLeuValTrpIleLeuArgIysAl 479  
| | | | |  
Db 1437 TGAGCCAGGACGCTGCTATAGAGGACTCAAGTACCTGTGTACATCCTCCGAAAGC 1496  
QY 479 aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerS 499  
| | | | |  
Db 1497 AGCCCGAAGGCTGGCCAGGCTCTTAGGGCTATAGGGGTGGGGCTGGCTCAGCAG 1556  
QY 499 rProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisAr 519  
| | | | |  
Db 1557 CCNAGTGGCCCGTAGTGGGAGAGCCCAAGCCAGTGGCAGCTGCATCGCTCACACCG 1616  
QY 519 gArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHis 539  
| | | | |  
Db 1617 TCGTCTGTCTGTCCACACCTGCTGCCACACATCACACACATCACACATCACACATCA 1676  
QY 539 uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAs 559  
| | | | |  
Db 1677 GGGTAATGGGACCTCAGAGTCTCCCGGGCACGCCAGATCCAGAGACGGATGGCAA 1736  
QY 559 nGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProP 579  
| | | | |  
Db 1737 TGGGTCTCGCGGGCTCATGCTTACCAACCTCTTACCAACCTCCTCTGGGGGCCCTCC 1796  
QY 579 cArgGlyAlaGluSerValHisSerPheTrpHisAlaAspCysHisLeuGluProValAr 599  
| | | | |  
Db 1797 GAGGGGGCGGAGTCTGTACACAGCTTCTACATGCTGACCTGCACCTGGAGCCAGTCCG 1856  
QY 599 gCysGlnAlaProProProArgCysProSerGlyAlaSerGlyArgThrValAlaLysG 619  
| | | | |  
Db 1857 TTGCCAGGCAACCCCTCCAGATGCCCATCGAGGCACTGTGTAGGACTGTGTGGTGTGG 1916  
QY 619 yLysValTrpProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLe 639  
| | | | |  
Db 1917 GAAGGTATACCCACTGTGTATACAGCCCTCCACAGAGATACTGAAGATTAAGCACT 1976  
QY 639 uValGlnValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProG 659  
| | | | |  
Db 1977 AGTGGAGGTGGCCGCCAGCCTGGGGCCCCCACCTCACAGCTTCAACATCCCACTGG 2036  
QY 659 yProPheSerSerMetHisLysLeuLeuGluuThrGlnSerThrGlyAlaLysHisSerS 679  
| | | | |  
Db 2037 GCCCTTCAAGCTCAGTACAAAGCTCTCGAGACACAGATACGAGAGCCCTGCATATGCTC 2096  
QY 679 rCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCy 699  
| | | | |  
Db 2097 CTCGAAATATTCAGCCCTTGTCTCCAAAGGACAGTGGAGCTTCGGGGCCGAGACAGTTG 2156  
QY 699 sProTrpCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAs 719  
| | | | |  
Db 2157 TCCCTACTGTGCCGAGACAGAGACAGAGACAGTCCGTGACCATATGCTCATGCTCTGA 2216  
QY 719 pSerAspSerGluAlaValTrpGluPheThrGlnAspAlaGlnHisSerAspLeuArgAs 739  
| | | | |  
Db 2217 CTCAGACAGGAGGCTGTGTATAGTTTCACAGAGAGCTGCACACACAGTACCTCCGGGA 2276  
QY 739 pProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLe 759

Db 2277 TCCCCACACCCGGCCGGACAGCGAGCCTGGGGCCCAAGATGACAGAGCTAGTTCTGTGCT 2336  
QY 759 uAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTrpPheG 779  
| | | | |  
Db 2337 GGCTTCTCGAAGCTGATGCTGTGACACATCCCGAAGATCGTAGATAGCAAAATACCTTTGG 2396  
QY 779 yArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTrpHisG 799  
| | | | |  
Db 2397 CCGGGAAATCATGATGCCATCTGGTCAATATACCTCAAGATGGGCATGAGTACACACA 2456  
QY 799 uGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuAs 819  
| | | | |  
Db 2457 GCAGCCCGAGAGAGCTACCAAGCCCTGGAAATTCAGCAACATGCTTACCAGCCTCTT 2516  
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Db 2517 CGCCTTGGAGATGCTGCTGAAACTGCTGTCTACAGCTCCCTTGGCTTACATTAGAAATCC 2576  
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| | | | |  
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QY 859 nGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValAr 879  
| | | | |  
Db 2637 GGGAGGTGGCTGTGCTGCTGCGGACCTTCGCGCTGATGCCGGTGTGAAGCTGGTGG 2696  
QY 879 gPheLeuProAlaLeuGlnArgGlnArgGlnLeuValLeuMetLysTrpMetAspAsnValAl 899  
| | | | |  
Db 2697 CTTCCTGCGGGCCCTGCAGCGCCAGCTCGTGGTGTCTCAAGAACCATGGAACAGTGGC 2756  
QY 899 aThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLe 919  
| | | | |  
Db 2757 CACCTTCTGATGCTCTCATGCTGTTCATCTTTCATCTTACAGATCCTGGGATGATCAT 2816  
QY 919 uPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnH 939  
| | | | |  
Db 2817 CTTTGGTTCAAGTTGGATCGATCGAAGCGGATGGGACAGTTGCCAGACCGGAAGATTT 2876  
QY 939 eAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAs 959  
| | | | |  
Db 2877 CGATCTCCCTGCTCTGGGCCATCGTCACTGCTCTTTCAGATTCGACTCAGAAAGACGGA 2936  
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| | | | |  
Db 2937 TAAAGTCTCTTCAACGAGGATGCTCCACATGCTTGGGCTGCTTATCTTCACTGCC 2996  
QY 979 aLeuMetThrPheGlyAsnTrpValLeuPheAsnLeuLeuValAlaIleLeuValGluG 999  
| | | | |  
Db 2997 CCTCATGACTTTTGGCAACTATGTGCTTTAACTGCTGTGGCATTTCTGTGGAAGC 3056  
QY 999 yPheGlnAlaGlu----- 1003  
| | | | |  
Db 3057 ATTCCAGGACAGAAATATCGGAAAACGGGAGATGCACTGACATTAAGCTGATTTCA 3116  
| | | | |  
QY 1004 -----GlyAspAlaThrLysSerGluSerGluProAspPhePh 1016  
| | | | |  
Db 3117 GCTGCTGTCAACTCTCAGGGGGGAGATCCACCAAGTGTGAGTCAAGAGCTGATTTCTT 3176  
QY 1016 eSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuG 1036  
| | | | |  
Db 3177 TTGCGCCCAATGTAGATGTGGGACAGAAAGAACGCTTGGCCCTGTGGCTTTGGG 3236  
QY 1036 yGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaH 1056  
| | | | |  
Db 3237 AGAAACAGCGGAACTACGAAAGAGCCTTTTGCACCCCTCATCATCTCAACAGCTGGCAGC 3296  
QY 1056 rProMetSerHisAspLysSerSerSerThrGlyValGlyAlaLeuGlySerGlyS 1076  
| | | | |  
Db 3297 ACCAATGTACTAACCAAGAGCTCCAGCACAGATGTGGGAAAGCATGGGCTTGGCTTC 3356  
QY 1076 rArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCy 1096  
| | | | |



Db 3357 TCAGCGTACGATGACAGTGGCTCCGCTGACCTCGAGCTCCGACCATGATGAAATC 3416  
Qy 1096 sProProSeRAlaArgSerSerProHisSerProTriSerAlaAlaSerSerTriPThrSe 1116  
Db 3417 TCCGCGCAAGGCCCGGAGCTCCCGGACAGTCCCTGGAGTGGCGGACAGACTGACAG 3476  
Qy 1116 rAArgArgSerSerArgAnsSerLeuGlyArgAlaProSerLeuArgArgArgSerProSe 1136  
Db 3477 CAGCGCTCCACGACGAGAACAGCTGGGCGGGGCCCCAGCCTTAAAGCGAGAGACCCGAG 3536  
Qy 1136 rGlyGlyArgArgSerLeuSerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 1156  
Db 3537 CGGGAGCGAGAGTCCCTGCTGCTGAGAGAGGCGGAGAGTGAAGTGAAGAGAGAG 3596  
Qy 1156 rSerGlyGlyArgArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGly 1176  
Db 3597 TTCGAGAGAGAGACCGGGCGACCCAGACGAGCATGACATCGCACAGGGGTTCTTGGA 3656  
Qy 1176 uArgGlyAlaLysSerSerPheAspLeuProAspThrLeuGlyAlaProGlyLeuHisArg 1196  
Db 3657 ACGTGAGGCGCAAGGATTCCTTGGACTGCTGACACTCTGCAGAGTGGCGGGCTGACCG 3716  
Qy 1196 gThrAlaSerGlyArgSerSerAlaSerGlyHisGlyHisProCysArgHisGlySerAlaSe 1216  
Db 3717 CACAGCGACGGCGCGAGCTGCTGCTGACACACCAAGCTGTAATGCAAGTGGCTTC 3776  
Qy 1216 rGlyArgLeuAlaArgThrLeuAlaArgThrAspAspProGlyLeuAspGlyAspAspAsp 1236  
Db 3777 AGGGCGTTGGCCCGGACCCCTGAGGACTGATGACCCCAACTGGATGGGATGATGACAA 3836  
Qy 1236 nAspGlyGlyAsnLeuSerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 1256  
Db 3837 TGATGAGGGAATGTGAGCAAGGGAAGGGAACGATACAACTGGGTCAGATCCCGCTTCC 3896  
Qy 1256 oAlaCysArgArgGlyArgAspSerTrpSerAlaTrpIlePheProProGlyInsArgPh 1276  
Db 3897 TGCGTGTGCGAGAGCGAGATCTCGGTCCGACTATCTTCTTCTCTCTGCTGACAGTT 3956  
Qy 1276 eArgLeuLeuCysHisArgIleIleThrHisGlyMetPheAspHisValValLeuValIle 1296  
Db 3957 TCGTCTCTGTGTACCGGATCATCACCAACAGATGTTTGACATGTGGTCTGCTGAT 4016  
Qy 1296 eIlePheLeuAnCysIleThrIleAlaMetGlyArgProLysIleAspProHisSerAl 1316  
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Db 4137 GACATGAAAGTGGTGGGACACTGGGCTGGTCTTGGGAGAGAGCGCTACCTGGCGAGAG 4196  
Qy 1356 rTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMe 1376  
Db 4197 CTGGAATGTGCTGAGCGGCTGCTGCTGCTCATCTCCGTCATCGCATCTGGTCTTCAT 4256  
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Db 4257 GGTCTCCACAGCGGACCAAGATCTTGGCATGTGAGGGGTGCGGCGCTGCTGGAGC 4316  
Qy 1396 rLeuArgProLeuArgValIleSerArgAlaGlyGlyLeuLysLeuValValGlyThrLe 1416  
Db 4317 CCTGGTCACTCACTGAGGTATCAAGCCGGGCGCAAGGACTGAAGCTGGTGTAGAGACT 4376  
Qy 1416 uMetSerSerLeuLysProIleGlyAsnIleValValIleCysCysValAspPheIleIle 1436  
Db 4377 GATGTCATCCCTCAAAACCATGTGGCAACATGTGTGCTATTTGCTGCTTCTTCATCAT 4436  
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Qy 1456 pThrArgAsnIleThrAsnLysSerAspCysAlaGlyAlaSerTrpArgTrpValArgHis 1476  
Db 4497 CACCAGGAACATCATTAACAAATCCGACTGAGGCCAGGCTTACCGATGGGTCCGGCA 4556  
Qy 1476 sLysTrpAsnPheAspAsnLeuGlyGlyAlaLeuMetSerLeuPheValLeuAlaSerLys 1496  
Db 4557 CAAGTCAACTTTGACAACTGGGGCCAGGCTCTGATGATGCTCTGTTTGTGCTGGCTCA 4616  
Qy 1496 sAspGlyTrpValAspIleMetTrpAspGlyLeuAspAlaValGlyValAspGlyHisPr 1516  
Db 4617 GGATGTTGGGTGATCATCATGATGATGATGGCTGAGATGCTGGGTGTGATGACGAGCC 4676  
Qy 1516 oIleMetAsnHisAsnProTrpMetLeuLeuTrpPheIleSerPheLeuLeuIleAlaI 1536  
Db 4677 CATCATAAACCAACACCCCTGAGATGTGTATACTTATCTTCTCTCTCATGTGGC 4736  
Qy 1536 aPhePheValLeuAsnMetPheValGlyValValValGlyAsnPheHisLysCysArgGly 1556  
Db 4737 CTTCCTTGTCTGAAACATGTTTGTGGCGCTGTGTGTGGAAGACTTCCATTAAGTCAGACA 4796  
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Db 4797 GCACCAAGAGAGAGAGGCGGAGCGCGGTGAGAGAGACGACTACGAGGCTGAGAA 4856  
Qy 1576 sLysArgArg-----SerLysGlyLysGlyMe 1585  
Db 4857 AAGAGAGAGAGATCTAAATGTTGACGATGTAATGCTTCCGCGAGCTTCACCGAGCTGC 4916  
Qy 1585 tAlaGlyAlaGlyCysLysProTrpTrpSerAspTrpSerArgPheArgLeuValHis 1605  
Db 4917 GTCAAGAGCCAGTGCAGAGCCCTACTACTGACTTACAGAGATTCGGGCTCTGTGCCA 4976  
Qy 1605 sHisLeuCysThrSerHisArgTrpLeuAspLeuPheIleThrGlyValIleGlyLeuAsnVa 1625  
Db 4977 CCACCTGTATACAGCCACTACCTGACCTTCTCATCATGTGTGTCAATCGGGCTGAAGCT 5036  
Qy 1625 lValIleMetAlaMetGlyHisArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 1645  
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Qy 1645 eCysAsnTrpIlePheThrValIlePheValPheGlySerValPheLysLeuValAlaPh 1665  
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Qy 1705 oThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMe 1725  
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Qy 1745 nLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValIleGlyLeuPh 1765  
Db 5397 CCTGGAGCTTCTCTTCAATGTAATGTTTTCATCTTGGACCTTGGCGGTGGAGCTCTT 5456  
Qy 1765 eGlyAspLeuGlyLysCysAspGlyTrpHisAspCysGlyGlyLeuGlyArgHisAlaIlePh 1785  
Db 5457 TGAGAGCTTGAGAGTGTATGAGACACACCTTGTGAGGGCTTGGGTGGCATGCCACTT 5516  
Qy 1785 eArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAs 1805  
Db 5517 TAGGAATTTGTGATGGCTTCTGACCTCTTCCAGTCTCCACTGCTGACCACTGGA 5576

QY	1805	nglyIYLewetLysAspProSerAArgAspCysAspGlnGluSerThrCysIYrAanThrVa	1825
Db	5577	TGGTAATATGTAAAGACACCTCTCCGGAGACTGTGACACGAGAGTCCACCTGGCTAACACACTGT	5636
QY	1825	IIIsSerProIleYrPheValIsSerPheValLeuThrValGlnPheValIleuValAsnVa	1845
Db	5637	CATCTCCCTTAATCTAATTGTGTCTTGTCTGTACGGCCCAAGTTTGTCTGTGTCAACT	5696
QY	1845	IVaIIleAlaValIleuMetLysSHIsLeuGluGluSerAsnLysGlnIaIaIySGIuGluIaI	1865
Db	5697	GGTCATAGCTGTGGCTGATGAAGACACTTGAAGAAAGACAAAGAGGCCCAAGAGGAGGAGC	5756
QY	1865	agluLeuGluIaIaGluLeuGluLeuGluMetLysThrIleuSerProGlnIProHisSerPr	1885
Db	5757	CGAGCTCGAGGCCGAGCTGGAGCTGGAGTAAAGCGCTCAAGCCCGGAGCCCACTCCCC	5816
QY	1885	oleuGIIysSerProPheLeuTrpProGluVAlGluGluVAlaAsnSerThraAspSerPoly	1905
Db	5817	GCTGGGAGCCCCCTCTCTCTGACCCGGGGGTGAGGGGTGTCAACAGTCTCTGACACCCCTAA	5876
QY	1905	sProGIIyAlaProHisThrThraIaHisIleGIIyAlaIaIsSerGIIyPheSerLeuGluHI	1925
Db	5877	GGCTGGGGCTCCACACACCACTGCCACATTGGAGACAGCTCTCGGCTTCTCCCTTGAACA	5936
QY	1925	sProThrMetValProHisProGluGluValProValProLeuGIIyProAspLeuLeuTh	1945
Db	5937	CCCCACAGATGNAACCCCAACCCCGAGAGAGGTCCAGTCCCTTACGAGCACAGCTGTAC	5996
QY	1945	rValArgIysSerGIIyValIsSerArgThHisSerLeuProAsnIleSerYrTrmetCysAR	1965
Db	5997	TGTGAGGAAGTCTGGTGTCAACCCGAGCCCACTCTCTGCCAATAGCACATCAATGTCCG	6056
QY	1965	gAsnGIIysSerThraIaGluArgSerLeuGIIyHisArgGIIyTrpGIIyLeuProPolyAlaGII	1985
Db	6057	CAATGGAGACACTGCTGAGAGATCCCTTAGACACAGGGGCTGGGGGCTCCCCAAAGCCCA	6116
QY	1985	nSerGIIysSerIleLeuSerValHisSerGlnProAlaAspThrSerCysIIleLeuGlnIe	2005
Db	6117	GTCAGGCTCCATCTTGTCCGTTCTCACTCCCAACAGACACACAGCTGCACTTCACTCAAGCT	6176
QY	2005	uProIyAspValHisYrIleuLeuGlnIProHisGIIyAlaProThrTrpGIIyAlaIlePr	2025
Db	6177	TCCCAAAATGTGCATATGCTTCCACACTGCATAGGGGCCCCCACTGGGGGCGCATCTCC	6236
QY	2025	olysLeuProProProGIIyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaI	2045
Db	6237	TAAACTACCCCACTGGCCGCTCCCTCTGGCTCAAGAGGCTCTCAAGCCCAAGCAGC	6296
QY	2045	aIIeArgThrAspSerIleuAspValGlnGIIyLeuGIIySerArgGluAspLeuLeuSerGI	2065
Db	6297	AATAAGACTGACTCTCTGGATGTGCAAGGCTGGGTAGCCGGAGAACACTGTTGTGAGA	6356
QY	2065	uValSerGIIyProSerCysProLeuThraIysSerSerSerPheTrpGIIyGIIysSerIle	2085
Db	6357	GGTGTGTGGGCTCTCTCCCTCTGACCCCGGTCTCACTCTTCTGGGGCGGAGTGCAGCAT	6416
QY	2085	eGlnValGlnGlnArgSerGIIyIleGlnSerIlyValSerIySHIsIleArgLeuProAl	2105
Db	6417	CGAGGTGACGACGCTTCCGGCATTCAGACAAAGCTCTTCAAGACACATCCGCTGCACGC	6476
QY	2105	aProCysProGIIyLeuGluProSerTrpAlaIyAspProProGluThraIysSerSerIe	2125
Db	6477	CCCTTGCCCAAGCCCTGGAACCCAGTGGGCCCAAGAACCTTCAAGAGACCAAGAGAGCTT	6536
QY	2125	uGluLeuAspThrGluLeuSerTrpIIsSerGIIyAspLeuLeuProSerSerGlnGluGII	2145
Db	6537	AGAGCTGACACGAGCTGAGCTGATTTACGAGAACCTCTCTCCACAGACCCAGAGAA	6596
QY	2145	uProLeuThraProAspLeuIyValCysTySerValGluThrArgIlnSerCysArgAR	2165
Db	6597	ACCCCTGTCCCAAGGAGACTGAAAGATGTCTCAAGTATAGACCCAGAGCTGTGAGGCG	6656
QY	2165	gARProGIIyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValIsSerCysLeuAs	2185

Db	6657	CAGGCTCGGCTCTGGCTTAATGAACAGCGAGACACTCCATTGCTGTCAAGTGTCTGGA	6716
Qy	2185	pSerGlySerGlnProArgLeuCySPSerProSerProSerLeuGlyGlyGlnProLeuG1	2205
Db	6717	CAGGGCTCCCAACCCCGGCTTAATGTCAAACCCCTCAAGCGCTGGGGGCCAACCTTTGG	6776
Qy	2205	YGIYProGlySerArgProIysIysIysLeuSerProProSerIleSerIleASPProP	2225
Db	6777	GGGTCCTGGAGGCGGGGCTTAAGAAATACTAGCCACCAAGTATCTCTTAAGACCCCC	6836
Qy	2225	oGluSerGlnGlySerArgProProCySerProGlyValCysLeuArgArgAlaPr	2245
Db	6837	GGAGAGCCAGAGGGCTCTCGGCCCATCATGACATCTGGTGTCTGCCTCAGAGAGAGGGCGCC	6896
Qy	2245	oAlaSerASPserIysASPProSerValSerSerProLeuASPserThrAlaIaSerPr	2265
Db	6897	GGCCAGAGACTCTAAGATCCCTCGGCTCCAGGCCCTTGACAGCAGCGGCTGCTTACC	6956
Qy	2265	oSerProIysIysASPThrLeuSerLeuSerGlyLeuSerSerASPProThraSPMeCAs	2285
Db	6957	CTCCCAAGAAAGACACGCTGAGTCTCTGGTTTGTCTTTCGACCCCAACAGACATGGA	7016
Qy	2285	pPro 2286	
Db	7017	CCCC 7020	

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RESULT 3
US-09-383-894-1
/ Sequence 1, Application US/09383894
/ Publication No. US20030125269A1
/ GENERAL INFORMATION:
/ APPLICANT: Li, Ming
/ TITLE OF INVENTION: T-Type Calcium Channel
/ FILE REFERENCE: 004 00191
/ CURRENT APPLICATION NUMBER: US/09/383,894
/ CURRENT FILING DATE: 1999-08-26
/ EARLIER APPLICATION NUMBER: US 60/098,004
/ EARLIER FILING DATE: 1998-08-26
/ EARLIER APPLICATION NUMBER: US 60/117,399
/ EARLIER FILING DATE: 1999-01-27
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 7129
/ TYPE: DNA
/ ORGANISM: Rattus sp.
US-09-383-894-1

Alignment Scores:
Pred. No.: 0 Length: 7129
Score: 11673.00 Matches: 2237
Percent Similarity: 97.77% Conservative: 1
Best Local Similarity: 97.73% Mismatches: 15
Query Match: 97.05% Indels: 36
DB: 10 Gaps: 2

US-09-611-257A-24 (1-2287) x US-09-383-894-1 (1-7129)

QY 34 TTTThTArGArGArGmEtCluArGAlaProArGSeRrArGaSpSeRProValAlaSeRrArG 53
Db 2 TGGACACGAGAGGAGCATGTGAGCGGCGCGCGAGGAGTCCGGACACACCCCGTAGCTTCACGC 61
QY 54 SeSeSeRrThThCyArProGlyProGlyVala-AlaGlyAla-GlySeRrThGluLysAsp 73
Db 62 AGGTCAACAGCACTGTCCGGGGGCGGGGGCCCGACAGGGGGCGGGGTCCAGCGAAAGGACC 121
QY 73 rGcLySeRrAlaSpSeRrGluAlaGluGlyLeuProTyProAlaLeuAlaProValValP 93
Db 122 CGGGCAGCGCGGACTCCAGCGCGAGGGGGCTGCGTACCGGGCCCTAGCCCCGGTGGTTT 181
QY 93 hePheTyLeuSeRrGluAspSeRrArProArGSeRrTyCyLeuArGTh-ValCyAsp 113

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[illegible]

QY	473	alYrrllleuArluysAlaAlaArgrleuAlaGlnValSerArgrAlalleglYala	493
Db	1332	TGTCATCTCTCCGAAAGACGCCGGAAGGCTGGCCGAGCTCTTAAGGCTATAGCGCTGC	1381
QY	493	rgAlaGlyleuLeuSerSerProValAlaAgsSerglYgIngluProGlnProSerglYs	513
Db	1382	GGGCTGGCTCTCAGCAGCCCAATGGCCGTATAGGAGGAGAGCCCAAGCCAGTGGCA	1441
QY	513	erCysThArGSerPthSarGrArGleuSerValHisHisleuValHisHisHisHisH	533
Db	1442	GCTGACCTCGCTCACACCGTGTCTGTCTGTCTGCACACACCTGTGTCCACACCATCACACC	1501
QY	533	lshIsHisHisleuGlylsleuGlylsleuGlylThleuArGValProArAlaSerProGlu	553
Db	1502	ACCATCACCACTTACCACTGGGTAATGGAGCGCTCAAGATTCCCCGGGGCCGACCAAGA	1561
QY	553	leglnaArGrArGrAlaAsnGlySerArGrArGleuLeuLeuProProSerSerThrProT	573
Db	1562	TCGAGGACGAGGAAATGCCAATGGGTCTGGCCGGCTCAATGCTTACACACACCCCTTACACCCA	1621
QY	573	hrProSerGlyGlyProProArGrGlylAlaGlnSerValHisSerPheThrHisAlaSPC	593
Db	1622	CTCCCTCTGGGGGGCCCTCCAGGGGTGGCGAGTGTGTATACAGAGTTCTACATCTACT	1681
QY	593	YshIsleuGluProValArGrCysGlnAlaProProProArGrCysProSerglAlaSerg	613
Db	1682	GCACTTGAGACCAAGTCCGTTGCCAGGACCCCTCCCAAGTGGCCCATTCGGAGGCATCTG	1741
QY	613	lyArGThValGlySerglylsVallyrProThrValHisThSerProProProGlu	633
Db	1742	GTAGGACTGTGGTGAATGGGAAAGGTGATCCCACTGTGCATATACAGCCCTTCCACAAAGA	1801
QY	633	leleuLYsArSlyArAlaleuValGluValAlaProSerProGlyProProThrleuThrs	653
Db	1802	TACTGAAAGATTAAGCACTATGTGAAGGTGGCCCCCAGCCCTGGGGCCCCCACTTACCA	1861
QY	653	erPheAsnIlleProProGlyProPheSerSerMetHislylsleuLeuGluThrGlnsert	673
Db	1862	GTTTCAACATCCCACTGGGGCCCTTACAGCTCATGCACAAGCTCTCGGAGACACAGATGA	1921
QY	673	hrGlyAlaCysHisSerSerCysAllylleSerSerProCysSerlyAlaAAspSerglyA	693
Db	1922	CGGGAGCTCGCATATGCTCTGCAAAATCTCCACCCCTTGTCTCCAAAGGCACAGTGAAG	1981
QY	693	laCysGlyProAspSerCysProProlyrCysAlaArGThnGlyAlaGlyluProGluSera	713
Db	1982	CCTGGGGCCCGAAGATTGCTCTTAATGTGGCCGACAGGACGAGGAGGACCAAGTCCG	2041
QY	713	laAspHisValMetProAspSerSerAspSerglAlaVallyrGluPheThrGlnAspAlaG	733
Db	2042	CTGACCAATGTATGCTGTACTCAACACAGAGCGCTGTATGATTTCAACAGGACGCTC	2101
QY	733	lnhiIsSerAspLeuArGrpProHisSerArGrArGrGlnArGSerleuGlyProAspA	753
Db	2102	AGCACAGTGAAGCTCGGGATCCCAACAGCCGGCGGCACAGCGGAGGCTGGGGCCAGATG	2161
QY	753	laGluProSerSerValleuAlaPheArGrArGleuLleCysAspThrPheArGrlylsIleV	773
Db	2162	CAGAGCCATGATTCGTGTGGCTTTCGGAAGCTGTGATCTGTGACACATTCGGAAAGATTG	2221
QY	773	AlaAspSerlyrTyPheGlyArGrGlylIleMetIleAlalleuValAsnThrleuSerm	793
Db	2222	TAGTATGCAATACTTGTGGCCGGGAGATCATGATCCGATCTGTGATATCATCTAGCA	2281
QY	793	etGlylleglyTyHisGlnGlnProGluGluLeuThrAsnAlaGluGluIleSeraAsnI	813
Db	2282	TGGGATGAGTATCACAGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAATCAGCAACA	2341
QY	813	leValPheThrSerleuPheAlaGluGluMetleuLeuIysleuLeuValTyrrGlyProp	833
Db	2342	TGGCTTACACAGGCTTTCGCTTGGAGATGCTGTGAATCTGCTTGTCTACAGGTCTCT	2401

QY	833	hegLYrTtLeuYaenProtyrAsnIlePheAspGlyValIleValValIleSerValT	853
Db	2402	TTGGGTACATTAAAGATCCCTCAACAACATCTTGAATGGTCAATGGTCAATCGATGT	2461
QY	853	TPGUILleValGlyGlnGlnGlyGlyGlyLeuSerValIleuArgThrPheArgLeuMetA	873
Db	2462	GCGAGATTGTGGCCAGCAGGGAGGTGGCTGTGGTCTCCGAGACTTCCGCTGTATGC	2521
QY	873	rgValIleuYLeuValArgPheIleuProAlaLeuGlnArgIleuValIleuMetL	893
Db	2522	GGGTGCTGAAGCTGGTGGCTTCCGTCCGGCCCTGCAGCGCCACACTCGTGGTGTCAATGA	2581
QY	893	ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS	913
Db	2582	AGACCAATGGACAAGTGGCCACTTTCGACAGCTCCATACCTGTTCATCTTCATCTTCA	2641
QY	913	erIleLeuGlyMetHisLeuPheGlyCysIysPheAlaSerGlyAlaArgAspGlyAspThrL	933
Db	2642	GCATCTGGGCAATGCATCTCTTTGGTTTCAGAGTTCCGACTCTGAACGGAGATGGGACACGT	2701
QY	933	euproAspArgIysAsnPheAspSerLeuLeuThrAlaIleValThrValPheGlnIleL	953
Db	2702	TGCCAGACCGGAAGATTTCGACTCCCGTCTGGGCGCATCGTCACTGCTTTCAATTC	2761
QY	953	euthrGlnGluAspTPraAsnYsValIeuthrAsnGlyMetAlaSerThrsSerThrPa	973
Db	2762	TGACTCAGAAAGACAGTAATAAGCTCTTCAACAGGATGGCCCTCCACATCGTCTTGGG	2821
QY	973	laAlaLeuThrPheIleAlaLeuMetThrPheGlyAsnThrValLeuPheAsnLeuY	993
Db	2822	CTGCTCTTACTTCATCGCCCTCATGACTTTTGGCACTATGTGCTCTTTAAGCTGCTGG	2881
QY	993	alAlaIleLeuValGluGlyPheGlnAlaGlu-----GlyAspAlaThrIysSerG	1003
Db	2882	TGGCATTTCTGTGTGAAGATTCCAGCAGAGAAATCGCAACGGGAATCGAGTG	2941
QY	1004	-----GlyAspAlaThrIysSerG	1010
Db	2942	GACAGTTAAGCTGTATTCAGCTGCCTCTCAACTCAGAGGGAGAGATGCCACCAAGCTCG	3001
QY	1010	IuSerGluProAspPheSerProSerValaAspGlyAspArgIysArgIysArgL	1030
Db	3002	AGTCAGACCTGATTTCTTTTGGCCAGATGTGAGGTGAGTGGAGACGAAGAAGAGCGCT	3061
QY	1030	euaAlaLeuValAlaLeuGlyGlnHisAlaGluLeuArgIysSerLeuLeuProIleuI	1050
Db	3062	TGGCCCTGTGGCTTTGGAGAGACACGGGAACACTAGAAAGAGCTTTTGCACCCCTCA	3121
QY	1050	IeIleHisThrAlaAlaThrProMetSerHisProIysSerSerSerThrGlyValGlyG	1070
Db	3122	TCATCCATAACGGCTGCGACACCAATGTCACTAACCCAAAGAGCTCCAGCACAAGTGTGGGGG	3181
QY	1070	IuaIaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaA	1090
Db	3182	AAGCACTGGAGCTGTGCTCTGACGTACAGAGAGAGTGGGTCGGCTGAGCTGAGAGCTG	3241
QY	1090	IaHisHisGluMetCysCysProProSerAlaArgSerSerProHisSerProThrPseRa	1110
Db	3242	CCCAACCAATGAATGAATCTCCGCCAATATGCCCCGAGAGTCCCCGACACAGTCCCTGGAGTG	3301
QY	1110	IaAlaSerSerThrPThrSerArgArgSerSerSerArgAsnSerLeuGlyArgAlaProSerL	1130
Db	3302	CGGCAGACAGCTGGACACAGAGCGCTCCAGACAGGAACAGCTGGGGCCGGGCCCCCAAGCC	3361
QY	1130	eulyArgArgSerProSerGlyIuArgArgSerLeuLeuSerGlyGlnIlyGlnIus	1150
Db	3362	TAAACCGAGAGGCCCGGAGCGGGAGCGAGAGTCCCTGTCTGTGAAGAGGACAGGAGGA	3421
QY	1150	erGlnAspGlnGluIuSerSerGluIuAspArgAlaSerProAlaGlySerAspHisA	1170
Db	3422	GTCAGAGATGAGGAGAAAGTTCAGAAAGAGACCGGGCCAGCCCAAGGACGTAACTATC	3481
QY	1170	rgHisArgGlySerLeuGluArgGluAlaYsSerSerPheAspLeuProAspThrLeuG	1190

Db	3482	GCACAGGGGTTCTTGGAACTGAGGCCAAGAGTTCTTTGACTGCTGCACACTTGC	3541
Oy	1190	InValProG1LeuH1sArGThra1aSerG1VaRgSerSer1aSerG1uH1eG1naSpC	1210
Db	3542	AGGTGGCGGGCTGCACTGGCAAGCCAGCGCGGAGACTCTGCTCTGACACCAAACT	3601
Oy	1210	yBaenG1yLySerAlaSerG1VaRgLeuAlaArGThraLeuArGThraAspAspProG1uL	1230
Db	3602	GTATGGCAAGTCGGCTTCAGGGGGTTGGCCCGCACCTCGAGAGATGATGACCCCAAC	3661
Oy	1230	euaSpG1YaAPAspAspAsnApG1uG1Yan1uSeuSerLySG1yG1uArG1eG1na1aT	1250
Db	3662	TGATGGGGATGATGACAAATGATGAGGAAATCTGACCAAGGGGAACGATCAAGACT	3721
Oy	1250	rPValaRgSerArGLeuProAlaCySyaRgG1uArGaSPSerTrpSerAlaTr1LeP	1270
Db	3722	GGGTCAAGATCCGGCTTCCTGCTGTTGCCAGAGCGAGATTCCTGGTCGACCTATCT	3781
Oy	1270	heP-roG1nSerArGPhaRgLeuCySh1aRg1e1IethR1uLyMeRhea	1290
Db	3782	TTCTCTCTCAAGTCMAAGTTTGCTCTCTGTGTCAACCGATCAATCACCAAGAATGTTTG	3841
Oy	1290	spH1sVal1LeuVal1Ie1IephLeuSnCyS1IeTr1IeAlaMeG1uArGProl	1310
Db	3842	ACCAATGGTCTCTGTATCATCTTCTTCACTGTATCACTATGATGAGCGCCCA	3901
Oy	1310	ys1IeaSPProH1aSerAlaG1uArG1IephLeuThraLeuSerAsnTr1IephThra	1330
Db	3902	AAATTTGACCCCAAGCGCTGAGGAGCATTTCTCGAACCTCCCAATCATCTTTCACGG	3961
Oy	1330	1aVal1PheLeuAlaG1uMeRThraLyS1aVala1a1e1uG1yTrpCyPheG1yG1uG	1350
Db	3962	CAGCTTCTTACGCTGAATGACAGTGAAGGTGGGACCTGGCTGTGCTTGGGGAGC	4021
Oy	1350	1na1aTr1LeuArGSeSerTrAsnVal1euaSpG1yLeuLeuVal1eul1eSerVal1	1370
Db	4022	AGGCTACCTGGCAGACGCTGGATGTGCTGGACGGCTGTGCTGTACTCTCGTCA	4081
Oy	1370	1eaSP1IeLeuVal1SerMeTValSerAspSerG1yThrLyS1eLeuG1yMeRLeuArGy	1390
Db	4082	TCGACATCTCGTCTCATAGTCTCCGACAGCGGCACCAAGATCTTGGCATGTGAGGG	4141
Oy	1390	a1LeuArGLeuLeuArGThraLeuArPro1euaRgVal11eSerArG1aG1nG1yLeuL	1410
Db	4142	TGCTGGCGGCTGTGGGACCTGTGCTCACTAGGGTCAATCAGCCGGGCCAGGGACGTGA	4201
Oy	1410	ys1LeuVal1Val1G1uThraLeuMeSerSer1euaRySProl1eG1Yan1I1eVal1a1IeC	1430
Db	4202	AGCTGGTGTGAGAACCTGTGATGTCAATCCCTCAAAACCATTTGGCAAAATGTGGTCAATTT	4261
Oy	1430	ysCySa1aPhePhe1e1IephG1y1IeLeuG1yVal1G1nLeuPheLyG1yLySPheP	1450
Db	4262	GCTGTGCTTCTTATCATTTTGGATTTCTCGGGGTGGAGCTTTCMAAGGGAAGTTCT	4321
Oy	1450	heVal1CySG1nG1yG1uAsPThraRgaSn1IethRasnLyS1eRAspCySa1aG1uLaS	1470
Db	4322	TCGTGTGTCAGGGTGAGAGACCCAGGAACATCTAACAATCCGACTGGCTGAGGCCCA	4381
Oy	1470	eRyTrArGTrPValArGh1uLySerYTrAsnPhaSPanLeuG1yG1nAlaLeuMeSerL	1490
Db	4382	GCTACCAATGGGTCTGGCACAAAGTGAACATTGCAACTGGGCCAGAGCTCTGATGTCC	4441
Oy	1490	eupheVal1LeuAlaSerLyAspG1yTrPValAsp1IeMeTrYzAspG1yLeuAspAlaV	1510
Db	4442	TGTTTGTGCTGGCTCCAAAGATGTGGGTGTGACATCATGTATGATGGCTGTGATCTGT	4501
Oy	1510	a1G1yValaSPG1nG1nPro1IeMeRAsnH1sAsnProTrpMeLeuLeuYrPhe1Ies	1530
Db	4502	TGGTGTGTGAATCAGCAAGCCATCATGAACCAACCCCTGGATGTCTGTATCTTCACTCT	4561
Oy	1530	ePheLeuLeu1IeVala1aPhePheVal1euaSnMeTPhaValG1yVala1a1aG1uA	1550

D	4562	CCTTCCTCCCTCAATCGCGCTTCCTTGTGCTGAACAATGTTTGTGGCGGTGGTGGAGA	4621
Q	1550	anphehislysvyavrglnihisglnlglnlglnlualaargrargrlnlglnlylva	1570
D	4622	ACTTCCATAAGTCAAGACAGCACAGAGAGAGAGAGCGGCGGTGAGAGAAC	4681
Q	1570	rgleuargargleuqlulvlylvaarg-----	1579
D	4682	GACTACGAGGCGTGGAGAAAAGAGAAATCTAAATGTTGACGATGTAATGCTTCG	4741
Q	1580	--serlysgulysglnmetalaaglualaglnlylsyaproytytyrseraptyrsera	1599
D	4742	GCAAGTCACGACCGACCGCTGCTCAAGAACCCAGTGCAGAGCCCTTAATCTGACTGAC	4801
Q	1599	rgpheargleuleuvalhishileuCythrserhistryleuapleupheillethrg	1619
D	4802	GATTCGGCGCTCTTGTTCACCACTGTGTACGAGCACTACCTGGACCTTTCATCACTG	4861
Q	1619	lyvalilleglyleuasnvalialthmetalameluhistyrnglnlnprognille	1639
D	4862	GTCACATCGGCGTGAAGCTGTGCTACATAGGCCATGAGACATTACAGACGCCCGAGATCC	4921
Q	1639	eulaprglualaleuylsileCyasnTyrllephethrvalillephevaliphegiuserv	1659
D	4922	TGACGAGGCTCTGAMAGATCTGCATTTCATCTTTACCTCATCTTTGTCTTTGAGTCAG	4981
Q	1659	alpheylsleuvalalaphelaphearghrphhegnlnasphrgttrpaenglnleua	1679
D	4982	TTTTCAAACTTGtggcctttggccttcggcgtttcttccagagacagtggaacagctgg	5041
Q	1679	spleualalilevallleuuserillemeqlyllethrleuglnlglnileglnvalant	1699
D	5042	ACCGGCTAATGTGCTTCTGTCCATCATGGGCATCACACTGAGAGAGATTTGAGTCATG	5101
Q	1699	euserleuproilleasnprothrillelphrgillemearyvalleuargillealaaryv	1719
D	5102	CTTGCGTGCACATACCCCAACATCCGATTCGATCAGAGGCTCCCGCATGCTCCAG	5161
Q	1719	alleuylsleuleuylsmetalavalglymearyghaleuuhisthrvalmeqina	1739
D	5162	TTCTGAAAGCTGTGGAATAGTGGCTGTGGGCATGCGGGCACGTGTCGACAGGTATGACAG	5221
Q	1739	laileuproglnvalglyasnleuglyleuleuphemeteuleuphepellepaelaah	1759
D	5222	CCCTGCCCGAGTGGGAGAACCTGGGACTTCTCTTCATGTATGTATTTTCATCTTTGACG	5281
Q	1759	laileuqlvvaligluelphegllyaspleuglucyabaprglunthrhisprocyaglunlyl	1779
D	5282	CTCTGGGCGTGGAGCTTTTGGAGACCTGGAGTGTATGAGACACCTCTGTGAGGGCT	5341
Q	1779	euglyacghisalatthPheArgAsnphelglymetalaPheleuthrleupheargvals	1799
D	5342	TGGGTCCGCATGCCACTTTAGGAACCTTGTGTATGGCTTTTCGACCCTTCCAGTCT	5401
Q	1799	erthrnglyaspaanttrpansnglyllemetlyaspproserargapcyasaprglnlus	1819
D	5402	CCACTGGGTGAACAATGGTAATGTATTAAGAGACACCTCCGGGACTGTGACCAAGAGT	5461
Q	1819	erthrCytyrtaenthrvaliliseserproilleyrthrevaliserPheValleuthrvalag	1839
D	5462	CCACCTCTACMACACTGTATCTCCCTCATCTACTTGTGTCTTCGTGTCGACGCGCC	5521
Q	1839	lnphevalleuvalasnvaliallealavallemuetyshislauglnuserasn	1859
D	5522	AGTTTGTGCTGGTCAAGCTGTCTAGCTGTCTGTATGAAGCACTCTGGAAGAAAGCACA	5581
Q	1859	ysglualalyeglulualagluuenglualagluuengluleuglnuetyrthrleus	1879
D	5582	AAAGGCGCAAGAGAGAGCGAGCTCGAGGCGGAGCTGAGAGTGAAGAAGCCCTCA	5641
Q	1879	erproglnprohisaserProleuglyserProphleuthrpproglvalaliglnlyvala	1899
D	5642	GCCCGACAGCCCATCCCGCTGGGACGCCCTTCTCTGTGCCCCGGGAGTGAAGGGTCTCA	5701
Q	1899	anserThrAspserProlyspProglvalaProhisethrThrAlahileileglvalaahlas	1919
D	5702	ACAGTCTGACAGCCCTTAAGCTGGGGCTTCACACACCACTGCCACATTTGAGACAGCT	5761
Q	1919	erGlyPheSerleuqlunhisprothrmetvalprohisproglunlglnvalprovalprol	1939
D	5762	CGGGCTTCTCCCTTAGACACCCCAAGATGATACCCACCCGAGAGAGGTGCAGTCCCC	5821
Q	1939	euglyProAspPleuLeuthrValArgdlysserglyvalaserArgThrHisSerleuProa	1959
D	5822	TAGACACAACTGCTGACTGTGAGGAAGTCTGTGTGTACGGCGGACCACTCTGCGCA	5881
Q	1959	snasSerTyrmetyCyasrghansglsyethrvalagluarsSerleuGlyhisarglylT	1979
D	5882	ATGACAGCTACATGTGCGCAATGGAGACACTGCTGAGAGATCCTTAGACACAGGGGCT	5941
Q	1979	proglyeupProlysalaglnserGlyserilleleuservalhisSerGlnProalaaPT	1999
D	5942	GGGGGCTCCCAAAAGCCAGTCAAGCTCATCTTGTCCGTTCATCTCCAAACAGACAGCA	6001
Q	1999	hserCyallleuglnleupProlysaapvalhislyrTleuenglnprohisgllyalP	2019
D	6002	CAAGCTGATCTTACAGCTTCCCAAGATGTGACTATCTGCTCCAGCTCATATGGGACCC	6061
Q	2019	rothrTtrpqlvalalleprolyslleupPropproproglvalargserProleuhalaglnarp	2039
D	6062	CCACCTGGGGCGGCATCCCTTAACATACCCCACTGGCGGCTCCCTCTGCTGACAGGC	6121
Q	2039	roleuargarglnalalaleaqrThrAspSerleuaspvalaglnlyleuGlysera	2059
D	6122	CTTTCAGGGCGCAAGGACGACATAGAGACTGACTCCTCGATGTGACAGGCTGGGTAGCC	6181
Q	2059	rglnaspleuaseuerglnvalaserGlyproserCyaproleuthrargserSerp	2079
D	6182	GGGAGACCTGTGTTCAGAGGTGAGTGGGCTCTCGCTCTGACCCGGGTCCATCATCT	6241
Q	2079	hettrpqllylserserilleglnvalglnlnargserGlylileglnserlyvalserl	2099
D	6242	TCTGGGGCGGCTCGAGCATCCAGTGCAGAGCTTCCGAGATCCAGGCAAAAGTCTCA	6301
Q	2099	yshisilleargleuproalpaProcyspProglyleuqluproserTtrpalaalsaspprop	2119
D	6302	AGCACAATCCGCTCGACGAGCCCTTGTCCAGAGCTGGAACCAAGCTGGGCGAAGACCTC	6361
Q	2119	roglunthrargserSerleuenglnleuasnprothrlnleuSerTtrpileserglyaspleu	2139
D	6362	CAGAGACAGAGAGCGTTAGAGCTGAGACAGAGACTAGCTGATTTCAAGAGACTCC	6421
Q	2139	euproserSerGlnlglnluproleupheproargAspleuylslyCytyrtyrserValg	2159
D	6422	TTCCCAAGCAGCAAGAGAAACCCCTGTCCCAAGGAGCTTAAGAAAGTCTACAGTATG	6481
Q	2159	lnthrlnserCyasargagargpProgllyphetrrpleuaspGlnlnarghrghisserl	2179
D	6482	AGACCCAGAGCTGCAGGCGCAGGCGCTGGGTCTGTGTAAGTAAGACGCGAGACACTCA	6541
Q	2179	lealavalserCyseuAspSerGlyserGlnProargleuCyaproserProserSerl	2199
D	6542	TTGCTGTAGCTGTCTGAGACAGCGGCTCCCAACCCCGCTATGTCTCAAGCCCTCAAGCC	6601
Q	2199	euglyglinProleuglyglyProglyserargProlyalylsleuSerPropos	2219
D	6602	TTCGGGGGCNAACCTTGGGGGTCTCTGGGAGCGCGCTTAAGAAAAAACTCAGCCACCCA	6661
Q	2219	erlleserilleasppropprogluserglnlyserArgProproCyserSerProglyvalC	2239
D	6662	GTAATCTTATAGACCCCGCGAGACCGAGGGCTCTCGGCGCCCAATGACATCTGATCT	6721
Q	2239	ysleuargargargalapaProalaserAspSerlysaapProserValserSerProleua	2259
D	6722	GCTTCAGAGAGAGGGCGGCGCATGATCTTAAGATCCCTCGGTCTCCAGGCCCTTG	6781









Db 4055 GCAACCTGAGCAAAAGGGGAACGGGATCCGGCGTGGATCCGAGCCGACCTCCCTGCTGCT 4114  
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Qy 1299 euAnCySIlleThrTlIeAlMeRGluArGProLySIlleAsPProHIsSeRAlAGluArGt 1319  
Db 4235 TTAACGTGCATCACCATGCGCATGGAGCGCCCAAAATTGACCCCAcAGCGCTGAAGCGCA 4294  
Qy 1319 lAePheLeuThrIleuSeArAntTyTlIePheThrAlAValPHeLMeAlAGluMeThThValL 1339  
Db 4295 TCTTCCTGACCCCTTCCAATTACATCTTCAcCGACGCTTTCGCGGAATACAGTGA 4354  
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Db 4595 CACTGAACCCATCGGCACTGTGTACTCATCTGTGCTTCCTTCATCATTTTCGGCA 4654  
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Db 4655 TCTTGGGGGTGCAAGCTCTTCAAGGAAAGTTTTCTGTGCCAGGGGAGAGATACCGGA 4714  
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Qy 1628 eCAlaMeRGlnHIsIyRGInGInProGlnIleIleuAsPGLuAlaLeuYsIlleCyAsAnt 1648  
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QY 1928 ----- MetValProHisProGluGluVal 1935  
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Db 6455 TGCCA-----GGAACAGACTTACTGACTGTGGGAACTGTGGGGTCCGGAAGC 6505  
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? Sequence 120, Application US/10786148  
? Publication No. US20050191634A1  
? GENERAL INFORMATION:  
? APPLICANT: LIN, SHIU-RU  
? APPLICANT: MANG, JAW-YUAN  
? TITLE OF INVENTION: GENES FOR DIAGNOSING COLORECTAL CANCER  
? FILE REFERENCE: BHT/3230-85  
? CURRENT APPLICATION NUMBER: US/10/786,148  
? NUMBER OF SEQ ID NOS: 142  
? SOFTWARE: PatentIn version 3.2  
? SEQ ID NO 120  
? LENGTH: 7825  
? TYPE: DNA  
? ORGANISM: Homo sapiens  
US-10-786-148-120  
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Score: 10963.50 Matches: 2128  
Percent Similarity: 89.56% Conservative: 34  
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Db 1841 CCGTCCACCACTGGGTGACACCAACCAACCATCAACCACTGAGCAATG 1900  
Qy 542 1YThrLeuAArgVal1ProAArgAla1SerProG1u11eG1AAspAArgAAsp11AaenG1YSerA 562  
Db 1901 GGAAGCTTCAAGGGCCCCCGGCGCAGCCGAGATCCAGACAGGAGATGCAATGGGATCCC 1960  
Qy 562 rGArgLeuMeTLeuProProPheSerThrProThrProSerG1YG1YProProAArg1Y 582  
Db 1961 GCGGCTCATGTGTGCACCACTTCGAGCGCTGCCCTCTCCGGGGCCCCCTGTGGGGG 2020  
Qy 582 1aG1uSerVal1H1sSerPheTyTyrH1sAlaAspCySPH1sLeuG1uProValAArgYSG1A 602  
Db 2021 CAGAGCTGTGCACAGCTTCTTACATGCCAGTGCACCTTAAAGCAGATCCCTGTGCAGG 2080  
Qy 602 1AProProProAArgCySPProSerG1uAlaSerG1YArgThrValG1YSerG1YLyValT 622  
Db 2081 CGGCCCTTCCAGGTCCCATCTGAGGCAATCGGAGCACTGTGGCGACGGGAAAGTGT 2140  
Qy 622 YrProThrVal1sPThrSerProProProG1u11eLeuLySPAspYsAlaLeuValG1uY 642  
Db 2141 ATCCACCGTGCACACACACCTTCCACCGGAGACGCTGAAGAGAAAGCATTAGTAAAG 2200  
Qy 642 a1A1AProSerProG1YProProThrLeuThrSerPheAAsn11eProProG1YProPheS 662  
Db 2201 TGGCTGCCAGCTCTGGGGCCCCCAACCTTCAACAGCTTCAACATCCACCCGGGCTTACA 2260  
Qy 662 eTserMeT11s1YsLeuLeuG1uThnG1nSerThG1YAlaCySPH1sSerSerCySP1Ys1 682  
Db 2261 GCTCCATGACAAAGCTGTGGAGACACAGATACAGTACGTGCTGCCAAACCTTTGCMAA 2320  
Qy 682 1eSerSerProCySPeSerLySAlaAspSerG1YAlaCySPG1YProAAspSerCySPProTyT 702  
Db 2321 TCTCCAGCCCTTGTCTTGAAGAAGACAGATGAGCGCTGTGTCAAGACAGCTGCCCTACT 2380  
Qy 702 YsAlaArgThrG1YalG1Y1uProG1uSerAlaAspH1sVal1MeTProAAspSerAAs 722  
Db 2381 GTGCCCGGCGCGGGGAGGAGTGAGTGCCTGCCCAACGTGAATGTCTGTACTGAGAA 2440  
Qy 722 eTGLuAlaVal1TyTg1uPheThnG1nAAspAlaG1H1sSerAAspLeuAArgAAspProH1s 742  
Db 2441 GCGAGGACGATTATGATGTTCACACAGATGCCAGACAGCAACCTTCCGGAAACCCCA 2500  
Qy 742 eTArGArgArgG1nAArgSerLeuG1YProAAspAlaG1uProSerSerVal1LeuAlaPheT 762  
Db 2501 GC---CGGCGGCAACGGAAGCTGTGGCCAGATGCAAGGCCAGCTGTGTGCTGGCTTCT 2557  
Qy 762 rPArgLeu11eCySPArThrPheAArgLyS11eValAAspSerLySP1ePheG1YArgG1Y 782  
Db 2558 GGAAGCTTAAATCTGTGACACCTTCCGAAAGATTGTGACAGCAAGTACTTGTGGCGGGGAA 2617  
Qy 782 1eMeT11eAla11eLeuVal1AenThrLeuSerMeTArg11eG1uTyTyrH1sG1uG1nProG 802  
Db 2618 TCATGTATCGGCATCTGTGTCAACACTCAGATGGGCAATCGAAATCCACAGACACCCG 2677  
Qy 802 1uG1uLeuThrAAsnAlaLeuG1u11eSerAAsn11eVal1PheThrSerLeuPheAlaLeuG 822  
Db 2678 AGAAGCTTACCAACGCGCTTGAATCAGCAACATGCTTTCACACAGCTCTTGGCCCTGG 2737  
Qy 822 1uMeTLeuLeuLySLeuLeuVal1TyTg1YProPheG1YTyT11eLyAAsnProTyTyrAAsn 842  
Db 2738 AGATGCTGTGAAGCTGTGTGTATGTCTCTTGGCTTACATCAAGAAATCCCTTAAACA 2797  
Qy 842 1ePheAAspG1YAla11eVal11eSerVal1TProG1u11eValG1YnG1nG1nG1Y 862  
Db 2798 TCTTCATAGGTGTCAATGTGTATGTATCAGGTGTGGAGATCGTGGCCACAGGGGGGGG 2857  
Qy 862 1YLeuSerVal1LeuAArgThrPheAArgLeuMeTArG1YAlaLeuLySLeuValAArgPheLeuP 882  
Db 2858 GCGTGTGGGTGTGCGGACCTTCCGCTGATGTGTGTGTAAGCTGTGTGCGCTTCTCTG 2917  
Qy 882 roAlaLeuG1nAArgG1nLeuVal1Val1LeuMeT1YsThrMeTAspAAsnVal1A1aThrPheC 902  
Db 2918 CGGCGCTGACGCGGCGAGCTGTGTGTCTCATGAAGACATGAGCAACGTGGCCACCTTCT 2977

Qy 902 ybMetLeuMeLeuPheIIePheSerIIeLeuGIyMeHisLeuPheGIyC 922  
Db 2978 GCATGCGCTTATGCTCTTCATCTTCATCTTCAGCATCTGGGCGATCATCTCTCGGCT 3037  
Qy 922 ybLybPheIIaSerGIuArGApGIyAsPThrLeuProAsPArGIyLyAsnPheAsPserL 942  
Db 3038 GCAGATTGCTCTGAGCGGGATGGGACACCTGCGACAGCGGAGAAATTTTACTCTCT 3097  
Qy 942 eueuTrrAlaIleValIThrValPheGInIIeLeuThrGInGIuAsPTrAsnLyValL 962  
Db 3098 TGCTCTGGCCATGTCACTGTCTTCATGATCTTCAGCCAGAGAGACTGGAACAATGCTC 3157  
Qy 962 euryArangIyMeAlaSerThSerSerTrpAlaAlaLeuTyrrPheIIeAlaLeuMet 982  
Db 3158 TCTTCAATGGATGGCTCCAGCTGCTCTGGCGGCTTTATTTTCATTTGCTCTCATGA 3217  
Qy 982 hrPheGIyAsnTyrrValLeuPheAsnLeuValAlaIIeLeuValGIuGIyPheGIna 1002  
Db 3218 CTTTCGGCACTACGTGCTCTTCATATTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3277  
Qy 1002 laGIu----- 1003  
Db 3278 CGGAGAAATCGAACAACGGGAAGATCGAGTGCAGCTTAAGCTGATTCAGCTGCTGCT 3337  
Qy 1004 -----GIyAsPAlaThrIySerGIuSerGIuProAsPhePheSerProS 1019  
Db 3338 TCGATCCCGAGGGGGAGATGCCAACAAGTCCGATCGAGAGCCCGATTTCTTCACCCA 3397  
Qy 1019 eValAsPGLyAsPGLyAsPArGIyLybArGIyLeuAlaLeuValAlaLeuGIyGIuHis 1039  
Db 3398 GCCGTGATGTGATGGGACAGGAAGAGTCTTGGCTTGGTGTCTTGGTGAAGAAGCA 3457  
Qy 1039 laGIuLeuArGIySerLeuLeuProProLeuIIeIIeIIeThrAlaAlaThrPromets 1059  
Db 3458 CGGAGCTCGGAAGAGCTGCTGCTGCTGCTTCATCATCATCAACGGCGCCACACCATGT 3517  
Qy 1059 eThAsProLySerSerSerThrGIyValGIyAlaAlaLeuGIySerGIySerArGIy 1079  
Db 3518 CGCTGCCAAGACAGCACAGCAAGGCGCTGGGAGGCGCTGCGCTGCTGCGCGCA 3577  
Qy 1079 hrSerSerSerGIySerAlaGIuProGIyAlaAlaHisIIeGIuMetLyCySProProS 1099  
Db 3578 CCACAGACGAGCGGTGCGCAGAGCTGGGGCGGCT---CACAGATGAAGTACCGGCCA 3634  
Qy 1099 eAlaArGIySerProIIeSerProTrpSerAlaAlaSerSerTrpThSerArGIyS 1119  
Db 3635 GCGCCCGAGCTCTCCGACAGCCCTGAGGCGTGCAGAGAGCTGAGCCAGCAGGCGCT 3694  
Qy 1119 eSerArGIyAsnSerLeuGIyArGIyAlaProSerLeuLyAsrGIySerProSerGIy 1139  
Db 3695 CCAAGCGGAACAGCTCGGCGGTGCACCCAGCTGTAAAGCGGAGAACCCCAAGTGAAGC 3754  
Qy 1139 rGIyArGIySerLeuLeuSerGIyGIuGIyGInGIySerGIyAsPGLyGIuGIySerSerGIy 1159  
Db 3755 GCGGCTCTCTTGTGCGGAGAGGCGCAGAGAGCAGAGATGAAGAGAGAGCTCAGAG 3814  
Qy 1159 luAsPArGIyAlaSerProIIeGIySerAsPArGIySArGIyArGIySerLeuGIyArGIy 1179  
Db 3815 AGGAGCGGGCGAGCCCTGCGGAGAGTGCATCGCACAGGGGCTCTCGAGCGGGAGG 3874  
Qy 1179 laLySerSerPheAsPLeuProAsPThrLeuGInValProGIyLeuHisArGIyThraIAs 1199  
Db 3875 CCAAGATGCTCTTGAACCTGCGACAGACACATGCAAGTGCAGGGCTGCATCGCATGCA 3934  
Qy 1199 eRGIyArGIySerSerAlaSerGIyHisIIeGInAsPArGIyLySerAlaSerGIyArGIy 1219  
Db 3935 GTGGCGAGGGGTCTCTCTGAGCACAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3994  
Qy 1219 euaIaArGIyThrLeuArGIyThrAsPArGIyProGInLeuAsPGLyAsPAsPAsPAsP 1239  
Db 3995 TGCGCGGCGCTGCGGCTGATGACCCCGCCTGATGGGATGACCGCCATGACGAGG 4054

Qy 1239 lyAsnLeuSerLySGIyGIuArGIyIleGInAlaTrpValArGIySerArGIyLeuProAlaCyS 1259  
Db 4055 GCACCTGAGCAAGAGGGGAACGGGATCGCGCTGATCCAGGCCAGCTCTCGCTGCT 4114  
Qy 1259 ybArGIyArGIyAsPserTrpSerAlaTyrrIlePheProProGInSerArGIyPheArGIy 1279  
Db 4115 GCGTCAGAGCAAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4174  
Qy 1279 eucYshIsArGIyIleThrHisLyMetPheAsPArGIyValIleLeuValIleIlePhe 1299  
Db 4175 TGATGACCGGATCATCACCAAGATGTTTCAACAGCGGCTCTTGTATCATCTTCTC 4234  
Qy 1299 eueuCyshIeThrIIeAlaMerGIuArGIyProLySIIeAsPProIIeSerAlaGIuArGIy 1319  
Db 4235 TTAACGTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4294  
Qy 1319 lePheLeuThrLeuSerAsnTyrrIlePheThraIaValPheLeuAlaGIuMetThrVal 1339  
Db 4295 TCTTCTGACCTCTCTCAATTATCATCTTCACCGAGCTTTCTGGTGAATGACATGA 4354  
Qy 1339 ybValValAlaLeuGIyTyrrCySbPheGIyGIuGIyAlaTyrrLeuArGIySerSer 1359  
Db 4355 AGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4414  
Qy 1359 alLeuAsPGLyLeuLeuValLeuIIeSerValIIeAsPIIeLeuValSerMetValSer 1379  
Db 4415 TGCTGACGGGCTGTGTGTCTCATCTCCATCATCATCATCTGATGATGATGATGATGAT 4474  
Qy 1379 bPserGIyThrLySIIeLeuGIyMetLeuArGIyValLeuArGIyLeuArGIyThrLeuArGIy 1399  
Db 4475 ACAGCGGACCAAGATCTCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 4534  
Qy 1399 roLeuArGIyAlaIleSerArGIyAlaGInGIyLeuLySLeuValAlaGIuThrLeuMet 1419  
Db 4535 CGCTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4594  
Qy 1419 eRLeuLyProIIeGIyAsnIIeValIleCySAsPAlaPhePheIIeIlePheGIy 1439  
Db 4595 CACTGAACCCATCGGAACATGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4654  
Qy 1439 leLeuGIyValGInLeuPheLybGIyLySbPhePheValCySGInGIyGIuAsPThrArGIy 1459  
Db 4655 TCTTGGGGGTGACCTCTTCAAGAGGAATTTTCGTGTGCGACAGGAGGATGACAGGA 4714  
Qy 1459 snIeThrAsnLySAsPArGIyAlaGIuAsPArGIyArGIyArGIyArGIyArGIyArGIy 1479  
Db 4715 ACATCACCAATTAATCGGATGCTGCGAGGCAAGTACCGGTGAGTCCGGACAAATGA 4774  
Qy 1479 snPheAsPAsnLeuGIyGInAlaLeuMetSerLeuPheValIleuAlaSerLySAsPGLy 1499  
Db 4775 ACTTTGACAACTTGGCGAGGCTGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4834  
Qy 1499 rPValAsPIIeMetTyrrAsPGLyLeuAsPAlaValaGIyValaAsPGLyGInProIIeMe 1519  
Db 4835 GGGTGCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4894  
Qy 1519 snHisAsnProTrpMetLeuLeuTyrrPheIIeSerPheLeuLeuIIeValaIaPhePhe 1539  
Db 4895 ACCCAACCCCTGATGCTGTGATCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4954  
Qy 1539 alLeuAsnMetPheValGIyValaValaGIuAsnPheHisLyCySArGIyGInHisIIeG 1559  
Db 4955 TCTTGAACATGTTGT 5014  
Qy 1559 luGIuGIuGIuAlaArGIyArGIyGIuGIyArGIyArGIyArGIyArGIyArGIyArGIy 1579  
Db 5015 AGGAGAGAGAGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5074  
Qy 1579 rG-----SerLySGIyLyGInMetAlaGIu 1588  
Db 5075 GGAATCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5134  
Qy 1588 laGInCySbPProTyrrTyrrSerAsPArGIySerArGIyPheArGIyLeuValHisIIe 1608

Db 5135 |CCGAGTGCACAACTTACTACTCCGACTACTCCGCTTCCGGCTCTCGTCCAGCACTTGT| 5194  
QY 1608 |ysthSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrM| 1628  
Db 5195 |GCACAGACCACTACCTGACCTTTCATCAAGGTGTCATCGGGCTGAAGTGTGCACCA| 5254  
QY 1628 |evLamMetGlnHisTyrGlnGlnProGlnIleLeuSerGlnIleAlaLeuLysIleCysAsnT| 1648  
Db 5255 |TGGCCATGAGGACATACAGACAGCCCAAGTTCTGAGTGAAGCTCTGAAGATCTGCAACT| 5314  
QY 1648 |YrIlePheThrValIlePheValPheGlnSerValPheLysLeuValAlaPheAlaPheA| 1668  
Db 5315 |ACATCTTCACTGTCATCTTGTCTTGAAGTCAGTTTCAAACTGTGGCTTGGTTTCC| 5374  
QY 1668 |rgHrgPhePheGlnAspArgTyrPAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleW| 1688  
Db 5375 |GTGGTTCTTCCAGGACAGGTGGAACAGCTGGACCTGGCCATTGTGCTGTCATCA| 5434  
QY 1688 |etGlyIleThrLeuGlnGlnIleGlyValAsnLeuSerLeuProIleAsnProThrIleI| 1708  
Db 5435 |TGGGCATCAGCTGAGGAATGAGGTCAAGCTCGCTGCCATCAACCCACATCA| 5494  
QY 1708 |leArgIleMetArgValIleuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValG| 1728  
Db 5495 |TCCGCATCATGAGGGGTCTGCGCATTCGCCAGTCTGGAAGCTGTGAAGATGGCTGTGG| 5554  
QY 1728 |YMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyL| 1748  
Db 5555 |GCATGCGGGCGCTGTGACAGCGGTGATGACGGCCCTGCCAGTGGGGAACCTGGGAC| 5614  
QY 1748 |eulePheMetLeuLeuPhePheIlePheAlaIleuGlyValGlyLeuPheGlyAsnL| 1768  
Db 5615 |TTCCTTCATGTTGTGTGTTTTCATCTTTCAGCTCTGGGCGTGAAGCTCTTGGAGACC| 5674  
QY 1768 |eugLysAspGlnThrHisProCysGlyGlyLeuGlyArgHisAlaIleThrPheArgAspN| 1788  
Db 5675 |TGAAGTGTGACGAGACACACCCCTGTGAAGGCTGTGGCCGTCAATGCACCTTTCGGAACT| 5734  
QY 1788 |heGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTyrPAsnGlyIleW| 1808  
Db 5735 |TTGGCATGGCTTCTTAACCTCTTCCGAGTCTCCACAGGTGACAAATTGGAATGGCATTA| 5794  
QY 1808 |etLysAspProSerArgAspCysAspGlnGlnSerThrCysTyrAsnThrValIleSerP| 1828  
Db 5795 |TGAAGACACCTTCGGGACTGTGACAGGAGTCCACTGTACAAACGCGTCATCTCGC| 5854  
QY 1828 |roIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleA| 1848  
Db 5855 |CTATCTAATTGTGTCTTGTGCTGTGACGGCCCAAGTTCTGCTAGTCAAGTGTGATCG| 5914  
QY 1848 |laValLeuMetLysHisLeuGlnGlnSerAsnLysGlnValAlaGlyGlnGlnIleuG| 1868  
Db 5915 |CCGTGCTGATGAGACACTGAGAGAGCAACAAAGGAGGCGCAAGGAGGCGGAGCTAG| 5974  
QY 1868 |IuAlaGlyLeuGlnIleuGlnMetLysThrLeuSerProGlnInProHisSerProLeuGlyS| 1888  
Db 5975 |AGGCTGAGCTGAGCTGGAATGAAGACCTTCAGCCCCCAGCCCCCACTGCCCACTGGGCA| 6034  
QY 1888 |erProPheLeuTyrProGlyValGlyGlyValAsnSerThrAspSerProLysProGlyVA| 1908  
Db 6035 |GCCCTTTCCTTGTGGCTCGGGGTGAGGGCCCGACAGCCCGACAGCCCGCAACCGTGGGG| 6094  
QY 1908 |laProHisThrThrAlaHisIleGlyAlaAlaSerGlyPheSerLeuGlnHisProThr-| 1927  
Db 6095 |CTGTGACCCAGCGGCGCCAGAGATCAAGCTTCCCACTTTCCTGTGAGCACCCCAACGG| 6154  
QY 1927 ----- 1927  
Db 6155 |ACAGGAGAGCTGTTGACACCAATATCCCTGTGATCCAGGGCTCCCTGGAAGTGGAGCTGA| 6214  
QY 1927 ----- 1927

Db 6215 |AGGTATGAGACGAGCTGGCAGGCGCCAGGGGGCCAGCCCTTGTCTTCCCTTGCCCCA| 6274  
QY 1927 ----- 1927  
Db 6275 |GCCTGGAGGCTCCGACCCACAGATCCCTTAGCTGAGATGAGAGCTGTGTCTGACGT| 6334  
QY 1927 ----- 1927  
Db 6335 |CAGAGATTGTGTGAACCGTCTGTCTTAGCTCTGACGAGATGACTCTTGGCTGATG| 6394  
QY 1928 -----MetValProHisProGlnGlyVal| 1935  
Db 6395 |ACATGCACACACTTACTTAGTGCCCTGAGAGCAATATGACGGCCCAACCCACAGGAG| 6454  
QY 1935 |aProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrH| 1955  
Db 6455 |TGCCA-----GAGACGACCTTACGTGACTGTGGGAAGTGTGGGGTCAGCCGAAAGCC| 6505  
QY 1955 |iSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGlnArgSerLeuG| 1975  
Db 6506 |ACTCTTGCCTCAATGACAGCTTACATGTGTGCGGATGGAGACACTGCCAGGGGCCCTGG| 6565  
QY 1975 |YHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerG| 1995  
Db 6566 |GACACAGGGGCTGGGGGCTCCCAAGCTCAGTCAAGCTCCGTTGTTCGTTCACTCCC| 6625  
QY 1995 |InProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrIleLeuLeuGlnP| 2015  
Db 6626 |AGCCAGACAGATACAGCTTACATCTGACAGCTTCCCAAAATACACCTCACTGCTCCAC| 6685  
QY 2015 |roHisGlyValProThrTyrPAsnIleProLysLeuProProGlyArgSerProL| 2035  
Db 6686 |CCACAGGCGCCCAACCTGGGGCACATGCCCAACTGCCCCCAACAGGACGCTCCCT| 6745  
QY 2035 |euaIaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnG| 2055  
Db 6746 |TGGCTCAGAGGCGACACTCAGGCGCCCAAGCAGCAATGAAGCTCACTTGGACGTTCCAG| 6805  
QY 2055 |YLeuGlySerArgGlyuAspLeuSerGlyValSerGlyProSerCysProLeuThrA| 2075  
Db 6806 |GTCTGGGCGCGGGAAGACTGTGCGAGAGGTGAAGTGGGCTTCCCGCCCTGGGCC| 6865  
QY 2075 |rGserSerSerPheThrPAsnGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnS| 2095  
Db 6866 |GGGCTTACTCTTTCGGGGCCAGTCAAGTACCAAGACAGACAGCACTCCGACAGCACA| 6925  
QY 2095 |etLysValSerLysHisIleArgLeuProAlaProCysPProGlyLeuGlnProSerTyrP| 2115  
Db 6926 |GCAGATCTCCAAAGCACATGACCCCGCAGCCCTTGGCCAGGGCCAGAAACCAACTGGG| 6985  
QY 2115 |laLysAspProProGlnThrArgSerSerLeuGlnLeuAspThrGlyLeuSerTyrPLeS| 2135  
Db 6986 |GCAAGGGCCCTCCAGAGACAGAAAGCACTTGAAGTTGACAGGAGCTGACCTGGATTT| 7045  
QY 2135 |erGlyAspLeuLeu---ProSerSerGlnGlnGlyProLeuPheProArgAspLeuLysL| 2154  
Db 7046 |CAGAGACCTTCTGCCCCCTTGGCGGCGCAGAGAGAGGCCCAATCCCAAGGAGACTGAAGA| 7105  
QY 2154 |YAspTyrSerValGlnThrGlnSerCysArgArgArgProGlyPheThrPLeuAspGlnG| 2174  
Db 7106 |AGTGTACAGCTGAGGCGCCAGAGCTGCAAGCGCGGCTTACGTCCTGCTGATGAGAC| 7165  
QY 2174 |InArgArgHisSerIleAlaValaSerCysLeuAspSerGlySerGlnProArgLeuCyP| 2194  
Db 7166 |AGAGGAGACACTTATTCGCGTCACTGCTGACAGCGGCTTCCCAACCCCACTGGGCA| 7225  
QY 2194 |roSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgProLysArgL| 2214  
Db 7226 |CAGACCCCTTCTAACCCTTGGGGGCGACCTCTTGGGGGGCTGTGGAGCCGGCCCAAGAAA| 7285  
QY 2214 |YLeuSerProProSerIleSerIleAspProProGlnuSerGlnGlySerArgProProC| 2234  
Db 7286 |AACTGAGCCCGCTAGTATCACCATGACCCCGGAGAGCAAGGTCTCGGAACCCCGC| 7345



Db	1502	ATACCAACCACTACCACTGGGCAATGGACGCTCAGGGCCCCCGGGCCAGCCGGAGA	1561
Qy	553	leglnaspaatgaapalaaanglyserarghlemueteupropioptoserthnprot	573
Db	1562	TCAGAGCAGAGGATGCAATGGGTCCCGCAGGCTCATGTGTCACCAACCTTCAGCCGCTG	1621
Qy	573	hnprosertglyypropioptarglyvalagluservallhisserphertyrhialaaspc	593
Db	1622	CCCTCTCCGGGGCCCCCGCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCAATGCCGACT	1681
Qy	593	yshisluengluuprovallargcyseglnalabpropioptargcysproserglualaserc	613
Db	1682	GCCACTTAGACCAATCCGCTGCGCAGCGCCCTCCCAAGTCCCAATGTGAGGCATCCG	1741
Qy	613	lyargthervalaglyserglylysevaltyrprothrhvalhisnhserserproproglui	633
Db	1742	GCAGGACTGTGGGCAAGGGAGAGGTGTATCCACCGTGACACACAGCCCTCCACCGGAGA	1801
Qy	633	leleulysaaplysalaleuvalgluvalalabproserproglipropioptothleuths	653
Db	1802	CGCTGAAGGAGGAGGCACTAGTAGAGGTGGCTGCCAGCTCTGG3CCCCCAACCTTACCA	1861
Qy	653	erpheanilepserproglipropheasersemethislyleuleugluuthrinsert	673
Db	1862	GCCTCAACATCCACCCGGGCCCTACAGCTCCATGCACAAAGCTGTGAGACACAGAGTA	1921
Qy	673	hrqlyalacyshisaserseyalysalaserseerprocysserlysalaspsertglya	693
Db	1922	CAGGTGCTCCCAAGCTCTTGCAAGATCTCCAGCCCTTGCTGAAAGCAGACAGTGCGAG	1981
Qy	693	lacysglylproaspseryserprotyrcysalarghrghyalaglygluprogliusera	713
Db	1982	CCGTGTGTCAGACAGTGCCTCTACTGTGCCGGCGGGGCGAGGGAGGTGAGCTCG	2041
Qy	713	laasphivalamcproaspsersersergluualavaltyrgluphetrhlnasplag	733
Db	2042	CCGACCGTGAAATGCTCGCATCAGACAGCGAGGCAAGTTATGAGTTACACAGATGCC	2101
Qy	733	lnhisserapleuargasprrohisserarghargharglnatgsertleuglyproaspa	753
Db	2102	AGCACAGCGACCTCCGGGAGCCCCCACAGC---CGGGCGGCAACCGAGCGCTGGGCCGAGATG	2158
Qy	753	lagluiproserservalaleualaphettharghleuliecyasapthrhpharxlysliev	773
Db	2159	CAGAGCCACAGCTGTGCTG3CCTCTGAGAGGCTAACTGTGAACCTTCCGAAAGATTG	2218
Qy	773	alaspserlysyrrpheglyargglyllemetllealaleuvalasnthrleuserm	793
Db	2219	TGGACAGCAAGTACTTTGGCCGGGGAAATCATGATCCGCATCCGTGTAAACACTCAGCA	2278
Qy	793	etqglylegluTyRHsgluGlnpProgluLeuthrAsnaalaleuGlnIleSerAsnI	813
Db	2279	TGGGCATCGAATACACAGACAGCCCGAGAGGCTTACCAAGCCCTTAAAGATACAGACA	2338
Qy	813	levaliphetrrsartleuphalaleuGlnmetleuLeuLeuValTyrglyProp	833
Db	2339	TCGCTTCACAGAGCTTTTGCCCTGGAGATGCTGTGAAAGCTGTGTGTATAGTCCCT	2398
Qy	833	heglyTyrllelysasnpProTyrrAsnIlePhaspglyvalIlevalalIleSerValT	853
Db	2399	TTGGCTACATCAAGAAATCCCTTAACAACATCTTCGATGGTGTCAATTGGTCATCAGGCTGT	2458
Qy	853	trpGluIleValIglYngIngIyglYleuSerValIleuargthrhPharxleuMeca	873
Db	2459	GGGAGAGTCGTGGCCAGACAGGGGGGCGGCTGTGCGGTGTGCGAGCACTTCCGCTGATGC	2518
Qy	873	rgfalleuylsleuValArgPheleuproblaleuGlnargGlnleuValIleuMethI	893
Db	2519	GTCGTGGAAGCTGTGGCTTCTCTGCGGCGGTGCAGCGGACAGCTGTGTGTCTCTATGA	2578
Qy	893	ysThrMecApsanValalathrhPheCysMecleuMecleuPheIlePhes	913
Db	2579	AGACATGAGCAACGNGGCCACTTCTGCAATGCTGTATGCTTTCATCTTCACTTCA	2638
Qy	913	erlleuGlnIleMethIleuPheGlyCylysePhealaserGluargaspGlyasppThl	933
Db	2639	GCATCTCGGAGCATGATCTCTTCGTGGTGCAAGTTTGCTCTAGCGGGATGGAGACACC	2698
Qy	933	euproaspaatrglysasnpheaspserserleuTriPalalilevalThrhValPheGlnIle	953
Db	2699	TGCCAGCCGGAAGAAATTTTGACTCTCTTGCTGTGGCCATGTGTACTGTCTTTCAGATCC	2758
Qy	953	euthrglnluasptipaenlyvalleuTyrrAsnGlyMecalaserThrserserTpa	973
Db	2759	TGACCCAGAGAGCTCGAACAAGTCTCTTAATATGTATGGCTTCCACAGTGTCTGTGG	2818
Qy	973	laalaleuTyrrheillealaleuMethrhPheGlyAsnTyrralleuPheanleuLeuV	993
Db	2819	CGGCCCTTATTTCAATGTGCCCTTCATGACCTTGCGCAACTGATGCTTCAATTTGCTGG	2878
Qy	993	alalalleuvalgluGlyPheGlnalaglu-----gluaspaalathrhlySerg	1003
Db	2879	TGCCATTTGTGTGAGGGCTTCCAGGCGGAGAAATCAGCAACGGGAAGATCGAGTG	2938
Qy	1004	-----gluaspaalathrhlySerg	1010
Db	2939	GACAGTTAAGCTGTATTCACTGCTGTGCACTCCAGGGGGAGATGCCCAAGTCCG	2998
Qy	1010	luserGluProasprPheSerProserValaspglyaspaGlylyaspaGlylyasgl	1030
Db	2999	AATCAGAGCCCATTTCTTCTCAACCAGCTG3ATGTATGTAGGGACAGAAAGATGCT	3058
Qy	1030	eualaleuvalaleuGlylunhisalagluLeuarglylserserleuLeupProleuI	1050
Db	3059	TGGCTTGTGTCTCCCTGGAGAGACCCCGAGCTGGGAAAGCTGTGCCGCTCTCA	3118
Qy	1050	lelleisethrallalathrpometSerhisProlysserserserThrhlyvalGlyG	1070
Db	3119	TCATCCACAGGCGCGCACACCATGTGCTGCCCAAGACACACAGCGGCTGGGGG	3178
Qy	1070	lunlaleuGlyserGlyserargharghThrserserGlyserlaserlgluproglyalad	1090
Db	3179	AGCGCTGG3CCTGCGTGCCTGCCGACAGACAGCGAGGTGGAGAGCCTGGGGCGG	3238
Qy	1090	lahisierGlnmetlyscysProProseralargserseerProhisserProtripsera	1110
Db	3239	CC---CACGAGATGAAGTACACGCCCGACGCCCGAGCTCTCGCACACCCCTGGAGGG	3295
Qy	1110	lalaserseerTprThrsersargargserSerarghanserleuGlyargalaproserL	1130
Db	3296	CTGCAGACAGCTGAGACACAGACAGCGCTCCAGCCGGAACAGCTCGGCGCTGCACCCAGCC	3355
Qy	1130	eulysarghargserProserGlyluargargserleuLeuSerGlygluGlnGlns	1150
Db	3356	TGAAGCGAGAAAGCCCAAGTGAAGAGCGGGGCTCTGTGTGTGGAGGAAGCCAGAGAA	3415
Qy	1150	erglnaspglugluGlnuserSerGluGluaspaarghIasercProalaglyseraspha	1170
Db	3416	GCCAGGATGAAGAGAGACTCAGAAAGAGCGGGCCAGCCCTGGGGCAATGACATC	3475
Qy	1170	rghtsargglyserleuGluargGluualalyserSerPheaspleuProlasppThrhLeug	1190
Db	3476	GCCACAGGGGGTCCCTGGAGCGGGAGGCCAAGAGTTCTTTGACCTGCAGACACACTCG	3535
Qy	1190	lnvalproglyleuHisargThrhIasercGlyArgserSerlaserGlnIleaglAspc	1210
Db	3536	AGGTGCGAAGGCTGCACTGCCACTGCGAGTGGCCGAGAGGTCTGTGTGAGCACAGGACT	3595
Qy	1210	lyasnglylysserlaserGlyArgleualargThrhuaargthrhAspaerProGlnL	1230
Db	3596	GCAATGGCAAGTCGCTTACAGGGCGGCTGTGGCCCTGTGGCGCTGTAGACCCCCAC	3655
Qy	1230	eulaspGlyaspaaspaaspaGluGlyAsnleuserlysglyluargllleglnalAT	1250
Db	3656	TGATGGGATGACGCCGATGACGAGGGCAACTGTAGCAAAAGGGGAACGGGTCCGCGCGT	3715



QY	1250	rpValaArgSerArgLeuProIlaCySyaArgIuaYgaSerTrpSerIaArgTrIleP	1270
Db	3716	GGATTCGACCGCACTCCCTGCTGCTGCTCGAGCAAGATCTCGTGAAGCTTCAACT	3775
QY	1270	heProProGInSerArgPheArgLeuLeuCyShIaArgIleIleThrIleIlyMetPheA	1290
Db	3776	TCCCTCTCACTCCAGGTTCGGCTCTCGTGTCAACGGATATACCAACAAGATGTTCC	3835
QY	1290	spHIsvalValLeuValIleIlePheLeuAncyIleThrIleAlaMetGluArgProI	1310
Db	3836	ACCAAGTGTCTTGTTCATCATCTTCTTAACTGCATCACCATGCATGAGAGGCCCA	3895
QY	1310	ysIleAerProHisSerIaGluArgIlePheLeuThrIleSerPheAsnTrIlePheThra	1330
Db	3896	AAATTTGACCCCAAGCGCTGAAGCAATCTTCCGACCTTCCAAATTAATCTTCAACG	3955
QY	1330	IaValIlePheAlaGluMetThrValIlySvaIValAlaLeuGlyTrpCysPheGlyGluG	1350
Db	3956	CAGTCTTCTTGCTGCAATGAACGTGAAGGTGTGTGCACCTGGCTGTGTTCGGGAGC	4015
QY	1350	IaaIaTyTrLeuArgSerSerTrpAsnValLeuAerGlyLeuLeuValIleuIleSerValI	1370
Db	4016	AGGCGTACCTCGGAGCAGTTGAAACGTGCAGCGGGCTGTGTGTCTCATCTCCGTCA	4075
QY	1370	IeaerPIleLeuValISerMetValSerAspSerGlyThrIlyIleLeuGlyMetLeuArgV	1390
Db	4076	TCGACATTCTGTGTGCATGTGTCTTCGACACGGGACCAAAATCTTGAGATGTGAAGG	4135
QY	1390	aIleuArgLeuLeuArgThrIleuArgProLeuArgValIleSerArgIaGInGlyLeuI	1410
Db	4136	TGCTGCGGCTCTCGGACCTGTGCGCCGCTCAAGGTATACGCGGGCGGAGGGCTGA	4195
QY	1410	ylSeuValIaGluThrIleuMetSerSerIleuLyPProIaGlyAsnIleValIalIec	1430
Db	4196	AGCTGTGTGTGAAGACGTGATGTCTTCACGAAACCATCGGCAACATTTAGTCACTCT	4255
QY	1430	ylSeuValaPhePheIleIlePheGlyIleLeuGlyValGInLeuPheIlyArgIlySPhP	1450
Db	4256	GCTGTGCTCTTCACTCATTTTCGGCATCTTGGGGGTCACTCTTCAAGAGAAATTTT	4315
QY	1450	heValCySGInGlyGluuAspThraArgAsnIleThrAsnIlySerAspCysAlaGluIaAs	1470
Db	4316	TGCTGTGCAAGGCGAGATACCAAGAACATCACAAATAAATTCGACTGTGCCAGGCCA	4375
QY	1470	eTyTyArgTrpValaArgHilySlyTyTrAsnPheAspAsnLeuGlyAlaLeuMetSerI	1490
Db	4376	GTTACCGGTGGGTCCGGCAACAAGTCAAACTTTGCAACCTTGGCGAGGCTCTGATGTCC	4435
QY	1490	eupHValIleuAlaSerIlySyaArgIyTrpValaAspIleMetTyraSpGlyLeuAspIaV	1510
Db	4436	TGTTTGTTTTGGCTCCCAAGATGTGTGGTGAATATATGATGATGGCTGGATGCTG	4495
QY	1510	aIaGlyValaSpGInGInProIleMetAsnHISAsnProTrpMetLeuLeuTyraPheIleS	1530
Db	4496	TGGGCTGTGACCAAGACGCATCATGAACACACACCTCGATGTGCTGTAATTCACTT	4555
QY	1530	erPheLeuLeuIleValaIlaPhePheValLeuAspMetPheValGlyValIValaGluA	1550
Db	4556	CGTTCCTGCTCATGTGTGGCTCTTCTTTGTCTGACATGTGTTGTGGTGTGTGTGAGAGA	4615
QY	1550	anPheHilySyaArgGInHISGInGluGInGluAlaArgArgArgGlyGluIlySva	1570
Db	4616	ACTTCACAAAGTGTGGAGCAACCAAGAGAAAGAGAGGCCCGGCGGAGAGAGAACG	4675
QY	1570	rgLeuArgArgLeuGluIlySlySvaArg-----	1579
Db	4676	GGCTACGAAGACTGAGAAAAAGAAAGAAATCTAATGCTGGACGATGAATTGCTTCCG	4735
QY	1580	--SerIyGluIlySglMetAlaGluAlaGInCySlyProTyTrSerAspTyTrSerA	1599
Db	4736	GCAGGTCAAGCCAGCTGCTCAGAAAGCCCAAGTGCAAACTTAACTATCTCGAATCTCC	4795

QY	1599	tgphreaqgleuValHiHfiHleucyphrshRi:stYrleuAapLePheIlethrg	1619
Db	4796	gcttccggctctctgtccacacattggacacacacacttaccactcttaccacag	4855
QY	1619	lyValIleeglyLeuAsnValValThrMetAlaMetGlnH:stYrGlnIleProGlnIlel	1639
Db	4856	gtgcacatcgagctgaaggtgtgtaccatggccatggagacactaccacagcccgagattcc	4915
QY	1639	euaaprglualaleuLysIleCyshantYrIlePheThrValIlePheValPheGlnserv	1659
Db	4916	tgcatgtagagctctgaagatctgcacacacacacacacttaccactcttaccacag	4975
QY	1659	alPheLysleuValAlaPheAlaPhehargrgrPhePheGlnaspArgTrpAsnGlnleua	1679
Db	4976	tttttcaactgtgagcctttgtgtgtccgtggtctttccagagacagggagacagcttcg	5035
QY	1679	apLeuAlaIleValleuLeuSerIleMetGlyIleThrleuGlnGluIleGluValAsnI	1699
Db	5036	acctggccattgtgtctgtctgtccatctatgggcacacagctggagaaatgaggtccaacg	5095
QY	1699	eusertleuProIleasnProThrIleileargIleMetArgValleuargIleAlaargv	1719
Db	5096	cctggcgcccatcaacccac	5155
QY	1719	alleuLysleuLeuLysMetAlaValGlyMetArgAlaleuLeuH:stYrValMetGlna	1739
Db	5156	tgctgaagactctgaagatggctgtggcagacggggcgctgtgacacagctgattgacag	5215
QY	1739	laleuProGlnIValGlyAsnleuGlyleuLeuPheMetleuLeuPheIlePheAla	1759
Db	5216	ccctggcccccagatggggaaacctgggaacttctcttcacatgtttgtttttaccatttgcag	5275
QY	1759	laleuGlyValGluLeuPheGlyAsnleuGlnYAsnArgIuThrH:stYrGlnGluIYL	1779
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QY	1779	euglyValGlnH:stYrPheArgAsnPheGlyMetAlaPheLeuThrleuPheArgValS	1799
Db	5336	tgggcgctgcac	5395
QY	1799	ertHrGlyAsnAsnTrpAsnGlyIleMetLysAsnProSerArgAspCyAsnGlnIus	1819
Db	5396	ccacagatgacaaattgaaatggcatttatgaagacacacctccgggacgtgtaccacagagt	5455
QY	1819	ertHrCyStYrAsnThrValIleSerProIleYrPheValSerPheValleuThrAlag	1839
Db	5456	ccactcgcttaccac	5515
QY	1839	lnPheValleuValAsnValIleAlaValleuMetLysH:stYrGlnIleuGlnserv	1859
Db	5516	agttcgctgctgctgacacgctgtgtgacccgctgtgacatgaacacacctggagagacac	5575
QY	1859	yGluAlaLysGlnGlnAlaGlnleuGlnAlaGlnleuGlnleuMetLysThrIeus	1879
Db	5576	aggaagcccaagagagagcccgagctgagagctgagctgagctgagatgaagacaccttca	5635
QY	1879	erProGlnIProH:stYrProleuGlySerProPheLeuTrpProGlyValGlnGluVala	1899
Db	5636	gccccacacccac	5695
QY	1899	asnertHrAsnSerProLysProGlyAlaProH:stYrThrAlaH:stYrleuAlaIas	1919
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QY	1919	erglyPheSerleuGlnH:stYrProHr	1922
Db	5756	ccacacttttccctggagacacccacacacacacacacacacacacacacacacacacac	5815
QY	1922	-----	1922
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QY	1927	-----	1927

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Db      5876 AGCCCTCTGCTTCCTTCCTGCCCCCAGGCTGGAGAGGCTCCAGCCAGATCCCTCTAG 5935
QY      1927 ----- 1927
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QY      1927 ----- 1927
Db      5996 CTCTGACGATGACTCTTTCCTTGATGACATGACACTCTTACTTACTGTCCTGAGAA 6055
QY      1928 -----MetValProHisProGluGluValProValProLeuGlyProAspLeuLeuThyV 1946
        6056 GCAATATGAGAGCCCAAGCCAGAGAGCTGCA-----GAGCCAGACTTACTGACCTG 6106
QY      1946 aATgLySserGlyValSerArgThiHisSerLeuProAsnAspSerTyMetCysArgA 1966
        6107 TCGGGAAGTCTGGGGTACAGCCGAACCACTCTGCCCCAATGACACTATGTGTGGC 6166
QY      1966 snGlySerThrAlaGluArgSerLeuGlyHisArgGlyTTPGlyLeuProValAlaGlnS 1986
        6167 ATGGAGGACTGCTCGAGGGGCCCCCTGGAGACAGAGGGCTGGGGCTCCCAAGACTCAG 6226
QY      1986 ergLySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuP 2006
        6227 CAGGCTCCGCTTGTCCGTTCACTCCAGCCAGCAGATACCACTACATCTGCACTTC 6286
QY      2006 roLyAspValHisTyLeuLeuGlnProHisGlyAlaProThrTPGlyAlaIleProL 2026
        6287 CCAAGATGACACCTCATCTGCTCAGGCCCAAGCCGCCCACTGGGGGCACTCATCCCA 6346
QY      2026 yLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaI 2046
        6347 AACTGCCCCCAAGAGCGCTCCCTTGGCTAGAGGCCACTCAGGCCAGCCAGCCAGCA 6406
QY      2046 leArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSerGlyV 2066
        6407 TAAAGACTGACTCTTGAGAGCTTCAAGGCTGGGCAAGCCGGAAGACTCTGCGAGAG 6466
QY      2066 aLserGlyProSerCysProLeuThrArgSerSerPheTTPGlyGlySerSerIleG 2086
        6467 TGAGTGGGCCCCCTCCGCCCCCTGAGCCCGGCGCTTCTTCTGGGGCACTCAAGTACC 6526
QY      2086 lnValGlnGlnArgSerGlyIleGlnSerIysValSerIysHisIleArgLeuProAlaP 2106
        6527 AGGCACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCAGCAGATACCCGCCAGGCC 6586
QY      2106 roCysProGlyLeuGluProSerTTPAlaIysAspProProGluThrArgSerSerLeuG 2126
        6587 CTGGCCAGGCCCAAGAACCACTGGGGGCAAGGGCCCTCCAGAGACCAAGAGCAGCTTAG 6646
QY      2126 luLeuAspThrGluLeuSerTTPIleSerGlyAspLeuLeu---ProSerSerGlnGluG 2145
        6647 AGTTGGACAGAGGAGCTGAGCTGATTTTCAGAGAACCTCCCTGCGCCCTGGGGCGCAGAGG 6706
QY      2145 luProLeuPheProArgAspAspLeuLysGlyCysTyrSerValGluThrGlnSerCysArgA 2165
        6707 AGCCCCCATCCCAAGGAGCTTGAAGAGTGTACAGCGTGGAGGCCCAAGCTTGCCAGC 6766
QY      2165 rGArgProGlyPheTTPLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuA 2185
        6767 GCGGGCTTACGTCTGCTGCTGATGAGCAGAGAGACACTTATCGCGCTCAGCTGCTGG 6826
QY      2185 spSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlnProLeuG 2205
        6827 ACAGCGGCTCCCAAGCCCACTGGGCAAGACCCCTTAACTTGGGGGCGCAGCCTTCTG 6886
QY      2205 lyGlyProGlySerArgProLysValLysLeuSerProProSerIleSerIleAspProP 2225
        6887 GGGGGCTTGGAGCGGCGCCCAAGAAAACTCAGCCCGCTTATATACCATGAGACCCC 6946
QY      2225 roGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgArgAlaP 2245

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Db      6947 CCGAGAGCAAGGTCTCTGAGACCCCGCCAGCCCTGTATCTGCTCCGAGAGAGGCTC 7006
QY      2245 roAlaSerAspSerIysAspProSerValSerSerProLeuAspSerThrAlaIAspP 2265
        7007 CGTCCAGCACTCCAAAGATCCCTTGGCTTGGCCCCCTGACAGCATGAGTGCCTGAC 7066
QY      2265 roSerProLysIysAspThrLeuSerLeuSerGlyLeuSerSerAspProThraAspMetA 2285
        7067 CTTCCCAAGAAAGATGTGCTGAGTCTCTCCGTTTATCTGACCAAGCAGACACTGG 7126
QY      2285 spPro 2286
        7127 ACCCC 7131
Db      7127 ACCCC 7131

RESULT 7
US-10-757-262-15
; Sequence 15, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karichef, Venkateswarlu
; APPLICANT: Siles-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16857, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 15547, 115, 579, 15985, 15625, 760, 16603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 615, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MP103-007P1RNMNM1N
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 7648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(7134)
; US-10-757-262-15

Alignment Scores:
Pred. No.: 0 Length: 7648
Score: 10845.50 Matches: 2105
Percent Similarity: 89.72% Conservatve: 33
Best Local Similarity: 88.338 Mismatches: 110
Query Match: 90.17% Indels: 135
DB: 19 Gaps: 7

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US-09-611-257a-24 (1-2287) x US-10-757-262-15 (1-7648)

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2 TGAACGAGAGAGAGATGAGCCGGCCCGAGAGTCCGGACACACCCCGAGCTTCAATGC 61  
54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73  
62 GGCTCAACGACCTCTCGGGGGCCGGGGGGCCGGCCGGGGCTCAGCAGAAAAGAACCC 121  
73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValAlaP 93  
122 CGGGCAGCCGGCATCCGAGCGGAGGGCTGCGTACCCGGCCCTGGCCCCGGGTGTTT 181  
93 hePheTyrLeuSerGluAspSerArgProArgSerTyrCysLeuArgThrValCysAsp 113  
182 TCTTCTACTTGAACGACGACGACCCCGCGAGCTGTCTCGCAGCGTCTGTAAAC 241  
113 roTrrPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133  
242 CCTGGTTTGAACGACATGATGTTGTCATCTTCTCAACTGGCGTGACCTGGGGCATGT 301  
133 heArgProCysGluAspIleAlaCysAspSerGluArgCysArgIleLeuGlnAlaPhe 153  
302 TCCGGCCATGGAGAGACATCGCTGTGACTCCAGCCGCTGCGGATCTGAGGCTTTG 361  
153 sPaAspPheIlePheAlaPhePheAlaValAlaGluMetValIleMetValAlaLeuGlyI 173  
362 ATGACTTCATCTTTGCTTCTTCTTCTTCTGAGATGTGTGTAAATGTGTGGCTTTGGCA 421  
173 IePheGlyLysCysTyrLeuGlyAspThrTrrPasnArgLeuAspPheIleValI 193  
422 TCTTTGGGAAAAGTTACCTGAGGAGACACTTGGAAACGGCTTGACTTTTCACTCGCA 481  
193 IeAlaGlyMetLeuGluTyrSerLeuAspLeuGluAsnValSerPheSerAlaValArgT 213  
482 TCGAGGGGATCTGGAGTACTCGCTGACCTGCAGAAAGTGACCTTCCACTGTGCAGAA 541  
213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233  
542 CAGTCCGTGTCTGCGACCGCTCAGGGCCATTAAACGGGTGCCCCAGCATGGCATCTTG 601  
233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253  
602 TCAGGTGCTCTGGATACGCTGCGCCATGCTGGGACACGTCGTGCTGCTTCTTCTCG 661  
253 alPhePheIlePheGlyIleValGlyValAlaGlnLeuTrrAlaGlyLeuLeuArgAsnAGC 273  
662 TCTTCTTCATCTTCGGCATCGTCGGCGCTGCAGCTGTGGGAGGGGCTGCTTGGAAACGAT 721  
273 ySPheLeuProGluAsnAspPheSerLeuProLeuSerValAspLeuGluProTyrTrrGlnT 293  
722 GCTTCTCACTGAGAAATTCAGCTCCCTCCGAGGTGTGAAGCTGGAAGCGCTTATTCAGA 781  
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782 CAGAGAAAGAGATAGAGACCCCTTCATCTGCTCCAGACCAAGCAGAAACGCGATGCGGT 841  
313 erCysArgSerValProThrLeuAlaGlyGluGlyValGlyGlyProProCysSerLeuAla 333  
842 CCTGAGAAAGCGGTGCCACGCTGCGCGGGAGCGGGGGCGGTGGCCCACTTGGCGGTGG 901  
333 sPyrrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrrAsnGlnTrrTrrT 353  
902 ACTATGAGGCTTACAAAGCTTCACAAACACCACTGTGTCACTGGAACAGTACTACA 961  
353 hrAsnCysSerAlaGlyGluIleAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373  
962 CCAATGCGTCAGCGGGGAGCAACCCCTTCAAGGGGCGCATCAACTTGAACAACATTG 1021  
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1022 GCTATGCTTGATGCCATCTTCCAGGTCAACGCTGAGAGGGCTGGTGCATCATCATGT 1081  
393 yrrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413  
1082 ACTTTGATGATGATGCTCATCTTCTACAAATTCATCTCACTTCATCTTCATCATCG 1141  
413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaTrrGlnPheSerGluT 433  
1142 TGGCTCTCTTCTTCATGATTAACCTGTGCTGGGTGATGTACAGCAGCACTTCTCAGAA 1201  
433 hrLysGlnArgGluSerGlnLeuMetArgGluGluGlnArgValArgPheLeuSerAsnAlaS 453  
1202 CCAAGCAGGGGAAAGCACTGATGGGAGAGCGGTGGCGGTCTCTGCCAACGCCCA 1261  
453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473  
1262 GCACCTGGCTACCTTCTTCAGACCCGGCAGCTGCTATGAGGAGCTGCTCAAGTACTGG 1321  
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1322 TGTACATCTTCTGTAGGAGCCCGCAGCTGTGCTCAGTCTCTCGGAGCAGAGTGTGC 1381  
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1382 GCGTTGGGCTGCTCAGACGCCAGCACCCCTCGGGGGCCAGAGACCCAGCCAGCAGCA 1441  
513 erCysThrArgSerHisArgArgLeuSerValHisIleLeuValHisHisHisHis 533  
1442 GCTGCTCTGCTCCACCGCCGCTATCCGTCCACCACTGGTGACACACACACACACAC 1501  
533 IHisHisHisTyrHisIleLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553  
1502 ATCACCAACCACTACCACTGGCAATGAGAGCTCAGAGGCCCCCCCGGACGCCAGAGA 1561  
553 IeGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573  
1562 TCCAGAGCAGAGATGCCAATGGGTCCGAGGGCTCATGTCGCACACCCCTCGACGCTTG 1621  
573 hrProSerGlyGlyProProArgGlyValaGluSerValHisSerPheTyrHisAlaAspC 593  
1622 CCTCTCCGGGGCCCCCTGTGTGGCCAGAGTGTGACAGAGCTTTCACATCTCCACT 1681  
593 ySHIleuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613  
1682 GCCACTTAGAGCCAGTCCGCTGCGAGGCGCCCTCCAGAGTCCCATCTGAGGCACTCG 1741  
613 IyArgThrValaGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633  
1742 GCAGAGCTGTGGAGCGGAGAGGTGTATCCACCGTGCACACCAAGCCCTCCACCGGAGA 1801  
633 IeLeuLysAspLysAlaLeuValaGluValaAlaProSerProGlyProProThrThrS 653  
1802 CGCTGAAGAGAAAGCACTAGTAGAGTGTGCTGCACCTGTGGGCCCCCAACCTTCACCA 1861  
653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSert 673  
1862 GCTTCACATCTCCACCGGGGCTTACAGCTTCATGACCAAGCTCTGAGACACAGAGTA 1921  
673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693  
1922 CAGTGTCTGCGAAAGCTCTTGCAGAAATCTCCAGCCCTTGTTGAAAAGCAGACAGTGGAG 1981  
693 IaCysGlyProAspSerCysArgProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713  
1982 CCTGTGTCCAGACAGCTGCCCTTACGTGTGCCCGGGGCGAGGAGGTGAGCTCG 2041  
713 IaaPheHisValMetProAspSerSerSerGluAlaValTyrGluPheThrGlnAspAlaG 733  
2042 CCGACCGGTGAATCTCGATCCAGACAGCAGAGGAGTTTATGAGTTCAACAGGATGCC 2101  
733 IHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753  
2102 AGCACAGGACCTCGGGAGCCCCCAACAGC---CGGGGCAACGGAAGCTGGGCCCAAGTG 2158

[illegible]

D	4316	TCGTGTCACAGGAGGAGATACAGAACATCACCAATAAATCCGACTGTCCAGGCCA	4375	D	5396	CCACAGGTGACAAATTGGATGCAATTATGAAGACACCTCCGGAGCTGTACAGGAGT	5455
Q	1470	ERTYATGTRPVALARSHISLYSTRANPHEASPNLEUGLYGALALEUWESERT	1490	Q	1819	ERTHCYSTRANTHVALLESERPROILETYRPHVALSERPHEVALLEUTHRALAG	1839
D	4376	GTTACCGGTGGGTCCGGCACAAGTACACTTTGACAACTTGGCCAGGCCCTGATGTCCC	4435	D	5456	CCACTGCTACAAACACGGTCATCTCGCTATTAATCTTGTGTCCTGTCGTACAGGCC	5515
Q	1490	EUPHEVALLEUALSERLYASAPGLYTRPVALASPILEMETYTRASPGLYLEUAPALAV	1510	Q	1839	INPHEVALLEUVALASPNVALIILEALVALLEUWESLYSHISLEUGLUSERASNL	1859
D	4436	TGTTGTTTTGGCTCCCAAGATGGTGGTGACATCATGTACGATGGCGTGATGTCTG	4495	D	5516	AGTTGCTAGTACACGCTGTGATGCCCTGCTGATGAAGACACTGGAGAGACACA	5575
Q	1510	ALGIVALLASPGIPLPROILEMETSNNISAPNPROTPMETLEUENUTYRPHIES	1530	Q	1859	YSGUALALYSGIUGLUALGLUENUGLUALGLULEUGLULEUGLULEUWESLYSTHREUS	1879
D	4496	TGGGCGTGACAGACGCCATCATGAACACAAACCCCTGGATGCTGTACTTCACTCT	4555	D	5576	AGAGAGCCAAAGAGAGAGCCGAGCTAGAGGCTGAGCTGAGATGAAGACCTCA	5635
Q	1530	ERPHEULEULLEVALIAPHEPHEVALLEUASMETPHEVALIYVALIYVALIUAL	1550	Q	1879	ERPROGILNPROHISERPROLEUGLYSERPROPHLEUTTPROGILYVALIYVALA	1899
D	4556	CGTTCCCTCATTTGTGGCTTTCTTGTCTGAAACATGTTTGTGGGTGTGGGTGAGA	4615	D	5636	GCCCCCAGCCCACTCCGACCTGGCGAGCCCTTCTCTGCTGGCTGGGGTGAAGGCCCG	5695
Q	1550	SNPHEHISLYSCYAAARGLNHISGNGIUGIUGIUGIUALAARGARGARGIUGIULYSA	1570	Q	1899	SNSETRHASPSEPROLYASPROGLYVALAPROHISTHRTHRALHISILEGIVALLAAS	1919
D	4616	ACTTCACAAATGTCGCGACAGCACAGAGAAAGAGAGGCCCGGCGCGGAGGAGAAGC	4675	D	5696	ACAGCCCCGACAGCCCCAAGCTGGGGCTGTGCACCCAGCGGCCACGAGATCAGCT	5755
Q	1570	TGLEUARGARGLEUGLULYSLYASARGA	1579	Q	1919	ERGLYPHESEULEUGLULHISPROTHR	1927
D	4676	GCCATACGAAGACTGGAGAAAAAGAAAGAAATCTAATCTGACGANTGAATTGCTTCG	4735	D	5756	CCCACTTTTCCCTGGACACCCACGAGCAGCTGTTTGAACACCATATCCCTGCTGA	5815
Q	1580	--SERLYSGILULYGLIMETALAGIUALAGIULYALYPROTYRSEASPTYRSERA	1599	Q	1927	TCCAGGCTCCCTGGAGTGGAGCTGAAGCTGATGACGAGCTGGCAGGCCAGGGGCC	5875
D	4736	GCACTCAGCCACGCGCTCGTCAGAACGCCCACTGAAACCTTACTACTCCACTACTCC	4795	D	5816	TCAGAGCTCCCTGGAGTGGAGCTGAAGCTGATGACGAGCTGGCAGGCCAGGGGCC	5875
Q	1599	TGPHEARGLEULEUVALHISHISLEUCYSTRHSETHISLYRLEUASPLEUHEILETHRG	1619	Q	1927	AGCCCTGCTCCCTTCCCTTGTGCCCCAGCTGGAGGCTCCGACCCACAGATCCCTTAG	5935
D	4796	GCTTCGGGCTCTCGTCCACCACTGTGTACACAGCCACTACTGGACCTTCTTACACAG	4855	Q	1927	CTGAGATGAGAGCTCTGTCTGTACGTCAGAGATTGTCGAAACGTCCTGCTCTAG	5995
Q	1619	LYVALIILEGLYLEUASPNVALIATHMETALAMETGLHISLYTGLINLPROGINILEL	1639	Q	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
D	4856	GTCATCATGGGCTGAACCTGTGTACCATGAGCCATGAGACACTACACGAGCCCAAGATTG	4915	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
Q	1639	EUAERGLUALALEUVALIECYASANTYRILEPHETHRVALIIEPHEVALPHEGUSERV	1659	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
D	4916	TGGATGAGGCTCTGAAGATCTGCACATCACTTCACTGATCTTTCTTGTGAGTACAG	4975	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
Q	1659	ALPHELYLEUVALIAPHEALAPHEARGARGPHEGLNASPARGTTPANGINLEUA	1679	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
D	4976	TTTTCAACTGTGGCTTTGGTTCCGTCGGTCTTCCAGGACAGGTGGAACCACTGCG	5035	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
Q	1679	SPLEUALIILEVALLEULEUSERTILEMETGLYIERTHLEUGLULILEGIVALLANL	1699	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
D	5036	ACCTGGCCATTGTGTGCTGTCCATCATGAGGCATCAGCTGAGGAAATCGAGGTCAACG	5095	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
Q	1699	EUSERLEUPROILEANPROTHRIEILEARGILEMETARGVALLEUARGILEALARGV	1719	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
D	5096	CCTGCTCCCTCATCAACCCACCATCATCCGATATAGGGTCTGGCCATTGCCCAAG	5155	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
Q	1719	ALILEUVALIEULEUVALIEUVALIYGLYMETARGVALLEUVALIESTHRVALMETGNA	1739	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
D	5156	TGCTGAAGCTGCTGAAGATGGCTGTGGGCATGCGGCGCTGTGACACGCGATGACAGG	5215	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
Q	1739	LALEUPROGLINVALIYANLEUGLYLEUENUPHEMETLEUENUPHEHEILEPHEALAA	1759	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
D	5216	CCCTGCCCAAGTGGGGAACCTGGGACTTCTTCAATGTGTGTGTTTTCATCTTTGAG	5275	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
Q	1759	LALEUGLYVALIYUENUPHEGLYASPLEUGLUCYASPGIUTHRIASPROCYSGIUGLYL	1779	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
D	5276	CTCTGGGCGTGAGCTCTTTGAGAGCTGTGAGATGTGAGAGACACACCCCTGTGAGGCC	5335	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
Q	1779	EUGLYARGHISALATHRPHARGANPHEGLYMETALAPHELEUTHRLEUPHEARGVALS	1799	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
D	5336	TGGGCGTCATATCCACTTTCCGAACCTTGGGATGAGCTTCTTAACCTCTTCCAGACTCT	5395	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055
Q	1799	ERTHGLYASPNANTTPANGIYIILEMETLYASPPROSERTRGASPCYASAPGNGIUS	1819	D	1927	CTTGACGGATGACTCTTTCCTGATGACATGACACACTCTTAATTAGTCCCTGAGA	6055

QY 2086 l n v a l g i n g l i n a s e r g l y l l e g l i n s e r l y s v a l s e r l y s h i s l e a r g l e u p r o h a p 2106  
Db 6527 a g c a c a g a c g a c t c c c g a c c a c a g a a g t c t c a a g a c a c a c c c c g a c c c 6586  
QY 2106 r o c y s p r o g l y l e u g l u p r o s e r t r p a l a l y a s p p r o p r o g l i u t h r a r g s e r l e u g 2126  
Db 6587 c t t g c c c a g g c c c a g a a c c a a c t g g g g c a a g g c c t c a g a g a c c a g a a g a c t t g a 6646  
QY 2126 l u l e u a p t h r g l u l e u s e r t r p l i s e r g l y a s p l e u e u - - - p r o s e r s e r g l i n g l u g 2145  
Db 6647 a g t t g a c a c a g a c t g a g c t g a t t c a g a g a c c t c t g c c c c t g g c g c c a g a g a g 6706  
QY 2145 l u p r o l e u p h e p r o a r g a s p l e u l y l e u c y s t y r s e r v a l g i u t h r i n s e r c y a r g a 2165  
Db 6707 a g c c c c a t c c c a c g a c c t a g a a g t c t a c a g c c t g a g g c c c a g a a g c t g c a g 6766  
QY 2165 r g a r p r o g l y p h e t r p l e u a s p g l u g l n a r g a r g h i s e r l e a l a v a l s e r c y a l e u a 2185  
Db 6767 g c c g g c c t a c g t c t g c t g a t g a c a g a g a g a c a c t t a t g c c g t a c t g c c t g g 6826  
QY 2185 s p s e r g l y s e r g i n p r o a r g l e u c y a p r o s e r p r o s e r s e r l e u g l y g l y g l i n p r o l e u g 2205  
Db 6827 a c a g c g c t c c c a a c c c a c c t g g c a c a g a c c c t t a c t t a c t t g g g g c c a g c c t t g g 6886  
QY 2205 l y g l y p r o g l y s e r a r g p r o l y l y l e u s e r p r o b r o s e r l i s e r l i e a s p p r o p 2225  
Db 6887 g g g g g c c t g g a c c c g g c c c a a g a a a a a c t c a g c c g c t t a t a t c a c a t a g a c c c c c 6946  
QY 2225 r o g l u s e r g i n g l y s e r a r g p r o c y s e r p r o g l y a l c y l e u a r g a r g a l a p 2245  
Db 6947 c c a g a g a c c a a g a g t c c t c g a a c c c c g c c a g c c c t g t a t c t c c t c c g a g a g a g g c t c 7006  
QY 2245 r o a l a s e r a s p s e r l y a s p p r o s e r v a l s e r s e r p r o l e u a s p s e r t h r a l a l a s e r p 2265  
Db 7007 c g t c a c g c g a t c c a a g a g a t c c t t g g c c t t g g c c c c t g a c a g a t g c t g c c t g c g 7066  
QY 2265 r o s e r p r o l y s l y s a s p t h r l e u s e r l e u s e r g l y l e u s e r s e r a p p r o t h a s m e t a 2285  
Db 7067 c c t c c c c a a a a a g a t g t c t a g t c t c t c c g g t t a t c t c t g a c c c a g a c c a c c t g g 7126  
QY 2285 s p p r o 2286  
Db 7127 a c c c c 7131

RESULT 8  
US-10-062-674-2011  
; Sequence 2011, Application US/10062674  
; Publication No. US20040005559A1  
; GENERAL INFORMATION:  
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.  
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS  
; FILE REFERENCE: PA-0026-1 CIP  
; CURRENT APPLICATION NUMBER: US/10/062,674  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: US 09/625,102  
; PRIOR FILING DATE: 2000-07-24  
; NUMBER OF SEQ ID NOS: 2217  
; SOFTWARE: PERL Program  
; SEQ ID NO 2011  
; LENGTH: 8116  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040005559A1 404183.1  
; NAME/KEY: unsure  
; LOCATION: (1) ... (8116)  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-062-674-2011

Alignment Scores:

Pred. No.: 0 Length: 8116  
Score: 10707.00 Matches: 2098  
Percent Similarity: 89.92% Conservative: 52  
Best Local Similarity: 87.75% Mismatches: 130  
Query Match: 89.02% Indels: 112  
DB: 17 Gaps: 6  
US-09-611-257a-24 (1-2287) x US-10-062-674-2011 (1-8116)  
QY 3 p r o h a r g v a l p r o a r g c y s v a l a r g t h r p r o p r o l e u a r g l y s e r a l a r g p r o s e r 22  
Db 321 c c g c c g g g c c c c c g g g t t g c c t g a g a c a c c t c t t e a g a g g g g c c c c t t g c c c t c t 380  
QY 23 s e r a s p p r o p r o g l y p r o a r g l e u a l a a r g l y t r p t h r a r g a r g m e t g l u a r g a l a 42  
Db 381 c c g a g a t c g c c c g a g g c c c c g c t g g c c a g a g a t g a c a g a g a g a t g a g a g c g g c g 440  
QY 43 p r o a r g s e r a r g a s p s e r p r o v a l a l a s e r a r g s e r t h r c y a p r o g l y p r o g l y 62  
Db 441 c c g a g a g a t c g g a c a g c c c c g a g a c t t a t g c g c t c a a c a c a c c t g t c g g g g c c g g g 500  
QY 63 a l a - a l a g l y a l a - g l y s e r t h r g l u l y a s p p r o g l y s e r a l a a s p s e r g l u a l a g l u g 82  
Db 501 g c c g g c c g g g c c g g g g t c a g a g a a a g a c c c g g c a g c c g a c t t c c g a g g c g a g 560  
QY 82 l y l e u p r o f y r p r o a l a l e u a l a p r o v a l a l a p h e t h r l e u s e r g l n a s p s e r a r g p 102  
Db 561 g e c t g c c g t a c c c g a g g c c t g c c c g a t g t t t c t t a c t t a g a c c a g a c a g c c c c c 620  
QY 102 r o a r g s e r t r p c y l e u a r g t h r v a l c y a s n p r o t r p h e g l u a r g v a l s e r m e t l e u v 122  
Db 621 c c g a g a g t c g a t c c g a c a g c t g t a c c c t g a t t a g c g a t c a g a c a t g t t g g 680  
QY 122 a l l l e u l e u a n c y s v a l t h r l e u g l y m e t p h e a r g p r o c y s e g l u a p l l e a l a c y a 142  
Db 681 t c a t c t t t c a a c t c c g a c c t g g a c c t g g a c a t g t t c c g c a g a g a c a t c g c t g g 740  
QY 142 s p s e r g l n a r g c y a r g l e l e u g l n a l a p h e a s p a s p h e t l e p h e a l a p h e a l a y 162  
Db 741 a c t c c a g c c g c t g c c g a t c t c a g a c c t t t g a t a c t t a c t t t g c c t t t t g c c g 800  
QY 162 a l g l u m e t v a l a l y s m e t v a l a l a l e u g l y l e p h e g l y l y s l y c y s t y r l e u g l y a 182  
Db 801 t g a g a t g t g g a a g a g a t g g c c t t g g c a t c t t t g g a a a a a g t t a c t t c t g a g 860  
QY 182 s p t h r t r p a s n a r g l e u a s p p h e p h e l l e a l l e a l a g i y m e t l e u g l u t y r s e r l e u a 202  
Db 861 a c a c t t g g a a c c g c t t g a c t t t t c a t c g t a t c g c a g a g a t g c t g a g t a c t g c t g g 920  
QY 202 s p l e u g l n a s n a l s e r p h e s e r a l a v a l a r g t h r v a l a r g v a l l e u a r g p r o l e u a r g a 222  
Db 921 a c c t g a g a a c g t c a g c t t c t a g c t g t a g a c a g t c c g t g t c t g c a c c g c t a g g 980  
QY 222 l a l l e a s n a r g v a l p r o s e r m e t a r g l l e u v a l t h r l e u l e u a s p t h r l e u p r o m 242  
Db 981 c c a t t a a c c g g g t c c c a c a c a t g c g a t c t t g t a c g t t g c t g a t a g a t c c t c c a 1040  
QY 242 e t l e u g l y a s n v a l l e u l e u c y s p h e p h e v a l p h e p h e l l e p h e g l y l l e v a l g l y v 262  
Db 1041 t g c t g g a a c g t c c t g c t g c t t g t t c g t t c t t c a t c t t c g g a c a t c g t g g g 1100  
QY 262 a l g l n e u t r p a l a g l y l e u a r g a s n a r g c y a s p h e l e u p r o g l u a n p h e s e r l e u p 282  
Db 1101 t c a g c t g t g g a c a g g c t g c t t c c a a c c a t g c t t c t a c t a g a t t t c a g c t t c c 1160  
QY 282 r o l e u s e r v a l a s p l e u g l u p r o t y r t y r g l i n t h r i u a n g l u a p g l u s e r p r o p h e i 302  
Db 1161 c c c t g a g c g t g a c c t g a g c c g t a t t a c c a g a c a g a a c a g a t a g a c c c c t t c a 1220  
QY 302 l e c y s s e r g l n p r o a r g l u a n g l y m e t a r g s e r c y a r g s e r v a l p r o t h r l e u a r g 322  
Db 1221 t c t g c t c c a g c a c c g a g a a c g g a t g c g t c t g c a g a a g c g t g c c a c a g c t g c g g 1280

QY	322	lygluylgylgylgylgylProProCysSerLeuAspTyrgluThrTyrAsnSerSer	342
QY	1281	gggacggggggggggggccaccttggcgagctgagcttgaagccctaacagagctccgacga	1340
QY	342	snThrTyrCysValAsnTTPAsnglnTyrTyrThrAsnCysSerAlaGlyGlnHisAsp	362
Db	1341	ACACCACCTGTGTCACTGGAAACAGTACTACCAACTGTCTACGCGGGGAGCAACC	1400
QY	362	roPheLysGlyAlaAlaAsnPheAspAsnIleGlyTyrAlaTyrAlaAlaIlePheGln	382
Db	1401	CCTTCAAGGGGGCCATCACTTTGACAAACATGGCTATGGCTGATCGCATCTTCACG	1460
QY	382	allIethrLeuGlnGlyTyrPValAspIleMetTyrPheValMetAspAlaHiserPheT	402
Db	1461	TCATCAGCGTGGAGGGCTGGGTGCACATCATGTACTTGTGATGAGTGCCTATTCCTCT	1520
QY	402	YrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPheMetIleAsnLeuC	422
Db	1521	ACAAATTCATTACTTCACTCTCTCTCATCATGTGGGCTCTTTTCAATGATCACTGT	1580
QY	422	ysLeuValAlaIleAlaThrGlnPheSerGluThrLysGlnArgLysSerGlnLeuMet	442
Db	1581	GCCTGGTGGTATTTGCCACGCGATTCAGAGACCAAGCGGGAAAGCAGCTGATGC	1640
QY	442	rgGlnGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG	462
Db	1641	GGGAGCAGCGGTGCGGTTCCTGTCCACACGCGACACCCCTGGCTAGCTTCTCTGAGCCG	1700
QY	462	LysSerCysTyrGlnGlnLeuLeuLysTyrLeuValTyrTyleuAlxValAlaArg	482
Db	1701	GCACCTGTAAGAGAGCTGCTCAAGTACCTGGTGTACATCTTCTGTAGGCAACCCGCA	1760
QY	482	rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProVal	502
Db	1761	GGCTGGCTCAGGTCTCTCTGGGACAGAGTGTGGGGTTGGGCTCTCAGACGCCACAC	1820
QY	502	LArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS	522
Db	1821	CCCTCGGGGGCCAGAGACCCAGCCCGACACACATGCTCTCCGCTCCACCGCCGCTAT	1880
QY	522	erValHisIleLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHis	542
Db	1881	CCGTCCACCACTGATGNN	1940
QY	542	LyrThrLeuArgValProArgLaserProGluIleGlnAspArgAspAlaAsnLysSer	562
Db	1941	GGAGCGTACAGGCCCCCGGGCGACCCCGGAGATCAGAGACAGGATGCCAATGGGTCC	2000
QY	562	rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgLys	582
Db	2001	GCGGCTCATGCTGGCACCACTTCGACGCTCGGCCCTCTCGGGAGCCCCCTGTGGCG	2060
QY	582	lAgLysValHisSerPheTyrHisAlaAspCysHisLeuGlnProValArgCysGln	602
Db	2061	CAGAGTGTGACACAGCTTCAACATGCGGACTGTGACCTTGAAGCCAGTCCGCTGACGG	2120
QY	602	lAProProArgCysProSerGlnAlaSerGlyArgThrValGlySerGlyHisValT	622
Db	2121	CGCCCCCTCCAGAGTCCCATCTTGAAGCATCCGGAGATCTGTGGGACCGGGAAAGTGT	2180
QY	622	YrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV	642
Db	2181	ATCCACCGTGCACACCAAGCCCTTCCACCGGAGACGCTGAAGAGAGGCACTAGTAGAGG	2240
QY	642	AlaIAProSerProGlyProProThrThrThrSerPheAsnIleProProGlyProPheS	662
Db	2241	TGGCTGCAGCTTGGGGCCCCCAACCTTCACCAAGCTCAACAATCCACCCGGGCGCTTACA	2300
QY	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2301	GCTCATGACACAGCTGCTGTGAGACACAGATGACAGTGTCTGTCCAAAGCTCTTGCAAGA	2360
QY	682	lSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC	702

Db	2361	TCCTCAAGCCCTGCTTGA	AAAGCAGACAGTGGAGCTTGCTGATCCAGACAGCGCCCTACT	2420
Qy	702	ysaIaargThgIyAlaGly	uProGluSerAlaaphiIsvaIeCProaPbSerAsps	722
Db	2421	GTGCCCGGGCCGGGGCAGGGGAGGTGAGCTCGCCGACCGTGAAATCTCGACTCAACACA		2480
Qy	722	ergIuAlaValTyrgIuPherThcIlnsplaIagi	nHisSerAspLeuArgAspProHis	742
Db	2481	GCGAGGCAAGTTTAAGATGTACACAGAGATGCCAGCACAGCAACTTCCTGGGAAACCCCAA		2540
Qy	742	eraTargArgGlnArgSerLeuGlyProaPbAlaGluProSerSerValleuAlaPheT		762
Db	2541	AGCGGG--GGGCAACGAGCCTGGGCCACAGATGACAGACCCAGCTGTGTGCGCTTCT		2598
Qy	762	TPaTgLeuIleCyAspThrPhea	rgIysIleValaAspSerLysTygPheGlyValrgIyI	782
Db	2599	GGAAGCTATCTGTGACACCTTCGAAAGATTTGGACAGCAAGTACTTTGGCCGGGGAA		2658
Qy	782	IeMeTIIeAlaIleleuValaAsnThrLeuSerMetGlyIleGluTyHieGluInnProG		802
Db	2659	TCATGATGCGCATCTGTGTCAACACTTCAGACAGTGGCATGAAATACACAGCAGCGCCG		2718
Qy	802	IuGluLeuThrAsnAlaLeuGluIleSerAsnIleValIpheThSerLeuPheAlaLeuG		822
Db	2719	AGGAGCTTACCAAGCGCCTAGAAATCAAGCAACATCGTCTTCAACAGCCTCTTCCCTCG		2778
Qy	822	IuMeTLeuLeuYsaIeLeuValTyrgIyProPheGlyTyrlIeYasAnProTyraSnI		842
Db	2779	AGATGCTGCTGACAGCTGCTGTGATGATGCTCCTTTGGCTACATCAAGAAATCTCAACAA		2838
Qy	842	IePheAspGlyValIleValaValIleSerValTrrGluIleValGlyGlnGlnIyGlyG		862
Db	2839	TCTTCGATGGGTCAATGTGTGTCTATCGACCGTGTGGAGATGTGTGGCCAGAGGGGGCG		2898
Qy	862	LyLeuSerValLeuArgThrPheArgLeuMetArgValLeuYsaLeuValArgPheLeuP		882
Db	2899	GCCGTGCGGTCTGTGGACCTTCGGGCTGATGCGTGTGCTGACAGCTGTGTGGCTTCTGC		2958
Qy	882	roAlaLeuGlnArgGlnleuValValleuMetLysrHMetAspAsnValaIaThrPheC		902
Db	2959	CGGCGCTGACAGCGGACGTGTGTGGTGCATGAAGACATGAGCAACGTTGCCACTTCT		3018
Qy	902	ysMeTLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisleuPheGlyC		922
Db	3019	GCATGCTCTTATGCTCTTCACTTCATCTTCATCTTCACAGATCTCGGAGATGATCTTCGGCT		3078
Qy	922	YelYsPhePbAlaSerGlnArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL		942
Db	3079	GCAAGTTTGGCTCTGAGCGGGATGGGACACCTTGCCAGACCGAGAAATTTGACTCT		3138
Qy	942	euleTrrPAlaIleValaThrValPheGlnIleLeuThngInGluIuAspTrrAsnYsaI		962
Db	3139	TGCTGTGGGCATGTCTACTCTCTTTCAGATCTCGAACCCAGAGAGACTGGAACAAAGTCC		3198
Qy	962	euryTAsnGlyMetAlaSerThrSerSerTrrPAlaAlaLeuTygPheIleAlaLeuMetT		982
Db	3199	TCTCAAAATGATAGGCTCCACAGTGTCTCTGGGGCGCCCTTATTTATTCATCCCTCATGA		3258
Qy	982	hrPheGlyAsnTygValleuPheAsnLeuLeuValaIleValaGluGlyPheGlnA		1002
Db	3259	CCTTGCGAACACTGCTCTTCAATTTGCTGTGGTCCATTCCTGGTAGGGACTTCCAGG		3318
Qy	1002	IaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValaAspG		1022
Db	3319	CGAGGGAGATGCCAACAAGTCCGAATCAGAGCCGAGATTTCTTTCACCCAGCGCTGGATG		3378
Qy	1022	IyAspGlyAspArgIyLysIaIrgLeuAlaLeuValaIaLeuGlyGluHisAlaGluLeuA		1042
Db	3379	GTGAATGGGAGACAGGAAGAAGTCTTGCTGTGTGCTCTGCGGAGAGACCCGAGAGCTGC		3438
Qy	1042	rgLysSerLeuLeuProIleuIleIleHISrrAlaIaThrProMetSerHisProL		1062



Db 3439 GGAAGAGCTGCTGCGGCTCTCATCATCCACAGCGGCCGACACCCCATGTGCTGCCCA 3498  
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Db 3499 AGAGACACACACAGCGGCGGCGAGCGCTGGGCGCTGCGTGCCTGCCGACACAGACGA 3558  
Qy 1082 erGIySerAlaGIuProGIyAlaAlaHISHisGIuMetLysCyProProSerAlaArgS 1102  
Db 3559 GCGGAGTCGAGAGCCCTGGGGCGGCGC---CACAGATGAAAGTCAACGCCACGCGCCGCA 3615  
Qy 1102 exSerProHISerProIrpSerAlaAlaSerSerIrpThSerAArgSerSerAArg 1122  
Db 3616 GCTCTCGGACAGCCCTGAGCGCTGACAGCTGACACAGACAGCGCTCCAGCCGGA 3675  
Qy 1122 snSerIeuGIyAArgAlaProSerIeuLysAArgArgSerProSerGIyGIuAArgSerL 1142  
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Db 3736 TGTTGTGGAGAAAGCCAGAGAGCCAGATGAAAGAGAGCTCAAGAGAGAGCGGG 3795  
Qy 1162 laSerProAlaGIySerAspHisAArgHisAArgGIySerIeuGIuAArgAlaLysSers 1182  
Db 3796 CCAAGCCCTGCGGGGAGTGCATCGCCACAGGGGGTCCCTGAGCGGGAGCGCAAGAGTT 3855  
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Qy 1222 hrLeuAArgThrAspAspProGIuLLeuAspGIyAspAspAspAsnAspGIuGIyAsnLys 1242  
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Qy 1242 erLysGIyGIuAArgIleGIuAlaIrpValAArgSerAArgLeuProAlaCyCyAArgGIuA 1262  
Db 4036 GCMAAGGGGAACGGGTCGGCGCGTGCATCCAGGCCCACTCCCTGCTGCTCGACG 4095  
Qy 1262 rgaAspSerTPSerAlaTyrlIephProProGIuSerAArgPheAArgLeuLysCyHisA 1282  
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Qy 1282 rgiIleIleThrHisLysMetPheAspHisValValIeuValIleIephLeuAsnCySI 1302  
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Qy 1302 leThrIleAlaMetGIuAArgProLysIleAspProHISerAlaGIuAArgIlePheLeuT 1322  
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Qy 1322 hrLeuSerAsnTyrlIephThrAlaValPheLeuAlaGIuMetThrValIyValAla 1342  
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Qy 1362 lyLeuLeuValIeuIleSerValIleAspIleLeuValSerMetValSerAspSerGIyT 1382  
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Qy 1382 hrLysIleLeuGIyMetLeuAArgValLeuAArgLeuAArgThrLeuAArgProLeuAArgV 1402  
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Qy 1442 alGIuLeuPheLysGIyLysPhePheValCySGIuGIyGIuAspThrAArgAsnIleThrA 1462  
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Qy 1482 snLeuGIyGIuAlaLeuMetSerIeuPheValIeuAlaSerLysAspGIyTPValAspI 1502  
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Qy 1582 GIuLysGIuMetAlaGIuAlaGIuLysLysProTyrlTyrlSerAspTyrlSerAArgPheA 1601  
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Qy 1602 leuLeuValHisHisIleuCySerThrSerHisSTYrLeuAspLeuPheIleThrGIyValIle 1621  
Db 5116 CTCTGTCTCACCACTTGTGCACAGCCACTACCTGGACCTTTCATCAACAGTGTCAATC 5175  
Qy 1622 GIyLeuAsnValIleThrMetAlaMetGIuHisSTYrGIuGIuInProGIuIleLeuAspGIu 1641  
Db 5176 GGGCTGAAGTGTGTGTCATGAGCGCATGGAGCACTACCAAGACCCCAAGTTCGGATGAG 5235  
Qy 1642 AlaleuLysIleCyAsnTyrlIephThrValIlePheValPheGIuSerValPheLys 1661  
Db 5236 GCTGTGAAGATCTGCAACTACATCTTCACTGATCTTGTGTGGAGTCAAGTTTTCANA 5295  
Qy 1662 leuValAlaPheAlaPheAArgPhePheGIuAspAArgTPAsnGIuLeuAspLeuAla 1681  
Db 5296 CTTGTGGCTTTGGTTCCTGTGGTTCCTTCCAGAGAGGTGAACCAAGTGAACCTGGGCC 5355  
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Qy 1722 leuLeuLysMetAlaValGIyMetAArgAlaLeuLeuHisSTHValMetGIuAlaLeuPro 1741  
Db 5476 CTGCTGAAGATGGCTGTGGGCATGGGGGCTGTGTGGACACCGGTATGAGCGCCCTGGCC 5535  
Qy 1742 GIuValGIyAsnLeuGIyLeuLeuPheMetLeuLeuPheIlePheAlaAlaLeuGIy 1761  
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QY 1782 HISAATHRPHeargaenphleglMetAlaPheleuthrleupheargValserThrcly 1801  
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DB 5656 CATGCCACCTTTCGGAAGCTTTGGCATGGCTTCTTAACCTCTTCCAGTCTCCACAGGT 5715  
QY 1802 AAspAntThraAnglylIemelyAspProserArgAspCyS---AapGlnLuserThr 1820  
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DB 5716 GACAAATTGAATGGCAATTATGAMAGACACCTCCGGAGCTGCACCCACAGACAGCGAGC 5775  
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DB 5776 TGCCGTGAGAGCCCTGAGATTGTGTCCGCCGTGTACTTCGTGAGACTTCGTGCTCACCGC 5835  
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DB 5836 CAGTTCTGTCTCAACCAAGTGTGTGTGTCTGTCTGAAGACCTGGAGACAGACAGAC 5895  
QY 1859 LyngluAlaLyngluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetlyThreLeu 1878  
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DB 5896 AAGGAGGGGCGAGAGAGCGCCGAGATGGATGCCAGCTCGAGCTGGAGATGAGACCTC 5955  
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DB 5956 AGCCCCAGGCCCTGCTGGCACTGGGCAAGCCCTTCTGCTGGCTGGGGGTGAGGGCCCC 6015  
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DB 6016 GACAGCCCCGACAGCCCCCAAGCTGGGGCTCTGACACCCAGCGCCCAAGCGAGATCAGC 6075  
QY 1918 aSerGlyPheSerLeuGlnHIsProThr----- 1927  
DB 6076 CTCCCACTTTCCTTGAGACACCCACGACAGCACTGTTTACACCAATATCCCTGCT 6135  
QY 1927 ----- 1927  
DB 6136 GATCCAGGGCTCCTCGAGTGGAGCTGAAGCTATGAGACGAGTGGGAGGCCAGGGGG 6195  
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DB 6196 CCAAGCCTCTGCTTCTCTTCTGCCCCAGCTGGAGGCTCCGAGCCACAGATCCCTCT 6255  
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DB 6316 AGCTTGAACGATGACTTCTTGCTGATGATGACATGACACACTCTTACTTATGCGCTGA 6375  
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DB 6376 GAGCAATATGACGCCACCCACGAGAGCTGCCA-----GGACCAAGCTTACTGAC 6426  
QY 1945 rValArgLySerGlyValaSerArgThrHisSerLeuProaPheSerlyrMetCyAr 1965  
DB 6427 TGTGCGGAAGTCTGGGTGACACCCCACTCTCTGCGCAATGACACTTCAATGATGTCG 6486  
QY 1965 gAnGlySerThraIaGluArgSerLeuGlyHisArgGlyTyRProGlyLeuProLySAlaG 1985  
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DB 6487 GCATGGAGGACCTGCGGAGGGGCCCCCTGGACACAGGGGCTGGGGGCTCCCAAGCTCA 6546  
QY 1985 nSerGlySerIleLeuSerValHisSerGlnProAlaAphTherCySIIleuGlnLe 2005  
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QY 2005 uProLyAspValHisTyRLeuLeuGlnProHIsGlyAlaProHIsTrpGlyAlaIlePr 2025  
DB 6607 TCCCAAAATGCACTCTGCTGCTCAGCCCAAGCCCAAGCCCAACTGGGGGACCATCC 6666  
QY 2025 OlyLeuLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAl 2045  
DB 6667 CAAATGCCCCCAAGAGAGCTGCTCCCTTGGCTCAGAGGGCACTCAAGGGCCAGGGAGC 6726  
QY 2045 aIleArgThraSpSerLeuAapValGlnGlyLeuGlySer-ArgGluAapLeuLeuSerG 2065

DB 6727 AATTAAGACTGACTCTCTTGAGCTTCAGGGTCTGGGCAAGCCGGGAAGACTCTGCGAG 6786  
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QY 2085 lGlnValGlnGlnAArgSerGlyIleGlnSerlyValSerlyshIleArgLeuProA 2105  
DB 6847 CCAAGGACAGGACACTCCCGCAGCCACAGCAAGATCTCAAGACATACACCCCGCAG 6906  
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QY 2125 euGlnLeuAapThrGlnLeuSerTrpIleSerGlyAapLeuLeu---ProSerSerGln 2144  
DB 6967 TAGAGTTGACACGAGAGCTGAGATTTCAGAGAGCTCTGCGCCCTGCGCGCCAGG 7026  
QY 2144 lGlnLProLeuPheProArgAapLeuLylyGcyTyRserValGluThrGlnSerCySA 2164  
DB 7027 AGAGAGCCCCATCCCAAGGAGCTGAGAGAGTGAAGAGTCAAGCGTGAAGGCCCAAGCTGCC 7086  
QY 2164 rGARArgProGlyPheTrpLeuAapGlnGlnArgArgHisSerIleAlaValSerCySL 2184  
DB 7087 AGGCGCGGCTTACGTCTGCTGATGAGAGAGAGACACTTATGCGCTGACGTGCC 7146  
QY 2184 euApsSerGly-SerGlnProArgLeuCySProSerProSerSerLeuGlyGlnPro 2203  
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QY 2223 pProProGlnSerGlnGlySerArgProProCySserPro-GlyValCySLeuAArgArg 2243  
DB 7267 CCCCCGAGAGGACAGAGTCTGAGACCCCGCCAGCGCTGGGTGCTGCTCCGAGGA 7326  
QY 2243 rGAlaProAlaSerAspSerLySAspProSerValSer--SerProLeuAapSerThraI 2262  
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US-10-483-467-3  
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; Publication No. US20050164161A1  
; GENERAL INFORMATION:  
; APPLICANT: Kath, Gary S.  
; APPLICANT: McManus, Owen  
; APPLICANT: Gervantes, Tina  
; APPLICANT: Bennett, Paul B., Jr.  
; APPLICANT: Imredy, John P.  
; APPLICANT: Augustine, Paul R.  
; APPLICANT: Bugianesi, Randal M.  
; TITLE OF INVENTION: ELECTRICAL FIELD STIMULATION OF  
; FILE REFERENCE: 20794YP  
; CURRENT APPLICATION NUMBER: US/10/483,467  
; PRIOR FILING DATE: 2004-01-12  
; PRIOR APPLICATION NUMBER: PCT/US02/22161  
; PRIOR FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: 60/304,955  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 7898  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-483-467-3

## Alignment Scores:

Pred. No.:	0	Length:	7898
Score:	6242.00	Matches:	1387
Percent Similarity:	65.00%	Conservative:	208
Best Local Similarity:	56.52%	Mismatches:	536
Query Match:	51.90%	Indels:	325
DB:	22	Gaps:	64

US-09-611-257A-24 (1-2287) x US-10-483-467-3 (1-7898)

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Db 188 CCGGGCGGATGCCCGGGGAGCGCCCGGCGAGAGCGAGAGGTCTGC-CGGCCG--- 243
QY 23 SerAspProProGlyProArgLeuAlaArgGly-----TTP 34
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QY 35 ThrArgArg-----ArgMetGluArgAlaProArgSer 45
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QY 46 ArgAspSerProValAlaSerArgSerSerThrCysProGlyProGlyAlaAlaGly 65
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QY 66 AlaGlySerThrGluYasPProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
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QY 86 ProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgProArgSerTP 105
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Db 465 CCGGCTTGGCGGCGCACGCTCTTCTTCTGCTCGGTAGACCAAGCGGCGCGCAGCTGG 524
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Db 525 TGCTCTCCGGCTGGTCTGCCAACCATGGTTGAGCAGCTGAGCATGCTGGTAATCATGCTC 584
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
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Db 585 AACTGCGTGAACCTGGGCGATGTTCCGGCCCTGTGAGGACGTGAGTGCGGCTCGAGCGC 644
QY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValIleMetVal 165
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QY 166 ValIleMetValAlaLeuGlyIlePheGlyLysIleCysTyrLeuGlyAspThrTPAsn 185
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QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
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Db 765 AGGCTGATTTCTTCATCGTCTGCGCGGCGATGATGATGATGCTTTGGACGAGACAAAC 824
QY 206 ValSerPheSerIleAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
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Db 825 GTGAGCTCTCTGGCTATCAGAGACCGTGCGGGTGTGGGCCCTTCGCGGCATCAACCGC 884
QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 885 GTGCTTAGCATGGGAGACTGTGATCACTCTGCTGTGATAGCGTGGCCATGCTCGGGAAC 944
QY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTP 265
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 945 GTCTTCTGCTGCTCTTCTGCTCTTCTTCAATTTTCGGCATGCTGGCGTCCAGCTCTGG 1004
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QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1005 GCTTGCTCTCTCGGAACCGCTGCTTCTCGACAGTGCCTTTGTGAGAAACAACACTGG 1064
QY 286 Asp---LeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSer 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1065 ACCTTCTCGGCGCGTACTACAGACGAGGAGGCGGAGAGAACCCGTTCACTGCTCC 1124
QY 305 GlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgIleGluGly 324
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1125 TCACGCCGAGAACCGGACATGGAGAGTCTGCACATCCG-----GGCGCGCGC 1175
QY 325 GlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsn----- 338
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1176 GAGCTGCGATGCTCTGACCTTGGCTGGAGGCGCTACACCGACCGGCGGAGGGG 1235
QY 339 ---SerSerAsnThrThrCysValAsnTPAsnGlnTyrTyrThrAsnCysSerAla 357
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1236 GTGGGCGCTGCACGCAACCGCTGCATCACTGAACCACTTACACAGTGGCGGCTCG 1295
QY 358 GlyGluLeuAsnProPheIleGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTPile 377
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1296 GGTGACTCCAAACCCCAACAGGTGCATCACTTCGACAAATCGGCTTACCGCTGGATT 1355
QY 378 AlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAsp 397
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Db 1356 GCCATTTCCAGTATATCACTGGAAGGCTGGGTGACATATGATACACTCATGGAC 1415
QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417
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Db 1416 GCCCACTCATTTACAACTTCATTTATTCATCCGCTCATCATGCTGGGCTCTTCTTC 1475
QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrArgGlnArgGlu 437
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1476 ATGATCAACTGTGCTGGTGTGATGTGCACGAGTTTCGAGACGAGAGCGGGGAG 1535
QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1536 AGTCACTATGCGGGAGAGCGGGGACGCCACCTGTCCAAGACAGACGCGTGGCGACG 1595
QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuYsTyrLeuValTyrIleLeuArg 477
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1596 TTCTCCGACCTGGCAGCTGTACGAGAGCTGTGAAGTACGTGGGCGACATATTCCCGC 1655
QY 478 TyrAlaIleArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1656 AAGGTCAAGCGGCGAGCTTGGCCTTACGCCCGCTGSCAGACGCGCGCAAGAG 1715
QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1716 GTGACCCCAAGTCTGTGCAAGGCCAGGCTCC-----GGG 1751
QY 518 HisArgArg-----LeuSerValHisHisLeuVal---HisHis 529
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1752 CACCGGCACGCGCGGCGAGGACGACACAGCCTCGGTGCACACCTGCTTACACACAC 1811
QY 530 HisHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAla 549
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1812 CATCACCAACACACACACCATTCATTCACCATGAGGAGCCCCCGGACGGCCCGGCCCC 1871
QY 550 SerProGluIleGluAspArgAspAlaAsnGlySerArgArgLeuMetLeu-----Pro 567
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1872 GAGCCAGGGCGCTGCAC-----ACAGGCTGTGTCCGACTGGCGCG 1913
QY 568 ProProSerThrProThrProSerGlyGlyProProArgGlyAlaGluSerValHisSer 587
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1914 CCCCCCTGCCACCTTCCCGCAGCGCGGAGCCCGCC---GAGCGAGAGCTGTGACACAC 1970
QY 588 PheTyrHisAlaAspCysHisIleGlu-----ProValArgCysGlnAlaProProPro 605
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1971 ATCTACCAATGCCAGTCCACATTAAGAGGGCGCGCAGAGAGGGCCCGGTGGCACTGCC 2030
QY 606 ArgCysProSerGluAlaSerGlyArg---ThrValGlySerGlyVal---TyrPro 623
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Db 2031 GCAGCACTGCGCTGCAGCTGAGCTGGCCACAGGCTGGGACCATTAACCTCC 2090
Qy 624 ThrVal -----HisThrSerProProGluIle 633
Db 2091 ACGATCTCGCTCAGGGGTGGGACGGCAAGGACAGACACCCCGGACCCAG--- 2147
Qy 634 LeuLysArgLysValAlaLeuValAlaProSerPro-----Gly 647
Db 2148 -----GGGAAGTGGGCGGATGGACCGCAGGACCGGCGGCGGACCGG 2189
Qy 648 ProProThrLeuThrSerPheAsnIleProProGluProPheSerSerMetHisLysLeu 667
Db 2190 CCGTTGAGCTTGAACAGC-----CCTGATCCCTACGAAAGATCCCGCATGTG 2237
Qy 668 LeuGluThrGlnSerThrGlyAlaCys-----HisSerSer-----Cys 680
Db 2238 GTCGGGAGAGCTGAGCTGGGCGGAGCCCTGGCCATCTGTGGGCTCAGTGTGCTGC 2297
Qy 681 LysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysPro 700
Db 2298 CCCCTGGCCAGCCCG-----CGAGCGGGGACACTGACTGTGAGCTGAAGAGCTGCCG 2351
Qy 701 TyrCysAlaArgThr---GlyAlaGlyLysProGluSerAlaAspHisValMetProAsp 719
Db 2352 TACTGCAACCCCTGCGCTGGAGAACCCGGAGGATGAGCTCAGCGGCTCGAAAGTGAGAC 2411
Qy 720 SerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAsp 739
Db 2412 TCAATGCGCGTGGCGTATATGAATTCACGAGACGTCGGCAGCGTGACCGCTGGGAC 2471
Qy 740 Pro-----HisSerArg 743
Db 2472 CCCACGCGACACCCCGTGCAGCGACACACAGGCGCCGACGCGGACCGCCAGCGG 2531
Qy 744 ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheThrArg 763
Db 2532 CGGGCACAGCAGAGGAGGAGCCCG---GGCAGACCGAGCTGAGTGGCGCGCTCGGGTT 2588
Qy 764 LeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMet 783
Db 2589 ACCTTACAGCGGACAGCTGCGCGCATCTGGACACAGACTTACAGCGCTGGCATCTG 2648
Qy 784 IleAlaIleLeuValAsnThrLeuSerMetGlyIleGlyTyrHisGluGlnProGluGln 803
Db 2649 ATGGCATCTTTGTCAACACGCTGAGATGGGCGTGAATCAATCAAGACAGCCGAGAG 2708
Qy 804 LeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGlnMet 823
Db 2709 CTGACTAATGCTCTGGAGATCAGCAACATCGTTTCACACAGCATGTGTCCTGGAGATG 2768
Qy 824 LeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAspProTyrAsnIlePhe 843
Db 2769 CTGCTGAAGCTGTGGCTGCGCGCCCTCTGGGCTACATCCGGAACCCGTACAACTTTC 2828
Qy 844 AspGlyValIleValIleSerValTyrGluIleValGlyGlnGlnGlyGlyLeu 863
Db 2829 GACGGCATCATCGTGTATCATGAGCTGTGGAGATCGTGGGCGAGCGGACGATGCTTG 2888
Qy 864 SerValIleLeuArgThrPheArgLeuMetCysValLeuLysLeuValArgPheLeuProAla 883
Db 2889 TCTGTGCTGGCGACCTTCGCGCTGCTGCTGCTGGAAGCTGGTGGCTTTCCTGCAACC 2948
Qy 884 LeuGlnArgGlnLeuValIleLeuMetLysThrMetAspAsnValAlaThrPheCysMet 903
Db 2949 CTGCGGCGCGCACTGTGGTGTGGTGAAGACATGACCAAGCTGCTTCTTGCAAG 3008
Qy 904 LeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLys 923
Db 3009 CTGCTCATGCTCTTCAATTTCATCTTCAGCATCTGGGACATGCACTTTTCGGCTGCAAG 3068
Qy 924 PheAlaSerGluArgAsp---GlyAspThrLeuProAspArgLysAspPheAspSerLeu 942

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Db 3069 TTCAAGCTTGAAGACAGACACCGGACACAGCTGTGCAGAGAACTTGACTCCCTG 3128
Qy 943 LeuThrAlaIleValThrValPheGlnIleLeuThrGlnLysArgThrAsnLysValLeu 962
Db 3129 CTGTGGGCGCATGCTGACCGGTGTTCCAGATCTTCAACCCAGAGAGACTTGAACGTGGTCTG 3188
Qy 963 TyrAsnGlyMetLysSerThrSerSerThrAlaAlaLeuThrPheIleAlaLeuMetThr 982
Db 3189 TACAAAGGACATGAGCTTCACCTCTCTGGGCGGCTTCACTTCGTGGCGCTCATAGCC 3248
Qy 983 PheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGlyLysPheGlnAla 1002
Db 3249 TTGGGCAACTATGTGCTTCAACCTGTGTGGCATCTCTCGTGAAGGGCTTCAGAGCG 3308
Qy 1003 GlnGlyAspAlaThrLysSerGlySerGlyLysProAspPhePheSerProSerValAspGly 1022
Db 3309 GAGGCGATGCTCAACAGATCCGACACGAGAGAGCAAGTGGTCCATTGCTGAGAGAG 3368
Qy 1023 AspGlyAspArgLysLysValArgLeuAlaLeuValAlaLeu----- 1035
Db 3369 GACTTCCACAGACTCAGAGAACTCCAGACCAAGAGCTGAAGATGTGTTCCCTGGCCCTG 3428
Qy 1036 -----GlyGlnHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleThr 1053
Db 3429 ACCCCCAACGGGCACTCGAGAGGACAGAGAGCTGTGCCCTCCCTCCATCATATGACACA 3488
Qy 1054 AlaAlaThrProMetSerHisProLysSerSerSer---ThrGlyValGlyLysAlaLeu 1072
Db 3489 GCTGCAAGCCGCAATGCTTACCCCAAGAGCTCAATCTCTGATGACAGCCCGGCTC 3548
Qy 1073 GlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGluAlaAlaHis 1092
Db 3549 CCAGACTCTGGCTGGACAGACAGCTCCGGGAGCCCGGCACTGGGA----- 3596
Qy 1093 GlnMetLysCysProProSerAlaArgSerSerProHisSerProThrSerAlaAlaSer 1112
Db 3597 GACCAAGAACCTCCGGGCAACCTCCGAAGTTCTCCGTGACCCCTGGGGCCGAGTGGC 3656
Qy 1113 SerThrSerArgArgSerSerArgAsnSerLeuGlyValArgAlaProSerLeuLysArg 1132
Db 3657 GCTGAGAGACAGCGGCGCTCAGCTGAGAGAGCTGGGCGGCTGCCCCAGCTCAAGCGC 3716
Qy 1133 ArgSerProSerGlyValArgArgSerLeuLeuSerLysGlnGlnGlnSerGlnAsp 1152
Db 3717 CGCGGCAAGTGTGGGAACGTGAATCTCTGTGTGGCAAGGCAAGGCGACAGAC 3776
Qy 1153 GlnGluGlnLysSerSerGlnGluAspArgAlaSerProAla-----GlySerAspHisArg 1170
Db 3777 GACGAA-----GCTGAGAGAGGAGGAGGCGCGCGCGCGCTGGCCACCCCATGGG 3830
Qy 1171 HisArgGlySerLeuGlnArgGluAlaLysSerSerPheAspLeuProAspThrLeu-- 1189
Db 3831 CGGGCGAGTCCCTGGAACCCAGCGGCGCTGCGGCGCGCGCTCCGCGCTACCAAGTGC 3890
Qy 1190 -----GlnValProGlyLeuHis-----ArgThrAlaSer 1199
Db 3891 CGCGATCGGACCGGAGAGGTGGTGGCCCTCGCCAGCATTTCTTCTCGGATGACAGC 3950
Qy 1200 GlyArgSerSerAlaSerGlnHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
Db 3951 CAGCTTGAAGATGACCGGAGCTTGAAGACATCGACATCGAGAGACAGCTGTGCTGCTG 4010
Qy 1220 AlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAspGlyLys 1239
Db 4011 CATAAAGTGTGGAGCCCTACAAAGCCCAAG----- 4040
Qy 1240 AsnLeuSerLysGlyLysGlnAlaThrValArgSerArgLeuProAlaCysCys 1259
Db 4041 -----TGC----- 4046
Qy 1260 ArgGluArgAspSerTyrSerAlaTyrIlePheProProGlnSerArgPheArgLeu 1279
Db 4047 CGAGCGCGCAGAGGCTGGGCGCTTACCTCTTCCCCACAGAACGGTTCGGGTCTCC 4106

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QY 1280 CyHhAArg1Le1LeThrHisLysMetPheAspHisValValIleuValIleIlePheLeu 1299  
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 Db 4107 TGCCAGAAAGGTCAACACCAAGATGTTGATCACTGGTCTCGTTCATCTTCCTC 4166  
 QY 1300 AsnCysIleThrlIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIle 1319  
 |||:::|||||  
 Db 4167 AACTGCGTCAACATCGCGCTGGAGAGCGCTGACATTACCCCGGACACCGAGCGGCTC 4226  
 QY 1320 PheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLys 1339  
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 Db 4227 TTCTCCAGCGCTTCATTCATTCATCTTCACCGGCATCTTCCTGGCGGAGATGGTGAAG 4286  
 QY 1340 ValValAlaLeuGlyTyrProCysPheGlyGluGlnAlaThrLeuArgSerSerTrpAsnVal 1359  
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 Db 4287 GTGGTGGCCCTGGGGCTGCTGCTCCGGGACGACCGCTTACCTGGACAGACCTGGAACCTG 4346  
 QY 1360 LeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAsp 1379  
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 Db 4347 CTGGATGGGCTGCTGGTGGTGGTCCCTGGTGACATTGTGGTGGCATGGGCTCGGCT 4406  
 QY 1380 SerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgPro 1399  
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 Db 4407 GGTGGCCGCAAGATCCCTGGGTGTTCTGGCGTGGCTGGCTGGCGAGACCTGGCGGCT 4466  
 QY 1400 LeuArgValIleSerArgAlaGlnGlyLeuLysLeuValAlaGlnThrLeuMetSerSer 1419  
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 Db 4467 CTAAAGGTCAATACGCGGCGCGCGGCTCAAGTGGTGGTGAAGAGCGATATACGTCG 4526  
 QY 1420 LeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIle 1439  
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 Db 4527 CTACAGGCCCATTTGGGAACATCGTCTCATCTGGCGGCTTCTTCATCATTTTGGATC 4586  
 QY 1440 LeuGlyValAlaLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsn 1459  
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 Db 4587 TTGGGTGTGACGCTCTTCAAGGGAGAGTTCTACTACGACGAGGCGCCGACACAGAGAAC 4646  
 QY 1460 IleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsn 1479  
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 Db 4647 ATCTCCACCAAGGACAGCTGCGGCGCGGCTCACTACCGCTGGGTGGACCAACAGTACAC 4706  
 QY 1480 PheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValIleuAlaSerLysAspGlyTyr 1499  
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 Db 4707 TTGCACAACTGGGCGACGCGCTGATGTCTGTGCTGTGATCATCAAGATGATGATG 4766  
 QY 1500 ValAspIleMetCysTyrAspGlyLeuAspAlaValAlaGlnGlnProIleMetAsn 1519  
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 Db 4767 GTGAACATCATGTACGACGCGGCTGGATGCGGTGGTGTGACACGACGCTGTGCAAGAC 4826  
 QY 1520 HisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheVal 1539  
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 Db 4827 CACAACCCCTGGATGCTGCTGATCTTCACTCTTCTGCTCATCGTCAAGCTTCTTCGTG 4886  
 QY 1540 LeuAsnMetPheValGlyValAlaGlnAsnPheHisLysCysArgGlnHisGlnGlu 1559  
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 Db 4887 CTCAACATGTTCTGGGCGGTGTGTGTGAGAACTTCCACAAGTGGCGGACGACGAGAG 4946  
 QY 1560 GluGlnGluAlaArgArgArgGluGlnLysArgLeuArgLeuGlyLysLysValArgArg 1579  
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 Db 4947 GCGGAGAGAGCGCGCGCGGACGAGAGAGAGCGGCTGGCGCTTACGAGAGAGCGGACG 5006  
 QY 1580 SerLysGlyLysGlnMetAlaGlnAlaGlnCysLysProTyrTyrSerAspTyrSerArg 1599  
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 Db 5007 AGGACTTTCCCGACG---CCAGAGGCCAGCGCGGCTTACTATGAGCATCTACCTCC 5063  
 QY 1600 PheArgLeuLeuValHisHisLysCysThrSerHisTyrLeuAspLeuPheIleThrGly 1619  
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 Db 5064 ACGGCGCGCTCCATCTCACTGCTGTGTGACACGACATCTCCAGCTTTCATACCTTC 5123  
 QY 1620 ValIleGlyLeuAsnValValThrMetAlaMetGlnHisTyrGlnGlnProGlnIleLeu 1639  
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 Db 5124 ATCATCTGTGTCAACGTATCATCAACCATGTGCATGAGACATATTAACCAACCAAGTCGCTG 5183

QY 1640 AspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerVal 1659  
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 Db 5184 GACGAGGCCCTCAAGACTGCACTACGCTTCAACCATGTGTGTGTGTGTGACGCTGCA 5243  
 QY 1660 PheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeuAsp 1679  
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 Db 5244 CTGAAGCTGTGATCATTTGGTTCGGTCCGTTCTTCAAGACAGGTGAAACAGCTGGAC 5303  
 QY 1680 LeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGluIleGluValAsnLeu 1699  
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 Db 5304 CTGGCCATGTGTGTGTCACTCAAGGACATCAGCTGGAGAGATGAGATGAGCGCC 5363  
 QY 1700 SerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgVal 1719  
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 Db 5364 GCGCTGCCATCAACCCACCATCATCCGACATACGCGGTCTTGGATTCGCGCTGG 5423  
 QY 1720 LeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAla 1739  
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 Db 5424 CTGAAGCTGTGAAGATGCTACGCGGCATGCGCGCTCTGGACACTGTGTGTCMAAGCT 5483  
 QY 1740 LeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuPhePheIlePheAlaAla 1759  
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 Db 5484 CTCCCCAGGTGGGAACTTGGGCTTCTTTCATGCTCTGTGTTTATCTATGCTGGG 5543  
 QY 1760 LeuGlyValGlyLeuPheGlyAspLeuGlyCysAspGlyThrHisProCysGluGlyLeu 1779  
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 Db 5544 CTGGAGTGGAGCTGTTCCGAGGCTGAGCTGACATGACAGAAACACCCCGGACGGGCTG 5603  
 QY 1780 GlyArgHisAlaThrPheArgAsnPheGlyMetValaPheLeuThrLeuPheArgValSer 1799  
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 Db 5604 AGCAGGCAAGCCCACTTCAGCAACTTCGGCATGCGCTTCTCAAGCTGTTCGCGGTGC 5663  
 QY 1800 ThrGlyAspAsnThrAsnGlyIleMetLysAspProSerArgAspCys-----Asp 1816  
 |||:::|||||  
 Db 5664 ACGGGGACAACTGGAACGGAGATCATGAAGAACACCTCGGAGAGTCCCTCGTAGAGAC 5723  
 QY 1817 GlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeu 1836  
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 Db 5724 AAGCATGCGCTAGACATCTGGCGGCGCTGTGCGCGCTTACTGTGTGATCTTCGTTG 5783  
 QY 1837 ThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlnGlu 1856  
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 Db 5784 GTGGCCAGCTGCTGTGTGTGAACGTGTGTGGCGGCTGCTCATATGAAGACCTGGAGAG 5843  
 QY 1857 SerAsnLysGluAlaLysGluGlnAlaGluLeuGluAlaGluLeuGluMetLys 1876  
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 Db 5844 AGCAACAGAGGACAGGAGAGTGGAGCTGAGCGGCGGACATTCAGCTGGAGATGGCG 5903  
 QY 1877 ThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGlu 1896  
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 Db 5904 -----CAGGGCCCCGGG 5915  
 QY 1897 GlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGly 1916  
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 Db 5916 AGTGACAGCGCGGTGACCGGACAGAGCT----- 5945  
 QY 1917 AlaAlaSerGlyPheSerLeuGlnHisProThrMetValProHisProGluGluValPro 1936  
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 Db 5946 -----CCCTTGGCCAGAGAGACTCG 5966  
 QY 1937 ValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValaSerArgThrHisSer 1956  
 |||:::|||||  
 Db 5967 GGGCGCAGGAGATCCCAAACTCGTTGATGACGAAAGTGTCCGTGTCCAGATGCTCTG 6026  
 QY 1957 LeuProAsnAspSerTyrMetCysArgAsnGlySerThrAla----- 1970  
 |||:::|||||  
 Db 6027 CTGCCCAAGACAGCTACATGTTCAAGGCCCGGTGCTCCGCTCGGCGGCCACCCCGC 6086  
 QY 1971 -----GluArgSerLeuGlnHisArgGlyTyrTrpGlyLeuProLysAlaGlnSerGly 1987  
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 Db 6087 CCGCTCAGAGAGGTGAGATGAGACCTATGGGGCGGACCCCC-----TTGGGC 6137  
 QY 1988 SerIleLeuSerValHisSerGlnProAlaSerThrSerCysIleLeuGlnLeuProLys 2007

Dh	6138	TTCCGTTCCCTGTGTGCACTCTCCGCGCGAGAGTCTGTGCTTCCTCCAGATCCCACTG	6137
Qy	2008	AspValHis-----TyrLeuLeuGlnProHisGlyAla	2018
Dh	6198	GCTGTGTGTCCTCCAGCGAGAGGCGGAGCGCTCCACGCGCTGTGCTCCCTCGGGGACA	6257
Qy	2019	ProThrTrrpGlyAlaIleProIlybLeuProProGlyIlyArgSerProLeuAlaGlnIlyArg	2038
Dh	6258	-----GCCCGCTCCCACTCCAGCGCG	6281
Qy	2039	ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyIlySer	2058
Dh	6282	CTGTCTGTGCAAGACAGAGCGTGTCAACCGATTCCTTGAAGGAAAG--ATTGAACAGC	6338
Qy	2059	ArgGluAspLeuLeuSerGluVal-----SerGlyProSerCysProLeuThr	2074
Dh	6339	CCTTAGGGACACCCCTGGATCTCGAGAGCGTGTGAGAAAACCCCGGAGAGCGGTGACC	6398
Qy	2075	ArgSerSerSerPheTrrpGlyIlySerSerIleGlnValGlnIlyArgSerGlyIleGln	2094
Dh	6399	CAG-----GGGGGGCTCCCTGACATCCCAACACCGCTCCCAACGCGCC	6440
Qy	2095	SerIlyVal-----SerIlyHis-----IleArgLeuProAlaPro	2106
Dh	6441	GCCAGCGCTCCGCACTCGTAGCAATACCTTCGAGACGACTGCGTCTCAGCGCGCGCG	6500
Qy	2107	CysProGlyIleuGlnProSerTrrpAlaIlyAspProProGluThrArgSerSerLeuGln	2126
Dh	6501	GCCCCAGCGGAGAGAGCGCGGAGGCTCCGACCA-----	6536
Qy	2127	LeuAspThrGluLeuSerTrrpIleSerGlyAspLeuLeuPro--SerSerGlnGlnI	2145
Dh	6537	GCGACGAGAGGATCAGCCACATACACAGTCCGCGTCCCTCGAGACCCACAGCCGAG	6596
Qy	2146	ProLeuPhePro-----ArgAspLeuIlybIlyCysEtyr	2156
Dh	6597	CCCCATGCGCCCGAAGCCTCTCCGGTGGCCGCGCGAGCGAGACTGTGCGAGGCTCTAC	6656
Qy	2157	SerValGluThrGlnSerCysArgArgArgProGlyPheTrrpLeuAspGlnGlnIlyArg	2176
Dh	6657	AGCGTGAAGCTCAGGCGCTTCCTGAGACAAGCCGGC---CGGACAGACAGACATGGCGG	6713
Qy	2177	HisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerPro	2196
Dh	6714	CCCTCGCGGAG-----CTGGGACGCGGGAG-----CTTGGGGAG	6749
Qy	2197	SerSerLeuGlyIlyGlnProLeuGlyIlyPro-----GlySerArgProIlybIlyb	2214
Dh	6750	GCGAAGGCGCTGGGCG---CCTGAGGCGCAGCGCCGCTCGGTGTGCGCGGAGAAAGAGAG	6806
Qy	2215	LeuSerProProSerIleSerIleAspProPro--GluSerGlnGlySer--ArgPro	2232
Dh	6807	ATGAGCCCCCTCGATCTCGGTGAAACCCCTCGGAGAGACAGAGGCTTCGCGCGGCC	6866
Qy	2233	ProCysSerProGlyIly-----ValCysLeuArgArgAlaProAla-----	2246
Dh	6867	TCCCGGAGAGAGGGGCGAGCAACCACTGAGGCGGACAGACCCGCTCTGTGAGGCGAG	6926
Qy	2247	-----SerAspSerIlyAspProSerValSerSerProLeuAspSerThrAlaIlySer	2264
Dh	6927	CCTCAGAGGAGACTCCCTGAGAGCCCAAGAGGCTCTAGCGCGCGGGGGAGACCTTCAGCC	6966
Qy	2265	-----ProSerProIlybAspThrLeuSerLeuSerGlyIlyLeu	2277
Dh	6967	AAAGGGAGCGCTGGGCGCAGGCGCTCTCGCGGGCTGAGACCTTACCGTCCCAAGCTTT	7046
Qy	2278	SerSerAspProThrAspMet-----AspPro	2286
Dh	7047	GCGCTTGAAGCGGTGACCTCGGGGCTCCCAAGTGAGAACCTT	7088

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Sequence 51: Application US/10930301
Publication No. US20050062607A1
GENERAL INFORMATION:
APPLICANT: Issa, Jean-Pierre
TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
METHODS OF USE THEREFOR
FILE REFERENCE: JH01590
CURRENT APPLICATION NUMBER: US/10/930,301
CURRENT FILING DATE: 2004-08-30
PRIOR APPLICATION NUMBER: US/09/396,522
PRIOR FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 120
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 3993
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel
FEATURE:
NAME/KEY: CDS
LOCATION: (373)...(3993)
US-10-930-301-51

Alignment Scores:
Pred. No.: 0
Score: 6103.00
Percent Similarity: 95.49%
Best Local Similarity: 94.52%
Query Match: 50.74%
DB: 21
Length: 3993
Matches: 117
Conservative: 12
Mismatch: 52
Indels: 4
Gaps: 2
US-09-611-257A-24 (1-2287) x US-10-930-301-51 (1-3993)

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US-09-611-257A-24 (1-2287) x US-10-930-301-51 (1-3993)

QY	3	ProHlaBValAProAqGcysValAArgThrProProLeuAaGgIysSerAlaArgProSer	22
Db	281	CCGCGCGGGGCCCCCGGGTGGCGTGGAGACACTCTCTGAGAGGGGCGCGCTTGCCCTCT	340
QY	23	SetAspProProGlyProAqGLeuAlaArgIyIThrAArgAGArgMetGluArgAla	42
Db	341	CCGGATCGCGCGGGGCCCCGGCTGGCCAGAGATGAGACAGAGAGAGATGAGACGGCGG	400
QY	43	ProArgSerArgAspSerProValAlaSerArgSerThrThrCy/ProGlyProGly	62
Db	401	CCGAGGAGTCGGGACAGCCCCCGAGACTTCATGCGGCTCAAGACACTGTCGGGGGCGGGG	460
QY	63	Ala-AlaGlyAla-AlaGlySerThrGlyuysAspProGlySerAlaAspSerGluAlaGlu	82
Db	461	GCGGCGCGGGGCGCGGGGTACGAGAAAGAGACCGGGCAGGCGGACCTCCAGAGCGGAGG	520
QY	82	LysLeuProTyrrProAlaLeuAlaProValAlaPhePheTyLeuSerGlnAspSerArgp	102
Db	521	GCGTGGCCGTAACCGGGCGTGGCCCCGGAGTGTTTTCTTACTTGAAGCAGGACAGCGCC	580
QY	102	roArgSerITrpCysLeuArgThrValCybaenProITrpPheGluArgValSerMetLeuV	122
Db	581	CGGGAGCTGGTGCTCCGACAGGTCTGTAAACCTCGGTTTGAGACGCATCAGCAATGTGG	640
QY	122	allIleLeuLeuLeuLeuValThirLeuGlyMetPheArgProCyGlnAspIleAlaCysA	142
Db	641	TCATCTCTTCAACTCGCGTACCTGGAGCATGTTCCGGACATGGAGGACATCCGCTGTG	700
QY	142	spSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaV	162
Db	701	ACTCCCAAGCGCTGCCGAGATCTGCAGAGGCTTTGATGATTCATCTTGGCTTTTTCGCG	760
QY	162	alGluMetValIValIysMetValAlaLeuGlyIlePheGlyLysLysCyArgTyLeuGluY	182
Db	761	TGGAGATGGGTGTAAGATGTGGCTTGGGATCTTGGGAAAAAGTGAACCTGGAGG	820
QY	182	spThrITrPheAspArgLeuAspPhePheIleValIleAlaGlyMetLeuGlyITyTysSerLeu	202
Db	821	ACACTGGAAACGGGCTTGACTTTTCATGTCATGTCAGAGGATGCTGGAGTATCTCGCTGG	880

QY 202 spleuGlnaenValSerPheSerAlaValArgThrValArgValLleuAroProLeuAla 222  
Db 881 ACCTGGAGAAAGTCAGTCTCTGAGCTGTCAAGACGCTGTGTGCGACCGCTCAAGG 940  
QY 222 LaIleAenAArgValProSerMetArgIleuValThrIleuLeuAAspThrLeuPro 242  
Db 941 CCATTAAACGGGATGCCAGATGCGCATCTTGTCAAGTTGTGTGCGATACCTGCCA 1000  
QY 242 etIeuGlyAenValLleuLeuLeuCySphPheValPhePheIlePheGlyIleValGly 262  
Db 1001 TGTGGGGCAACGTCTGCTCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1060  
QY 262 aIeGlnLeuTPAlaGlyLeuLeuAArgSnaArgCySphLeuProGluAAspPheSerLeu 282  
Db 1061 TCAGAGGTGGGCAAGGCTCTTGGAAACGATGCTTCTTCACTGAGAAATTCAGCTCC 1120  
QY 282 roLeuSerValAAspLeuGluProTyrTyrGlnThrGluAenGluAAspGluSerProPhe 302  
Db 1121 CCTGAGCGTGGACCTGGAGCGCTATTACAGACAGAGAAAGAGATGAGAGCCCTTCA 1180  
QY 302 IeCySerGlnProAArgGluAAsnGlyMetAArgSerCySArgSerValProThrLeuAArg 322  
Db 1181 TCTGCTCCAGACCAAGCGAGAAACGAGCATGCGGCTCTGCAAGAGCGTGGCCACGCTGCGCG 1240  
QY 322 IyGluGlyGlyGlyProProCySerLeuAAspTyrGluThrTyrAAspSerSerA 342  
Db 1241 GGGACGGGGCGGGGCGCCACCTTGGCTGCAATGAGCGCTTCAACAACAGCTCCAGCA 1300  
QY 342 snThrThrCyValAAspThrAAsnGlnTyrTyrThrAenCySerAlaGlyLysAsn 362  
Db 1301 ACACCACTGTGTAACTGGAAACCAATCAACCAACTGCTCAAGCGGGAGAGACACAC 1360  
QY 362 roPheIyGlyAlaIleAAsnPheAAsnIleGlyTyrAlaATPLeaIlePheGln 382  
Db 1361 CCTTCAAGGGGGCATCACTTGAACAATTGGCTATGCTGATGCGCATCTTCAGG 1420  
QY 382 aIIeThrIeuGluGlyTyrValAAspIleMetTyrPheValMetAAspAlaHisSerPhe 402  
Db 1421 TCATCACGCTGGAGGCTGGGTGCATCATGATCTTGTGATGATGATGCTCATTCCTTCT 1480  
QY 402 yRAsnPheIleTyrPheIleuLeuIleIleValGlySerPhePheMetIleAsnLeu 422  
Db 1481 ACAATTTCAATCTTCAATCTCTCTCATCATCGTGGCTCTCTTCTTATGATCACTGT 1540  
QY 422 ySLeuValValIleAlaThrGlnPheSerGluThrIyGlnAArgGluSerGlnLeuMet 442  
Db 1541 GCTGTGTGTGATGGCAAGCATTTCTCAAGACCAAGCAGGGGAAAGCCAGCTGATGC 1600  
QY 442 rGluGluAArgValAArgPheLeuSerAAsnIleAspThrLeuAlaSerPheSerGluPro 462  
Db 1601 GGGAGCAGCGGTGGGTCTCTGTTCACAGCCAGCACCCTGGCTTCTCTGAGCCG 1660  
QY 462 IySerCyTyrGluGluLeuLeuLeuTyrIleuValTyrIleLeuAArgLysAlaIArg 482  
Db 1661 GCACTGTGTATGAGAGCTGTCTCAAGTACCTGTGTATCATCTTCTGTAAGCCCGCA 1720  
QY 482 rGluLeuAArgValAArgValAlaIleGlyValAArgAlaGlyLeuLeuSerSerProVal 502  
Db 1721 GGTGTGTGTCAAGTCTCTCGGGCAGCAGGTGTGGGGTGGGCTCTCAAGCAGCCACAC 1780  
QY 502 IAAArgSerGlyGlnGluProGlnProSerGlySerCySThrAArgSerHisAArgGlu 522  
Db 1781 CCTGTGGGGGCAAGAGCCAGCCAGCAGCAGCTGCTGTGTCTCCACCGCGCTTAT 1840  
QY 522 etValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHis 542  
Db 1841 CCGTCCACCACTGTGTGACCAACCAACCAACCAACCAACCAACCAACCAACCACTGGGCA 1900  
QY 542 IyThrLeuAArgValProAArgLaseProGluIleGlnAAspAArgAAsnGlySerA 562  
Db 1901 GGAAGCTCAGGGCCCCCGGGCCAGCCCGAGATCCAGGACAGGAGATCCCAATGGTGTCC 1960

QY 562 rGArgLeuMetLeuProProSerThrProThrProSerGlyGlyProProAArgIyA 582  
Db 1961 GCGGGGTATAGTGGCAACACCTCGAGCGCTCGCCCTCTCGGGGGCCCCCTGTGTGGCG 2020  
QY 582 IAGluserValHisSerPheTyrHisAlaAAspCyHisIleuGluProValAArgCySglnA 602  
Db 2021 CAGAGCTGTGTGACAGCTTCAACATGGCGCATGTGCACATTGAGCAATCGCTGCCAGG 2080  
QY 602 IaProProAArgCySProSerGluAAspGlyAArgThrValGlySerGlyLysValT 622  
Db 2081 CGCCCCCTCCAGGTCCCATGTGAGGATCCGGAGAGCTGTGGGCGAGGGGAAGTGT 2140  
QY 622 yRProThrValHisThrSerProProGluIleLeuLysAAspLysAlaLeuValGlu 642  
Db 2141 ATCCACCGGTGACACAGCCCTCCACCGGAGACCTGAGAGAAAGGACATAAGAGG 2200  
QY 642 aAlAAspSerProGlyProProThrLeuThrSerPheAAsnIleProProGlyProPhe 662  
Db 2201 TGGCTGCCAGCTCTGGGCCCCCAACCTTCAACAGCTCAACATCCACCCGGGCTTCA 2260  
QY 662 eRSeMetHisLysLeuLeuGluThrGlnSerThrGlyValaCyHisSerSerCySly 682  
Db 2261 GCTTCATGCAAGAGCTGTGGAGACACAGATACAGTGTCTGCCAAGCTTTGCAAGA 2320  
QY 682 IeSerSerProCySerLysAlaAspSerGlyAlaCyAspLysProAAspSerCyProTyr 702  
Db 2321 TCTCCAGCCCTTGCTTGAAGACAGACAGTGGAGCTGTGTCTCAAGCTGCCCTACT 2380  
QY 702 ySAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAAspSerA 722  
Db 2381 GTGCCCGGGCGGGGAGGGAGGTGAGCTCGCAGCCGTGAATGCTTGACTCAGACA 2440  
QY 722 eRGlulAlaValTyrGluPheThrGlnAAspAlaGlnHisSerAAspLeuAArgAAspProHis 742  
Db 2441 GCGAGCAGATTATGATGTTCACACAGATGCCAGACAGCACTCCGGGACCCCA 2500  
QY 742 eRArgArgArgGlnAArgSerLeuGlyProAAspAlaGluProSerSerValLeuAlaPhe 762  
Db 2501 GC---CGGGGCAAGGAGCCCTGGGCCAGATGCAGAGCCAGCTGTGTGCTGCTCT 2557  
QY 762 rPArgLeuIleCyAAspThrPheAArgLysIleValAAspSerLysTyrPheGlyAArgGly 782  
Db 2558 GGAAGCTTAATCTGTGACACCTTCGAAAGATTGTGACAGCAAGTCTTGGCCGGGAA 2617  
QY 782 IeMetIleAlaIleLeuValAAsnThrLeuSerMetGlyIleGluTyrHisGluGlnPro 802  
Db 2618 TCATGATCGCATCTGTGTCAACACTCAGATGGGCAATCCAAATCCACGAGACCCG 2677  
QY 802 IuGluLeuThrAAsnAlaLeuGluIleSerAAsnIleValPheThrSerLeuPheAlaLeu 822  
Db 2678 AGGAGCTTACCAAGCGCCCTTGAATCAGACATGTGCTTCAACAGCCTTTGGCCCTG 2737  
QY 822 IuMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAAspProTyrAAsn 842  
Db 2738 AGATGCTGTGAAGCTGTGTGTATGTCTCTTGGCTTACATCAAGATCCCTTACAA 2797  
QY 842 IePheAAspGlyValIleValIleIleSerValTrogIuIleValGlyGlnGlnGly 862  
Db 2798 TCTTCATAGGTGTCATGTGTGATCAGGCTGTGTGAGATCGTGGCCAGCAGGGGGGG 2857  
QY 862 IyLeuSerValLeuAArgThrPheAArgLeuMetAArgValLeuLysLeuValAArgPheLeu 882  
Db 2858 GCTGTGTGTGTGCGGAGCTTCCGCTATGTGTGTGTGTAAGCTGTGTGCTTCTG 2917  
QY 882 roAlaLeuGlnAArgGlnLeuValValLeuMetLysThrMetAAspAAsnValAlaThrPhe 902  
Db 2918 CCGCGCTGCAAGCGGAGCTGTGTGTCTCATGAAAGCAATGACCAACGTCGCACTTCT 2977  
QY 902 ySMetLeuLeuMetLeuPheIlePheSerIleIeuGlyMetHisIlePheGlyC 922  
Db 2978 GCATGTGTGTATGCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTT 3037  
QY 922 ySlySphLeuAAspGluAArgAAspGlyAAspThrLeuProAAspAArgLysAAsnPheAAspSer 942





QY 266 AlaGlyLeuLeuAlaArgAnaArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285  
 Db 694 GCGGGCTGCTGGTAACCGCTGCTCTGAGAGAACTTCAACACAGAGGATG 753  
 QY 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305  
 Db 754 GCCTTGCCCAATCTACAGCCGAGAGAGATGATGAGATGCCCTTCACTGCTGCTG 813  
 QY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325  
 Db 814 TCGGGCAACATGAGATGAATGGGCTGCATGAGATCCCGCTCAAGAGGACAG----- 867  
 QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339  
 Db 868 ---GGCGTGAAGTCTGCTGCTGCCAAGACGACCTTACACATTTGGGGGGGGCCGAC 924  
 QY 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357  
 Db 925 GACCTCAATGCCAGCGGCTCTGTGTCACTGGAAACGTTACTACATGATGCTCCGACG 984  
 QY 358 GlyGluHisAsnProPheGlyGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377  
 Db 985 GGCAGCGCCCAACCCCAAGAGGTCATCACTTGACAAACATCGGTTATGCTTGAT 1044  
 QY 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397  
 Db 1045 GTCTCTTCCAGGATGATCACTGGAAGGCTGGTGAAGATCATGATCATGATGAGAT 1104  
 QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417  
 Db 1105 GCTCACTCTTTCATCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCTTC 1164  
 QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437  
 Db 1165 ATGATCAACTGTGCTCGTGTGATAGCAGACCACTTCGAGACCAAGCAACGGAG 1224  
 QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457  
 Db 1225 CACCGGCTGATCTGGAGACGCGGACGCTACTCTGCTC---TCCACACGCTGGCCAGC 1281  
 QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477  
 Db 1282 TAGCCGAGCTGGCGACTGTGATGAGAGATCTTCCAGTATGCTGCGACATCTGCTGCG 1341  
 QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValAlaGlyLeuLeu 497  
 Db 1342 AAGGCCAAGCGCGCGCTGGGCTCTACAGGCTCTGACAGAGCCGCGCCAGGCCCTG 1401  
 QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517  
 Db 1402 ---GGCCGAGGCGCCGCGCCCGCCAAACCTGGGCGC----- 1437  
 QY 518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHis----- 533  
 Db 1438 -----CACGCCAAGAGCGCCGCGACCTACCATGGGAAGACTAAG 1476  
 QY 534 -----HisHisHisTyrHisLeuGlyAsn-----GlyThrLeuArgValPro 547  
 Db 1477 GGTCAAGAGATGAAGGAGGACATCTCGGAAGCGCGCATTCGACACTTGGAGCT 1536  
 QY 548 ArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuPro 567  
 Db 1537 ---GCTTCCCTGGAAATGATCACTCGGGAAGAGAGCTGCGCGCAACTA---GCCCC 1590  
 QY 567 OProProSerThrProThrPro-----SerGlyGlyProProArgGlyAlaGluSerVal 585  
 Db 1591 CTGATCGCAGCGCCCAACACCTGTGTGACAGCCCATCCCGCCAGC----- 1636  
 QY 585 HisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPr 605  
 Db 1637 -----TGCTTCCGATCC 1650

QY 605 oArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrVal 625  
 Db 1651 GCCAGCTGCCCTTGTGCTGCCAGATGAGAGCGCCGCGGCTCCGAGCTCG----- 1702  
 QY 625 HisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluValAlaProse 645  
 Db 1703 -----GCAGACCCGACTCGGCGCAAGAGGCTCGGCTG----- 1735  
 QY 645 rProGlyProProThrThrThrSerPheAsnIleProProGlyProPheSerSerMetHis 665  
 Db 1736 -CCGGAGCTCGCTGCTGCGC----- 1756  
 QY 665 sLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysIleSerSerPr 685  
 Db 1757 -----AGGACGAGCGGATGGCG----- 1774  
 QY 685 oCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgTh 705  
 Db 1775 -----AC 1776  
 QY 705 rGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAspSerGluAlaVal 725  
 Db 1777 GGGCCCGGAGCGGAGG----- 1795  
 QY 725 lTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg 745  
 Db 1796 -----ACGAGACCTCTCAGAACCTGGGGAAGAGAG-----AGGAGGAGAG 1836  
 QY 745 gGlnArgSerLeuGlyProAspAlaGluProSerSerValIleuAlaPheTrpArgLeuI 765  
 Db 1837 GAGCAGCGGATGCGGCGCTGCTGCTG---TGCAGGAGATGG-----TGCAGGAGAGC 1886  
 QY 765 eCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAl 785  
 Db 1887 GCGAGCCAAAGCTCGCGGCACTTGGAGACAGAGTCTTCAACCGGAGCATCATGATGCG 1946  
 QY 785 aIleLeuValAsnThrLeuSerMetGlyIleGlyTyrHisGluGlnProGluGluLeuTh 805  
 Db 1947 CATCTGTGTCAACACCGTCAAGATGGAGATCGAGCAACGAGAGCGGAGAGACTGAC 2006  
 QY 805 rAsnAlaLeuGluIleSerAsnIleValaPheThrSerLeuPheAlaLeuGluMetLeuLe 825  
 Db 2007 CAACATCTCGAGATGTGCAATGTGTCTTCAACAGCATGTTGCTCGTGAAGATGATCT 2066  
 QY 825 uLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGl 845  
 Db 2067 GAGGCTGCTGCACTTGGGCTCTTGCATCACTGCTTAACCTTACACATCTTGCACAG 2126  
 QY 845 yValIleValAlaIleSerValTrpGluIleValGlyGlnGlnGlyGlyLeuSerVal 865  
 Db 2127 CATCATTTGATCATCATGAGCATCTGGAGATCGTGGGCGAGCGGAGCGGTGGCTGCTG 2186  
 QY 865 lLeuArgThrPheArgLeuMetArgValaLeuLysLeuValaArgPheLeuProAlaLeuGl 885  
 Db 2187 GCTGCGAGCTTCCGCTGCTGCTGCTGCTGAAACGTGGCTTCATGCTGCTGCTGCG 2246  
 QY 885 rArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLe 905  
 Db 2247 GCGCCAGCTCGTGGTCTATGAAACATGAGCAACGAGGCAACCTTGTGACAGCTGCT 2306  
 QY 905 uMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysAlaPheAl 925  
 Db 2307 CATGCTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 2366  
 QY 925 aSerGluArgAsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTr 944  
 Db 2367 CTTCCCGACAGCACTGAGACACGCTGCGCCAGAGGAACCTTCACTTCCCTGCTGAG 2426  
 QY 944 pAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAs 964  
 Db 2427 GGCATGTGATCACTGATCTCAATCTCAACCCAGAGAGCTGAAGCTGTTCTTCAACA 2486  
 QY 964 nGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGl 984

Db	2487	TGGATGAGCCCTCCACTTCTCCCTGAGGCTCCCTTACTTGTGCGCCCTATGACTTCG	2546
Oy	984	YASrTYValLeuPheAenLeuValAlaIleLeuValGluIlePheGlnAlaGluI	1004
Db	2547	CACATATGTGCTCTTCAACCTGCTGTGTGSCCATCTCTGTGAGAGGCTTCCAGCGGAGG	2606
Oy	1004	YASpAlaThrIysSerGluSerGluProAapPheSerProSerVal-----	1020
Db	2607	TGACGCCCAATGCTCTCTACTCGACGAGGACCAAGACTCAACCAATAGACAGTTTGA	2666
Oy	1021	-----AapGlyAapGlyAapArgIlyAapArgIlyAapArgIlyAlaLeuValAla	1034
Db	2667	TMACTCCAGAGAGGCTTGACACAGCGGAGATCCCAAG-----CTCTGCCCAATCC	2720
Oy	1034	AlaGluIlyGluIleAlaGluLeuAlyGlySerLeuLeuProProIleIleIleIsthr--	1053
Db	2721	CATAGACCCCAATAGGACACTTGACCCCACTCTC-----CCACTGGGTGGGACCTAGG	2774
Oy	1054	-----AlaAlaThrProMetSerHisProIysSerSerSerThrGlyValGlyI	1070
Db	2775	TCCTGTGTGGCTGGGGAGCTGCC-----CCCGCACTCATCTGCAGCGGACCCCAT	2828
Oy	1070	uAlaLeuGlySerGlySerArgArgGlyThrSerSerSerGlySerAlaGluProGlyAlaI	1090
Db	2829	GCTGGTGGCCCTGGAGCTCCGAAAGAGAGATCATGTCTCTA-----GGAGAGAT	2879
Oy	1090	AlaHisGluMetIlyScyProProSerAlaArgSerSerProHisSerProIsthrSerAl	1110
Db	2880	GAGCTATACACAGCGCTCTCTGTCCAGCTCCCGAGACTCTTAACAGGCGCATAGGCGCG	2939
Oy	1110	AlaSerSerTrpThrSerArgArgSerSerArgAmsSerLeuGlyAlaAlaProSerIle	1130
Db	2940	CAGGCGGCGCTGGGGCAGCGCGCTCCAGCTGAGAAC-----AGCCT	2981
Oy	1130	uLysArgArgSerProSerGlyIlyAlaArgArgSerLeuLeuSerGlyIly--GlyGlnG	1149
Db	2982	CAGAGACAGCGCGCTGCGGCGGAGCATAGATCCCTGTCTCTCGGAGCGGCGCGCGG	3041
Oy	1149	uSerGlnAapGluGluGluSerSerGluGlu-----AapArgAlaSerProAlaGlySe	1167
Db	3042	CGCCCGGCTGTGCGAGGTTGCCCGGACGAGGAGCGCGCGGCGCGCACCCCTGCACAC	3101
Oy	1167	rAspHis-----ArgHisAr	1172
Db	3102	CCCAACAGCCCAACCATTCATCAAGGGCCCATCTGGCGACCGCCACCGCCACACCG	3161
Oy	1172	gGlySerLeuGluArgIlyAlaLysSerSerPheAapLeuProAapThrLeuGlnValPr	1192
Db	3162	CCGGACGCTGTCCCTCGACAAACAGGAGCATCGGTGACCTGGCGCGAGCTGTGCCCGGT	3221
Oy	1192	oGlyLeuHisArgThrAlaSerGlyArgSerSer-----AlaSerGluHisGlnAapCy	1210
Db	3222	GGGCGCCCAACCCCGGGCGCGCTGGAGGAGCGGACCGCGGCGCCCGGGCATAGAGACTG	3281
Oy	1210	aAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAap--AspProG	1229
Db	3282	CAATGGCAGAGTCCACG-----ATGGCAAAACGCTTTCACCAAGATGGGAGACG	3353
Oy	1229	nLeuAapGlyAapAapAapAapAapGlyIlyAmsLeuSerIlyGlyIlyAlaI	1249
Db	3336	CGGGATCGCGGAGAGATGAGAGAAATCACTACACCTGTGCTTCCGGTCCGCA	3399
Oy	1249	aTrpValArgSerArgLeuProAlaCyCyArgArgIlyArgAapSerTrpSerAlaTrpI	1269
Db	3396	GATGATGCACGCTTAAAGCCGACCTGGTCAGAGTCGCGCAAGACTGCTGTACTCT	3455
Oy	1269	aPheProProGlnInsArgPheArgLeuLeuCyHisIArgIleIleIsthrHisIlyMetPh	1289
Db	3456	CTTCTCTCCCGAAGACAGTTCGGGGTCTGTGTCAAGACATTAATGGCCCAAACTCTT	3515
Oy	1289	aAapHisValValLeuValIleIlePheLeuAmsCyIleThrIleAlaMetGluArgPr	1306

Db	3516	CGACTACGTGTCCTGGCCTTCATCTTTCTCACTGATCAACATCGCCCTGGAGCGCC	3515
Oy	1309	OLYSIIAASPProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheTh	1329
Db	3576	TCAGATGAGGCCGGGACAGCAACGAGCATCTTTCTCAACGGTGGCCAACTACATCTTCAC	3635
Oy	1329	ALAValAlaPheLeuAlaGluMetThrValLysValValAlaAlaLeuGlyTyrProAspPheGlyGly	1349
Db	3636	GGCATCTCTCGTGGGACAGATGACATTGGAAGTATGTCGTGGGCGCTGATCATTCCTGGCGCA	3695
Oy	1349	UGlnAlaTyrLeuArgSerSerTyrPasnValIleuAspGlyLeuMetValIleuIleSerVal	1369
Db	3696	GCAGGCGGACTACGACAGCAAGCTGGAACAGTCTGAAGGCTTTCTTGCTTCGTGTCAT	3755
Oy	1369	IIleAspIleLeuValSerMetValIserAspSerGlyThrLysIleLeuGlyMetLeuArg	1389
Db	3756	CATGACATCTCGTGTGTCTCGGCTCAGACCGGGGGAGCCAAAGATCTTGGGGGTCCTCCG	3815
Oy	1389	GValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLe	1409
Db	3816	AGTCTTGGGCTCTCGGCGCACCCCTACGCCCTTCGTCATCAAGCGGGGGCGGGCT	3875
Oy	1409	ULysLeuValValGlnThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleI	1429
Db	3876	GAAAGCTGGTGGTGGAGACATCACTCATCTCTCCCTCAAGCCCATCGGCAACATCGTCTCAT	3935
Oy	1429	ECysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1449
Db	3936	CTGCTGTGCTCTTCTTCATCATCTTTGGCATCTCGGAGTGAGCATGCTTCAGAGGCAAGTT	3995
Oy	1449	EPheValCysGlnGlyLysAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAl	1465
Db	3996	CTACCACTGTGTGGGCGTGGACACCCGGAACATCAACAAACCGCTCGGACTGCATGGCCGC	4055
Oy	1469	ASerTyrArgThrValArgHisLysTyrArgPheAspAsnLeuGlyGlnAlaLeuMetSe	1489
Db	4056	CAACTACCGCTGGGTCATCAACAAATACAACTTGGACAACTGGGCGCAGGCTTGATGTC	4115
Oy	1489	ILeuPheValIleuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAl	1509
Db	4116	CCTCTTGTCTCGGATCCAAAGATGGTGGGTGAACATCATGTATCAATGACATCGATGAC	4175
Oy	1509	AVAlGlyValAspGlnGlnProIleMetAsnHisAsnProThrMetLeuLeuTyrPheAl	1529
Db	4176	TGTTGCTGTGGACACGACCTGTGGACCAACAAACCCCTGGATGCTGCTGATCTTAT	4235
Oy	1529	ESerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValAlaGly	1549
Db	4236	CTCTCTCTGCTCATGTCAGCTCTTTTGCTCAACATGTTTGGGTGTCGTGTGTGA	4299
Oy	1549	UAsnPheHisLysCysArgGlnHisGlnGlyGlnGlyLysAlaArgArgGlyGlyLys	1569
Db	4296	GAACTTCCACAAGTCCCGGACGACACAGGAAGCTGGAAGAAGGACGCGCGGTGAGAGA	4355
Oy	1569	SArgLeuArgArgLeuGlyLysLysValArgSerLysLysGlyLysGlnMetAlaGluAlaGly	1589
Db	4356	GCGGCTGGGGCGCTCGGAGAAAGACGCGCG-----AAAGCCCA	4399
Oy	1589	NCysLysProTyrTyrSerArgPyrSerArgPheArgLeuLeuValHisLysCysThr	1609
Db	4396	GCGGCTGCCCTACTATGACCACTATTGTCACACCGGCTGCTCATCCATCGATGTGAC	4455
Oy	1609	ISerHisTyrILeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThiMetAl	1629
Db	4455	CAGGCACATACCTGAGCATCTTCATCATCTTGCTCATCTGCTCAACGTGGTCACCATATTC	4514
Oy	1629	AMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIle	1649
Db	4515	CTTGAGACATCAATCAACGCCACGTCCTTGAGAGCACCCCTCAAGATCTGCAACTATAT	4574
Oy	1649	EPheThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArg	1669
Db	4575	GTTTCAACACTGCTTTTGCTGGAGGCTGTGCTGAAGCTGGTGGGATTTGGTGTGAGGCG	4633



PRIOR FILING DATE: 1999-09-23  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 1  
 LENGTH: 6816  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURES:  
 NAME/KEY: CDS  
 LOCATION: (192)..(6716)  
 US-09-935-541-1

Alignment Scores:  
 Pred. No.: 0 Length: 6816  
 Score: 5420.00 Matches: 1223  
 Percent Similarity: 61.74% Conservative: 234  
 Best Local Similarity: 51.82% Mismatches: 494  
 Query Match: 45.06% Indels: 413  
 DB: Gaps: 60

US-09-611-257a-24 (1-2287) x US-09-935-541-1 (1-6816)

QY	12	ThrProProLeuAaArgGlySerAlaArgProSerSerAspPro-----	25
DB	207	TCCTCCGCTCTCTCTATCTGACAGCCGCCGCTGAGCCAGAGTCAACGAGACG	266
QY	26	ProGlyProArgLeuAlaArgGlyTyrThrArgArgMetGluArgAlaProArgSer	45
DB	267	CCCGGACCCCGG-----	278
QY	46	ArgAspSerProValAlaSerArgSerThrThrCysProGlyProGlyAlaAlaGly	65
DB	279	-----AGCCCCCATCTCCCGCCAGCGCTGAGAGAGCTCTGATGAGCT-----	326
QY	66	AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGlyLysLeuProTyr	85
DB	327	-----GATCTCT-----CATGTCCACAC	344
QY	86	ProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgProArgSerTyr	105
DB	345	CCAGACCTGGCGCCATTGCTCTTCTGCTGCGACAGACACACGAGCCCGGAACTGG	404
QY	106	CysLeuArgThrValCysAsnProTyrPheGluArgValSerMetLeuValIleLeuLeu	125
DB	405	TGCATCAAGATGCTGTGCAACCCGCTGTTGATGTGCAGATCTGTGATCTCTGCTG	464
QY	126	AsnGlyValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg	145
DB	465	AACTGCGTGACACTTGAGATGTACAGCCGTGCGACGACATGACTGCTGTCCGACCGC	524
QY	146	CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal	165
DB	555	TGCAGATCTCTGACAGCTCTTGTATGACTTCTTATCTCTTCTTCCATGAGATGCTG	584
QY	166	ValLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeuGlyAspThrTyrAsn	185
DB	585	CTCAAGATGCTGCGCTGGGATTTTGGCAAGAGTGCTGCTGCGGACCATGCAAC	644
QY	186	ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn	205
DB	645	CGCTCGATTTCTTATCGTATGTCAGAGGATGTGAGTACTCTCTGACCTTCAAGAC	704
QY	206	ValSerPheSerAlaValArgThrValArgValLeuAspProLeuArgAlaIleAsnArg	225
DB	705	ATCAACCTGTGACGCACTGCGACCTGCGCTCTGAGGCCCCCTCAAAACCATCAACGC	764
QY	226	ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn	245
DB	765	GTGCCCAAGATCGGATCTGTGTAACCTGCTCGACACACTGCCCATGCTGGGGGAT	824
QY	246	ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTyr	265
DB	825	GTCTGCTGCTGCTCTTGTGTTCTTTCATCTTGGCATATAGGTGTGAGCTCTGG	884

QY	266	AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal	285
DB	885	GGGGGCTGTGTGGTAACGCTCTCTGAGAGAACTTCAACCAAGGAGATGTG	944
QY	286	AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln	305
DB	945	GCCTTGCCCATATCTACAGCCGAGAGAGATGATGATGCTTCACTGCTGCTGCTG	1004
QY	306	ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGlyGly	325
DB	1005	TCGGCGCAATGAGATGATGAGCTGCTCATGATATCCCGCTCAAGAGGACG-----	1058
QY	326	GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer	339
DB	1059	---GGCGGTAGGCTGCTGCTGCTCAAGAGACGCTTACATGAGGCGGGCGCCAG	1115
QY	340	SerSerAsnThrThr-----CysValAsnTyrAsnGlnTyrTyrThrAsnCysSerAla	357
DB	1116	GACCTCAATGCCAGCGCTCTGTGTCACTGAAACCGTTACTACATGTGTGCGGACG	1175
QY	358	GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTyrIle	377
DB	1176	GGCAGCGCCCAACCCCAAGAGGTCATCACTTGAACAATCGGTATGCTTGAT	1235
QY	378	AlaIlePheGlnValIleThrLeuGlyTyrValAspIleMetTyrPheValMetAsp	397
DB	1236	GTCACTTCCAGGATGATCTGTGAGGCTGGTGAATCATGTACTGATGATGAT	1295
QY	398	AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe	417
DB	1296	GCTACTCTTCAACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCTTC	1355
QY	418	MetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGlu	437
DB	1356	ATGATCAACCTGTGCTCGTTGTATGACGACCACTTTCGAGACCAAGCAAGCGGAG	1415
QY	438	SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer	457
DB	1416	CACCGCTGATGTGCGAGCGGCGGACGCTTACCTGTC-----TCCACACGCTGGCAGC	1472
QY	458	PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg	477
DB	1473	TACGCCAGGCTTGGCACTGCTACAGAGATCTTCCAGATGTCTGCGACATCTGCGC	1532
QY	478	LysAlaIleArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu	497
DB	1533	AAAGCCAAAGCC-----CGGCGCTGGGCTCTACAGGCGCTGCAG	1574
QY	498	SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer	517
DB	1575	AGC-----	1577
QY	518	HisArgArgLeuSerValHisIleLeuValHisIleHisIleHisIleHisIleTyr	537
DB	1578	---CGGCGCCAGGCGCTG-----	1592
QY	538	HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp	557
DB	1593	-----GGCCGGAG-----	1601
QY	558	AlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGly	577
DB	1602	-----GCCCGGCGCCCGCCCAACCTGGGCGCC-----	1628
QY	578	ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro	597
DB	1629	-----CAGCGCAAG-----GAGCC	1643
QY	598	ValArgCysGlnAlaProProProArgCysAspSerGluAlaSerGlyArgThrValGly	617
DB	1644	CGGCACTACCAAGCTGTGCCCAACATAGCCCTCGATGG-----	1685

QY 618 SerGlyLysValTyrProThValHisThrSerProProGluIleuLysAspLys 637  
DB 1686 -----ACGCCCCACACC----- 1697  
QY 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657  
DB 1698 ---CTGGTGCAG-----CCCATCCCGCCACGCTGGCTTCC----- 1730  
QY 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676  
DB 1731 -----GATCCCGCCAGCTGCTTCCTGCTCCAG 1757  
QY 677 HisSerSerCysLysHisLeuSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696  
DB 1758 CATGAGGACGCGCGCGCGCTCGGCGCTGGGACGACCGACTTCGGGCGAGGAGGCTCG 1817  
QY 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716  
DB 1818 GGCTCC-----GGAGGCTCGGCTGGTGGGAGGAGCGAGGCG----- 1853  
QY 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736  
DB 1854 -----GATGGGACGCGGCGC-----CGAGCGAGCGAGACGAGCCTCTCGAGAA 1898  
QY 737 LeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756  
DB 1899 CTGGGGAGAGGAGAGGAGAGGAGAGAGCAG-----GCCGATGGGCGG 1940  
QY 757 SerValLeuAla-----PheTyrArgLeuIleCysAspThrPheArgLysIleValAsp 774  
DB 1941 GTCTGGCTGTGGGGGATGTGTGGCGGGAGACGCGAGCCAAAGCTGGCGGCGCATCTGTGAC 2000  
QY 775 SerLysLysThrPheGlyAlaArgGlyIleMetIleAlaIleuValAsnThrLeuSerMetGly 794  
DB 2001 AGAAGAAGACTTCAACCGGGCATCATGATGAGCCATCTGTGTCAACCGGTCAGCATGGGC 2060  
QY 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814  
DB 2061 ATGAGAGACACACAGAGCGCGGAGAGCTACCAACATCTGGAGATCTGCATGTGCTC 2120  
QY 815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGly 834  
DB 2121 TTCACCGACATGTTCCTCGAGATGATCTCTGAAGCTGGCTGATTTGGGCTCTTCGAC 2180  
QY 835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValITrGlu 854  
DB 2181 TACCTGGTAAACCTTCAACATCTTCGACAGCATTTGTCTATCATCAGCATCTGGAG 2240  
QY 855 IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874  
DB 2241 ATGCTGGGGGAGCGGAGCGGTGGGCTGTCCGTGCTGGGACCTTCGCGGCTGCTGGCTG 2300  
QY 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValIleuValIleuMetLysThr 894  
DB 2301 CTGAAACTGGTGGCTTCATGCTCGCTCGGCGGCGAGCTCGGGTCTCATGAAGAC 2360  
QY 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIle 914  
DB 2361 ATGACAACAGTGGCACCTTCTGATGCTCTCATGCTTCATCTTCATCTTCAGATC 2420  
QY 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu 933  
DB 2421 CTGGGATGCAATTTTGGCTGCAAGTTCAGCTCCGCGACGAGACTGAGACAGCGGTG 2480  
QY 934 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953  
DB 2481 CCGGACGAGAAAGCTTCGACTCCCTGCTGTGGGCGCATCGTCACTGTTCCAGATCTC 2540  
QY 954 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 973  
DB 2541 ACCGAGGAGGAGCTGGAGCGTTCCTCTTACAATGGACGTGGCTCCACTTCTCCCTGGGC 2600  
QY 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993

DB 2601 TCCCTTACTTTGTGGCGCTCATGACCTTGGCAACTATGTCTCTTCAACTGGCTGGTG 2660  
QY 994 AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013  
DB 2661 GCCATCTCTGTGAGGAGCTTCCAGGCGGAGGTGACGCCAATCGCTCTTACTCGACGAG 2720  
QY 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023  
DB 2721 GACGAGCTCATTCACATACAGAGTTGATTAAGCTCCAGAAAGCCTGACAGAC 2780  
QY 1024 GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGlnHisAlaGluLeuArgLys 1043  
DB 2781 GGAGATCCGAG-----CTTGCCCAATCCCAATGACCCCAATGGGACCTGGAGCCCC 2834  
QY 1044 SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrProMetSer 1059  
DB 2835 AGTCTC-----CACTGGGTGGGACCTAAGGTCTGTGGGGCTGGGAGACTTGC--- 2885  
QY 1060 HisProLysSerSerSerThrGlyValGlyAlaLeuGlySerGlySerArgThr 1079  
DB 2886 ---CCCGACTCTCATGCGAGCGGACCCCATGTGTGGCTCGGCTCCGAAAGAGC 2942  
QY 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysAspProSer 1099  
DB 2943 AGTGCATGTCTTA-----GGAGAGATGAGCTATGACAGCGCTCCGTTCAC 2993  
QY 1100 AlaArgSerSerProHisSerProTrpSerAlaAlaAspSerTrpThrSerArgArgSer 1119  
DB 2994 TCCCGAGCTCTTACTACAGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3053  
QY 1120 SerArgAspSerLeuGluYargAlaProSerLeuLysArgArgSerProSerGlyArg 1139  
DB 3054 AGCTGAGAC-----ACCTTCAAGCACAAAGCCGCTCGGCGAGCAT 3095  
QY 1140 ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluSerSerGlu 1158  
DB 3096 GAGTCCCTCTCTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAG 3155  
QY 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169  
DB 3156 GAGGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3215  
QY 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181  
DB 3216 CCCCATCTGGCGGACCGGCAACCGGCAACCGGCGGAGCTGTCTCTGCACAACAGGAGC 3275  
QY 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201  
DB 3276 TCGGTGAGCTGGCGGAGCTGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAG 3335  
QY 1202 SerSer-----AlaSerGluHisGlnAspCysAlaAspGlyLysSerAlaSerGlyArgLeu 1219  
DB 3336 GCGGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3389  
QY 1220 AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAspAspAspGlu 1238  
DB 3390 GCCAAGAGCTTTCACCAAGATGGGCGACCGGAGGATCGGGGAGGATGAGAGAGAA 3449  
QY 1239 GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys 1258  
DB 3450 ATGAGATACACCTGTGCTTCGCGGTCGCGCAAGATGATGAGGTCTATTAAGCCGAGCTGG 3509  
QY 1259 CysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeu 1278  
DB 3510 TCGGAGCTCGGAGAGACTGTGTCTTCACTCTCTCCCGAGAAAGGTTCCGCGGCTC 3569  
QY 1279 LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePhe 1298  
DB 3570 CTGTGTCAACCAATTAATCCCAAACTCTTGCAGTACGTGTGCTGTGCTTCTTCTTCTT 3629  
QY 1299 LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg 1318

Db 3630 CTCAATGCGATCCACCATCGCCCTGAGCGGCTCATGATCGAGCCCGGACAGACCGGAACGC 3689  
Qy 11ePheLeuThrLeuSerAsnTyr11ePheThrAlaValPheLeuAlaGluMetThrVal 1338  
Qy 1319 I1ePheLeuThrLeuSerAsnTyr11ePheThrAlaValPheLeuAlaGluMetThrVal 1338  
Db 3690 ATCTTTCACACCGGTCCACATCATCTTTCACGGGCATCTTCGTGGGGGATGACATGCAATG 3749  
Qy 1339 LysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn 1358  
Db 3750 AAGGTAGCTCGCTGGGCTTACTTCGGCGACGAGGGCTGACTTACGACGACGCTGGGAAAC 3809  
Qy 1359 ValLeuAspGlyLeuLeuValLeuLeuSerVal11eAsp11eLeuVal1SerMetValSer 1378  
Db 3810 GTGCTGAGTGGCTTCTTCTGCTTCGTGCATCATGCATCGATGAGTGGTCCCTGACCTCA 3869  
Qy 1379 AspSerGlyThrLys11eLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 1398  
Db 3870 GCCGGGGAGCGCAAGATCTTGGGGGTCTCCGAGTCTTGGGGCTTCGCGACCCCTAGC 3929  
Qy 1399 ProLeuArgVal11eSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer 1418  
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Db 3990 TCCCTCAAGCCCATCGGCAACATCGTCTCATCTGCTGCTGCTTCATCATCTTGGC 4049  
Qy 1439 11eLeuGlyValGlnLeuPheLeuGlyLysPhePheValCysGlnGlyGluAspThrArg 1458  
Db 4050 ATCTCGGAGTGCAGCTCTTCAAGGGCAAGTTCTACCATCTGCTGGGGGTGAGACCCGC 4109  
Qy 1459 Asn11eThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr 1478  
Db 4110 AACATCAACCAACCGCTCGAGCTGAGTGGCCGCAACTACCGCTGGTCCATCACAAATAC 4169  
Qy 1479 AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly 1498  
Db 4170 AACTTCGACCAACTGGGCCAGGCTGTGATGCTCTTGTGCTGTGGCATCCAAAGATGT 4229  
Qy 1499 TrpValAsp11eMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnPro11eMet 1518  
Db 4230 TGGGTGAACATCATGTTACATGAGTGAATGCTGTGTGCTGTGAGACACAGAGCTGTGACC 4289  
Qy 1519 AsnHisAsnProTrpMetLeuLeuTyrPhe11eSerPheLeuLeu11eValAlaPhePhe 1538  
Db 4290 AACCAACAACCCCTGATGCTGTGACTTCACTCTTCCTGCTCATGTGACGCTTCTT 4349  
Qy 1539 ValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGln 1558  
Db 4350 GTGCTCAACATGTTGTGGGTGTGCTGTGAGAACTTCCACAAAGTGCCTGGACAGCAG 4409  
Qy 1559 GluGluGluGluAlaArgArgArgGluLysArgLysArgArgArgLeuGlyLysLysArg 1578  
Db 4410 GAGGTGAAGAGGACCGGCGGCTGAGAGAGAGAGCGGCTGCGGCGCTGGAGAGAGAGCGC 4469  
Qy 1579 ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSer 1598  
Db 4470 CGG-----AAGGCCAGCGGCTGCTGCTTACTAGTCCACTATGTT 4508  
Qy 1599 ArgPheArgLeuLeuValHisHisLysLeuCysThrSerHisTyrTyrLeuAspLeuPhe11eThr 1618  
Db 4509 CACACCCGCGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATC 4568  
Qy 1619 GlyVal11eGlyLeuAsnValVal11eThrMetAlaMetGluHisTyrGlnGlnProGln11e 1638  
Db 4569 TTTCATCATCTGCTCACTGCTGCTCAACATGCTCCGAGAGCACTACATCAAGCCAGCGTCC 4628  
Qy 1639 LeuAspGluAlaLeuLys11eCysAsnTyr11ePheThrVal11ePheValPheGluSer 1658  
Db 4629 CTGGAGACAGCCCTCAAGTACTGCAACTATATGTTACACCATGCTTTGTGTGAGGCT 4688  
Qy 1659 ValPheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeu 1678  
Db 4689 GTGCTGAAGCTGTGCTATTTGTCTGAGGCGCTTCTTCAAGAACCGATGGAACGAGCTG 4748

Qy 1679 AspLeuAla11eValLeuLeuSer11eMetGly11eThrLeuGluGlu11eGluValAsn 1698  
Db 4749 GACCTGGCCCATTTGCTACTAGTCAATGAGATGATCACTTGAAGGAGATGAGATCAAT 4808  
Qy 1699 LeuSerLeuPro11eAsnProThr11eLeuArg11eMetArgValLeuArg11eAlaArg 1718  
Db 4809 GCGGCGCTGGCCCATCAATCCACCATATATCCGATCATAGAGGTTCTGCGCATTTGCCGA 4868  
Qy 1719 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln 1738  
Db 4869 GTGCTGAAGCTGTGAAGATGGCCACAGAGATGGGCGCTGCTGACACGATGTCAA 4928  
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Db 4929 GCTTTCGCCAGGGGGCAACTGGGCTCTCTTCAATGCTGCTCTTCTTCACTATAGCT 4988  
Qy 1759 AlaLeuGlyValGluLeuPheGlyAspLeuGlyCysAspGluThrHisProCysGluGly 1778  
Db 4989 GCTTCGGGGTGAAGCTCTTGGGAAGCTGTGTGCAACAGACAGAACCCGTGAGGGC 5048  
Qy 1779 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1798  
Db 5049 ATGAGCGCGGATGCACTTCGAGAACTTCGCGATGGCTTCCACACTTTCAGAGTC 5108  
Qy 1799 SerThrGlyAsnAsnTrpAsnGly11eMetLysAspProSerArgAspCys---AspGln 1817  
Db 5109 TCCACGGGTGCACTGGAACGGGATCATGAAAGCAGCGTGGGAGCTGACCCACGAC 5168  
Qy 1818 GluSerThrCysTyrAsnThrVal-----11eSerPro11eTyrPheValSerPheVal 1835  
Db 5169 GAGGCAAGCTGCTGAGCAGGCTGCAAGTGTGTGTGCTGCGCGCTGACTTCTGTAGCTTGTG 5228  
Qy 1836 LeuThrAlaGlnPheValLeuValAsnValVal11eAlaValLeuMetLysHisLeuGlu 1855  
Db 5229 CTCACCGGAGATTGCGTGCATCATCAAGCTGTGTGTGCTGTGCTCATGAGACCTGGAC 5288  
Qy 1856 GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluGluMet 1875  
Db 5289 GACAGCAACAAAGGAGGGGAGAGAGAGCCGAGATGAGTCCGAGCTGAGCTGGAATG 5348  
Qy 1876 ---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGly 1894  
Db 5349 GCCCATGCGCTGGGCGCTGGCGCCGAGGCTGTAACGGCTCC----- 5390  
Qy 1895 ValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHis 1914  
Db 5391 -----CGGGGCGCGCTGGCCGAGGGCGG--- 5414  
Qy 1915 11eGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValPro----- 1930  
Db 5415 ---GAGGGGCGGGCGGGCGG-GGGCGAACCCGAGGGCGGCTGTGGCGGCGCTGACTC 5470  
Qy 1931 -----HisProGluGluValProValPro 1938  
Db 5471 GCTGCGCCAGGACTCTTGGAGGGGAGAGCTGACCATATGACAAACCTGTGGGCTCAT 5530  
Qy 1939 LeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1958  
Db 5531 CTTCCACCATCAATCTCTCGCTGCGGCTGCAAGAGTCA-----CCA 5575  
Qy 1959 AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGly 1978  
Db 5576 CGACAA-----GCAAGAGGTGAGCTGTGTGAGACGGA 5608  
Qy 1979 TrpGlyLeuProLysAlaGlnSerGlySer11eLeuSerValHisSerGlnProAlaAsp 1998  
Db 5609 GAGCTTCTCCCTGAAGTCAAGACAGTCTCTGCTCATCTGTGGGTACACACTGAGTCT 5668  
Qy 1999 ThrSerCys11eLeuGlnLeuProLysArgValHisTyrLeuLeuGlnProHisGlyAla 2018  
Db 5669 CGAGGA-----CCSCACAGGCTGTG 5686



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Qy      2019 ProthThrProglYalAalleProlys----- 2026
      |||||
Db      5687 CCCACCTGG-----CCGCAAGACACAGAGGTGAGCTGAGCCACCTGAGCCCAT 5737
Qy      2027 ---LeuProProProglYArGserProLeuAlaGlnArgProLeuArgArGlnAlaA 2045
      |||||
Db      5738 GCGGTGGAGAGACTGTGGCGCAATGCTTCTCCCTTGT-CCTCTACGCGCGCTCGCGGG 5796
Qy      2046 ILeArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGlu 2065
      |||||
Db      5797 ATCCAGAGAACTTCTCTGT---GTGAGATGAGAGAGATCCCAT-----TCACCC 5841
Qy      2066 ValSerGlyProSerCysProLeuThrArgSerSerSerSerSerThrProGlyGlySerSerIle 2085
      |||||
Db      5842 CTGTCGGGTCTGCTGCTAAACATGACA----- 5868
Qy      2086 GlnValGlnGlnArgSerGlyIleGlnSerGlyValSerIleValSerIleArgLeuProAla 2105
      |||||
Db      5869 -----GCAGTCAAGACACCCCAAGTCCCTTCT 5895
Qy      2106 ProCysProGlyLeuGluProSerTerTrpAlaLeuAspProProGluThrArgSerSerLeu 2125
      |||||
Db      5896 CCC-----CGGATGCTCCAGCC----- 5913
Qy      2126 GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2145
      |||||
Db      5914 -----CTCTCTGCCCATGCCAGCCGAGTCTTCCACCCCTG 5949
Qy      2146 ProLeuPhePro-----ArgAspLeuAlaLeuCysTySerValGluThrGlnSerCys 2163
      |||||
Db      5950 CAGGTGTGCGACGACAGAAAGCCCAAGAAAGGCACTGGACACTGGAAACCTCCCAAGA 6009
Qy      2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCys 2183
      |||||
Db      6010 TTGGGCTTG-CAGGCTCTCTGGGCACTC-----CTGGGATCCACCAAGGATCAACTGT 6059
Qy      2184 Leu-----AapSerGlySerGlnProArgLeuCysProSerProSerSerLeu 2199
      |||||
Db      6060 ACCCTCTCCGGACGAGCCACCGGAGGAGGACAGTCTGAGACGCCACCCCAAGCAG-CTC 6118
Qy      2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLeuAlaLeuSerProSer 2219
      |||||
Db      6119 CGCGGCGAGCTGTGACACACGCTCGAGACAGCTCACCCTGAGCAGACCCCGCGCG 6178
Qy      2220 IleSerIleAspProProGluSerGlnGlySerArgProCysSer-----ProGly 2237
      |||||
Db      6179 -----TGCCCTGGGGCGCCCGCGCTGCTCCAGAACCCCGGCG 6217
Qy      2238 ValCysLeuArgArgArgAlaProAlaSerAspSerLeuAspProSerValSerSerPro 2257
      |||||
Db      6218 CGGCTGTCTCCCGCCCTGCGCGCGCTGAGCTCGCGCGCGGCGCTTTCAGCTT 6277
Qy      2258 LeuAspSerThrAlaAlaSerProSerProLeuAlaSerThrLeuSerLeuSerGlyLeu 2277
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Db      6278 GCGGGGCGCTGGGGCGCATCAGCGCACGACGAGCGGGGCGCTCCACGACCGCGGCTG 6337

RESULT 13
US-10-425-800-1
; Sequence 1, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: AND USES
; CURRENT APPLICATION NUMBER: US/10/425,800
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192) ..(6716)
US-10-425-800-1

Alignment Scores:
Pred. No.: 0
Score: 5420.00
Percent Similarity: 61.74%
Best Local Similarity: 51.82%
Query Match: 45.06%
DB: 16 Gaps: 60

US-09-611-257a-24 (1-2287) x US-10-425-800-1 (1-6816)
Qy      12 ThrProLeuArgGlySerAlaArgProSerSerAspPro----- 25
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Db      207 TCCCGGCTCTCTCATCTGACGAGCCCAAGCCGCTGAGCCAGATCACACGAGACAG 266
Qy      26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
      |||||
Db      267 CCGGAGCCCGG----- 278
Qy      46 ArgAspSerProValAlaSerArgSerSerThrTrpCysProGlyProGlyValAlaGly 65
      |||||
Db      279 -----AGCCCCCATCTTCCCGCCAGGCTGAGAGACCTTGAGATGAGCT----- 326
Qy      66 AlaGlySerThrGluAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
      |||||
Db      327 -----GATCT-----CATGCCACAC 344
Qy      86 ProAlaLeuAlaProValAlaPhePheTyrlleuSerGlnAspSerArgProArgSerTrp 105
      |||||
Db      345 CCAGACCTGCGCGCTATCTCTCTGCTGCGACAGACCAACCAAGCCCGGAACTGG 404
Qy      106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
      |||||
Db      405 TGCATMAATGTTGTCACACCGGTGTTGAATGTGAGATGCTGTGATGATCTGCTG 464
Qy      126 AsnCyValThrleuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
      |||||
Db      465 AACTGCTGACACTTGGCATGTACACAGCCCTGCGACGATGACTGCTGTCGACCCG 524
Qy      146 CysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePheAlaValGluMetVal 165
      |||||
Db      525 TGCMAATCTTGACAGGTCTTGTATGACTTCATCTTATCTTGTGCCATGAGATGGTG 584
Qy      166 ValIleMetValAlaLeuGlyIlePheGlyIleValCysTyrlleuGlyAspThrTrpAsn 185
      |||||
Db      585 CTCMAATGTTGCTGCGGAGATTTTGGCAAGAGTGTACTCGGGGACACATGGAAC 644
Qy      186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGlyTyrlleuAspLeuGlnAsn 205
      |||||
Db      645 CGCTGATTTCTTCACTCTCATGCGAGGAGATGTGAGATCTCTCGAGCTTCAGAAC 704
Qy      206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
      |||||
Db      705 ATCAACCTGTACAGCCATCCGCAACCGGCGGCTCTGAGAGCCCTCAAAACCAACCCG 764
Qy      226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
      |||||
Db      765 GTGCCAGATAGTGGATCTCTGGAACCTGCTTCGACACACTGCGCCATGCTGGGGAAAT 824
Qy      246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
      |||||
Db      825 GTCTCTGTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 884
Qy      266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnAspSerLeuProLeuSerVal 285
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Db      885 GCGGCGCTGTGTGTATCCGCTGCTTCTGAGAGAGAACTTCAACCATCAAGAGGAGATGTG 944
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QY 286 AspleuGluProTyrrTyrgInthrGluAanGluaspGluSerProPheIleCysSerGln 305  
 |||||  
 945 GCCTGGCCCCCATCTACACGCGGAGAGATGATGATGCCCTTCATCTGCTCCCTG 1004  
 QY 306 ProArgGluAanGluMetArgSerCysArgSerValProThrLeuAanGlyGluGly 325  
 |||||  
 1005 TCGGAGCCACATGGATATGGCTGCCATGATCCCGCTCCAGAGAGAG- 1058  
 QY 326 GlyGlyProProCysSerLeu-----AspTyrgIuThrTyraAsnSer 339  
 |||||  
 1059 ---GGCGTAGAGCTGCTCTGTCCAGAGACGCTTACATCTTGGGGGGGGCGGAG 1115  
 QY 340 SerSerAsnThrThr-----CysValAsnTPraasnIntTyrrThraanCysSerAla 357  
 |||||  
 1116 GACCTCAATGCGAGCGGCTCTGTGTCACTGAAACGTTACTTACATGTGTGCGCAGC 1175  
 Db 358 GlyGluHisAsnProPheIlyGlyAlaIleAsnPheAsnIleGlyTyrrAlaThrIle 377  
 |||||  
 1176 GCGAGCCCAACCCCAAGGGTGCATCAACTTGACAAATCGGTTATGCTTGATTT 1235  
 QY 378 AlaIlePheGluValIleThrLeuGluGlyTrpValAspIleMetTyrrPheValMetAsp 397  
 |||||  
 1236 GTCAATCTTCAGAGTATCACTGTAAAGCTGGGTGGAGATCATGTACTACATGAT 1295  
 QY 398 AlaHisSerPheTyrrAsnPheIleTyrrPheIleLeuLeuIleValGlySerPhePhe 417  
 1296 GCTCACTCTTTCACAACTTCACTTACTTCACTGCTTATCATAGTGGCTCTCTTC 1355  
 QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrIlyGlnArgGlu 437  
 |||||  
 1356 ATGATCAACCTGTGCTGCTGTGTATGCGAGCCAGTTCGAGACCAACCAAGCGGAG 1415  
 QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457  
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 1416 CACCGGCTGATGTGAGACAGCGGAGGCTACCTGTCC---TCCAGACGCGTGGCAGC 1472  
 Db 458 PheSerGluProGlySerCysTyrrGluIleuLeuLeuTyrrLeuValTyrrIleuAarg 477  
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 1473 TACGCCAGAGCTGGAGACTGCTGACAGAGATCTTCCAGTATGTCTGCACATCTGTGGC 1532  
 QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497  
 |||||  
 1533 AAGGCCAAGGCC-----CGCGCCCTGGGCTCTACAGAGCCCTGAG 1574  
 QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517  
 |||||  
 1575 AGC----- 1577  
 Db 518 HisArgArgLeuSerValHisIleLeuValHisIleHisIleHisIleHisIle 537  
 |||||  
 1578 ---CGGCCCGCAGGCCCTG- 1592  
 QY 538 HisLeuGluAanGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557  
 |||||  
 1593 --- 1601  
 Db 558 AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly 577  
 |||||  
 1602 ---GCCCGGCGCCCGCCCAAGCGGCGCC- 1628  
 QY 578 ProProArgGlyAlaGluSerValHisSerPheTyrrHisAlaAspCysHisIleuGluPro 597  
 |||||  
 1629 ---CAAGCCCAAG-----GAGCCC 1643  
 QY 598 ValArgCysGlnAlaProProProArgArgCysProSerGlyAlaSerGlyArgThrValGly 617  
 |||||  
 1644 CGGCACTACCAAGCTGTGCGCAACATAGCCCGCTGATGCG- 1685  
 QY 618 SerGlyLysValTyrrProThrValHisIleSerProProProGluIleLeuLysAspLys 637  
 |||||  
 1686 ---ACGCCCCACAC- 1697

QY 638 AlaLeuValGluValAlaProSerProGlyProProThrThrLeuThrSerPheAsnIlePro 657  
 |||||  
 1698 ---CTGATGAG-----CCATCCCGCCACGCTGCTTCC----- 1730  
 Db 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676  
 |||||  
 1731 ---GATCCCGCCAGCTGCTTCTCCAG 1757  
 QY 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696  
 |||||  
 1758 CATGAGACGCGCGCGGCTCTGCGCAGCAGCAGCAGCTCGGCGCAGAGAGGCTCG 1817  
 QY 697 AspSerCysProTyrrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716  
 |||||  
 1818 GGCTCC-----GGAGCTTCGCTGTGGGAGAGCAGAGCC- 1853  
 Db 717 MetProAspSerAspSerGluAlaValTyrgIuPheThrGlnAspAlaGlnHisSerAsp 736  
 |||||  
 1854 ---GATGGGACGGGGCC-----CGAGCAGCAGAGCAGAGCTTCTCAGAA 1898  
 QY 737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756  
 |||||  
 1899 CTGGGAGAGAGAGAGAGAGAGAGAGAG-----GCGATGGGGCG 1940  
 Db 757 SerValLeuAla-----PheTPraGluIleCysAspThrPheArgLysIleValAsp 774  
 |||||  
 1941 GTCTGCTGTGCGGGATGTGTGCGGAGACCGGAGCCAGCTGCGGCGCATGTGGAC 2000  
 QY 775 SerIleTyrrPheGlyArgGlyIleMetIleAlileuValAsnThrLeuSerMetGly 794  
 |||||  
 2001 AGCAAGTACTTCAACCGGGCATCATGATGCCATCTGCTCAACCCGACAGATGGC 2060  
 Db 795 IleGluTyrrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814  
 |||||  
 2061 ATGAGACACACAGCAGCGCGAGAGCTGACCAACATCTCGAGAGTCCCAATGTGTCT 2120  
 QY 815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrgIyProPheGly 834  
 |||||  
 2121 TTCAACGACATGTTTGCCGTGAGATGATCTGAAGCTGGCTGCATTTGGAGCTTTCAG 2180  
 QY 835 TyrrIleLysAsnProTyrrAsnIlePheAspGlyValIleValIleSerValTrrGlu 854  
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 2181 TACTGTGTAACCCCTTACACATCTTGCACAGCATATTTGTATCATACAGATCTGGAG 2240  
 Db 855 IleValGlyGlnGlnGlyGlyLysLeuSerValLeuArgThrPheArgLeuMetArgVal 874  
 |||||  
 2241 ATGTTGGGACAGGCGGAGCGTGGGCTGTCCGTCTCGGAGCTTCCGCTGTCCGCGTG 2300  
 QY 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValLeuMetLysThr 894  
 |||||  
 2301 CTGAACCTGTGGCTTCAATGCTGCTCGCGGCGGCGGAGCTGTGGCTCATGAAGACC 2360  
 QY 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIle 914  
 |||||  
 2361 ATGGACACGTGGCACCCTTCTGATCTGTGTCTATGCTCTTCACTTCACTTCAAGATC 2420  
 Db 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu 933  
 |||||  
 2421 CTGTGATGATATTTTGGCTGTGCAAGTCAAGCTTCGCGACGAGCAGTGGAGACCGGTG 2480  
 QY 934 ProAspArgLysAsnPheAspSerLeuLeuThrAlaIleValThrValPheGlnIleLeu 953  
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 2481 CCCGACAGAAACCTTCACTCTGTCTGTGGGCAATCGTCACTGTGTTCACATCTC 2540  
 QY 954 ThrGlnGluAspTPraAsnLysValLeuTyrrAsnGlyMetAlaSerThrSerSerTrrAla 973  
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 2541 ACCAGAGAGACTGAACGTCTTCTTACATGAGCATGAGCTTCACTTCTCCCTGGGCG 2600  
 Db 974 AlaLeuTyrrPheIleAlaLeuMetThrPheGlyAsnTyrrValLeuPheAsnLeuVal 993  
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 2601 TCCTTACTTGTGCGCCCTCATGACCTTGGGCAACATGATGTGCTTCAACCTGTGTGT 2660  
 QY 994 AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013

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Db      2661  |||||GCGATCTGGTGGAGGCTTCCAGGCGGAGGTGAGCGCAATGCTCTCACTGAGCAGG 2720
QY      1014  |||||AerpPheserProserVal-----AerpGlyAsp 1023
Db      2721  |||||GACCAGAGCTCATCCAACTAGAAAGATTGATAGCTCCAGAGAGCGCTGACACAGC 2780
QY      1024  |||||GlyAspArgGlyValArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgGly 1043
Db      2781  |||||GGAGATCCCAAG-----CTCTGCCCAATCCCATAGACCCCAATGGAGCACTGGACCCC 2834
QY      1044  |||||SerLeuLeuProProLeuIleIleHisThr-----AlaIleThrPrometSer 1059
Db      2835  |||||AGTCTC-----CCACTGGGTGGGCACTAGAGCTCGTGGGGCTGGGGAGCTGGCC--- 2885
QY      1060  |||||HisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr 1079
Db      2886  |||||-----CCCCGACTCTCAGTCAGCGGACCCCATGCTGGTGCCCTGGGCTCCCGAAAGAGC 2942
QY      1080  |||||SerSerSerGlySerAlaGluProGlyValAlaAlaHisIleGluMetLysCysProProSer 1099
Db      2943  |||||AGTGTATGTTCTTA-----GGAGGATGAGCTATATACAGCGCTCTGTCCAGC 2993
QY      1100  |||||AlaArgSerSerProHisSerProTIPSerAlaAlaSerSerTIPThrSerArgArgSer 1119
Db      2994  |||||TCCGGAGGCTCTTAATAAGGCGCATGGAGCGCGGAGCGGCTGGGCGAGCGCTGCTCC 3053
QY      1120  |||||SerArgHisSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg 1139
Db      3054  |||||AGCTGGAAC-----AGCTCAACGACAAAGCGCGCTGCGGGGAGCANT 3095
QY      1140  |||||ArgSerLeuLeuSerGlyGlu---GlyGluGluSerGlnAspGluGluGluSerSerGlu 1158
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QY      1159  |||||Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
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QY      1170  |||||-----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181
Db      3216  |||||CCCCATCTGGCGGACCGGCGCACCGCCACCGCGCGGAGCGCTGCTCCGCAACAGGAGAC 3275
QY      1182  |||||SerPhaAspLeuProAspThrLeuGluValProGlyLeuHisArgThrAlaSerGlyArg 1201
Db      3276  |||||TGGGTGAGCTTGGCGGAGCTGCTGCGCGCGGTGGGCGCGGCGCGGCGGCTGGAGG 3335
QY      1202  |||||SerSer-----AlaSerGluHisGluAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
Db      3336  |||||GCGGAGGCGCGGCGCGCGGCGCATGAGACTGCAATGGCAGATGCCAGC-----ATC 3389
QY      1220  |||||AlaArgThrLeuArgThrAsp---AspProGluLeuAspGlyAspAspAspAspAspGlu 1238
Db      3390  |||||GCCAAGAAGCTCTTCCACCAAGATGGGCGACCGCGGGATGCGGGAGATGAGAGAA 3449
QY      1239  |||||GlyAsnLeuSerLysGlyGluArgGluAlaArgValArgSerArgLeuProAlaCys 1258
Db      3450  |||||ATGAGCTACACCTGTCCTTCCGCTCCGCAAGATGATGACGTCTATAAGCCGAGTGG 3509
QY      1259  |||||CysArgGluArgAspSerTIPSerAlaTyrIlePheProGluInserArgPheArgLeu 1278
Db      3510  |||||TGGGAGGTCCGGAAGACTGCTGCTTACCTTCTCTCCGAGAAACAGAGTTCGCGGTC 3569
QY      1279  |||||LeuCysHisArgGlyIleIleThrHisLysMetPheAspHisValIleLeuValIleIlePhe 1298
Db      3570  |||||CTGTGTGAGCCATTAATGCGCAACACTTTCGAGCTACGTCGTCTGCGCTTCACTTTT 3629
QY      1299  |||||LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg 1318
Db      3630  |||||CTAACTGCACTACCATGCGCTGGAGCGGCTCAAGTCAAGTCAGAGCGGCGGAGCAACG 3689
QY      1319  |||||IlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVal 1338

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Db      3690  |||||ATCTTTCACCGGTGTCCAACTACATCTTACGCGCATCTTGTGGGCGAGATGACATTTG 3749
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Db      3750  |||||AAGTAGTCTCGCTGGGCGCTGTATCTCGCGAGCGAGCGGTACTTACGCGAGCTGGAAC 3809
QY      1359  |||||ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer 1378
Db      3810  |||||GTGCTGAGAGGCTTCTTCTGTCGTGTCATCATGACATGATGATGATGATGATGATGATG 3869
QY      1379  |||||AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 1398
Db      3870  |||||GCCGGGGAGCCCAAGATCTTGGGGGGCTCCGAGCTTGGCGCTCTGGGCAACCTTACCC 3929
QY      1399  |||||ProLeuArgValIleSerArgAlaGluGlyLeuLysLeuValValGluThrLeuMetSer 1418
Db      3930  |||||CCCTGCTGTATACGCGCGGCGCGGCGCGGAGCTGAAAGCTGATGAGACACTCATCTCC 3989
QY      1419  |||||SerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGly 1438
Db      3990  |||||TCCCTCAAGCCCATGGGCAACATCGTGCATCTGCTGTGCTTTCATCATCTTGGC 4049
QY      1439  |||||IleLeuGlyValGluLeuPheLysGlyLysPhePheValCysGluGlyGluAspThrArg 1458
Db      4050  |||||ATCTGGAGTCAAGCTTTCAAAGGCAAGTTCACACTGTCTGGCGTGGCGTGGACACCCGC 4109
QY      1459  |||||AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTyrValArgHisLysTyr 1478
Db      4110  |||||AACATACCAACCGCTGGAGCTGCATGGCGGCCCAACTACCGCTGGGTCCATACAAATAC 4169
QY      1479  |||||AspPheAspAsnLeuGlyGluAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly 1498
Db      4170  |||||AACTTGACAACTGGGCGAGGCTGATGTCCTCTTGTCTGGGCACTCAAGATGTGT 4229
QY      1499  |||||TyrValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGluInProIleMet 1518
Db      4230  |||||TGGGTGAAATATGATGACATGACATGATGATGATGATGATGATGATGATGATGATGATG 4289
QY      1519  |||||AsnHisAsnProTIPMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe 1538
Db      4290  |||||AACCAACACCCCTGATGCTGCTGATCTTCACTCTCTCTGCTGCTGCTGCTGCTGCTGCT 4349
QY      1539  |||||ValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGluHisGlu 1558
Db      4350  |||||GTGCTCAATGTTTGTGGGTGTCGTGCGTGAAGACTTCCACAAAGTCCGCGGAGCAGCAG 4409
QY      1559  |||||GluGluGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysValArg 1578
Db      4410  |||||GAGGCTGAAGAGGCAAGCGGCGGTGAGGAAGCGGCTGCGCGCTGGAGGAAGAGCGCGC 4469
QY      1579  |||||ArgSerLysGluLysGluMetAlaGluAlaGluCysLysProTyrTyrSerAspTyrSer 1598
Db      4470  |||||CGG-----AAGGCCAGCGGCTGCTCTATGCTCACTTGTGT 4508
QY      1599  |||||ArgPheArgLeuLeuValHisLysCysGlyHisSerHisTyrLeuAspLeuPheIleThr 1618
Db      4509  |||||CACACCGGCTGCTGATCCACTGCAATGTCACACGCACTTACCTGGAACATCTTCAACACC 4568
QY      1619  |||||GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGluInProGluIle 1638
Db      4569  |||||TTCATATGTGCTCAACGTGTGACCAATGCTCTGGAGCACTACCAATGAGCCACGTCC 4628
QY      1639  |||||LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSer 1658
Db      4629  |||||CTGGAGACAGCCCTCAAGTACTGCAACTATATGTTTCAACACATGCTTGTGTGCGAGGCT 4688
QY      1659  |||||ValPheLysLeuValAlaPheAlaPheArgArgPheGluAspArgTIPAsnGluLeu 1678
Db      4689  |||||GTGCTGAACCTGGTGCATTTGTGTGAAGCGCTTCTTCAAGGACCGAGTGAACAGCAGTGTG 4748
QY      1679  |||||AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1698
Db      4749  |||||GACCTGGCATGTGTCTACTGTCACTGATGAGGATCAACCTTGAAGAGATGAGATCAAT 4808

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Qy	1699	LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	1718
Db	4809	GGCGCCCTGGCCCAATCAATCCACCATATCCGACATCAATGAGGGTTGTGGCGATTGCCGA	4868
Qy	1719	ValLeuLeuLeuLeuLeuLeuMetAlaValGIWetArgAlaLeuLeuLHisThrValMetGIh	1738
Db	4869	GTGCTGAAGAGCTTTGAAGATGGCCACAGAAATGGGGCCCTGCTGGACACGGTGGTCAA	4928
Qy	1739	AlaLeuProGlnValGIYAsnLeuGIYLeuLeuPheMetLeuLeuPhePheIlePheAla	1758
Db	4929	GCTTTGGCCCAAGTGGGAACTGGAGCTCTCTTCAATGCTGTCTTTCTTATCATATGCT	4988
Qy	1759	AlaLeuGIYValGIuLeuPheGIYAspLeuGIYAspArgIleUtrHHisProCysGIuGIY	1778
Db	4989	GCTCTCGGGGTGGAGCTCTTTGGGAAGCTGGTCTTGCAACGACGAAACCCGTGGAAAGGC	5048
Qy	1779	LeuGIYArgHISAlaThrPheArgAsnPheGIYMetAlaPheLeuThrLeuPheArgVal	1798
Db	5049	ATGAGCGGACATGGCACTTCTGAAAGTCTGGAGATGGCTTCCTTCACACTCTTCAGAGTC	5108
Qy	1799	SerThrGIYAspAsnProPAsnGIYIleMetIYAspProSerArgAspCys---AspGIh	1817
Db	5109	TTCACGGGTGACAACTGGAAAGGGATATGAAGACACGCTGGGGATCGTGAACCCAGAC	5168
Qy	1818	GIuSerThrCysTYrAsnThrVal-----IleSerProIleTYrPheValSerPheVal	1835
Db	5169	GAGCGCACTGCTCCGAGACAGCTCAGTTGATGTGTGCGCGCTGTACTTCGTGAAGCTTGCTG	5228
Qy	1836	LeuThrArgIAsnPheValLeuValAsnValValIleAlaValLeuMetIYHisLeuGIu	1855
Db	5229	CTACCCGCGAGTTGCTGCTCATATCAAGCTGGTGGTGGCTGTGCTCATGAACACCTGAC	5288
Qy	1856	GIuSerAsnTYrSGIuAlaTYrSGIuValaGIuLeuLeuGIuAlaGIuLeuGIuLeuGIYMet	1875
Db	5289	GACAGCAACAGAGAGCGCCAGAGAGACCGCAATGATGCCAGCTCGAGCTGGAATG	5348
Qy	1876	---LYrThrLeuSerProGlnProHIsSerProLeuGIYSerProPheLeuTrpProGIY	1894
Db	5349	GCCCATGGCTGGGCGCTGGCCGAGGCTGCTACCGGCTCC-----	5390
Qy	1895	ValGIuGIYValAsnSerThrAspSerProLYrProGIYAlaProHIsThrThAlaHis	1914
Db	5391	-----CCGGCGCGCCCTGGCGCGAGGCGCG--	5414
Qy	1925	IleGIYAlaIleAsnArgIYpHeSerLeuGlnHisProThrMetAlaPro-----	1930
Db	5415	---GGAGGGGCGGGCGGCGCG--GGCGACACCGAAGGCGGCTTGCGCGGCGCTCTATC	5470
Qy	1931	-----HisProGIuGIuValaProValPro	1938
Db	5471	GGCTGGCCAGGACCTCCTTGAGGGGGAGCTGACCATATGCAACAACTGTGGGCTCAT	5530
Qy	1939	LeuGIYProAspLeuLeuThrValArgIYSerGIYValSerArgThrHisSerLeuPro	1958
Db	5531	CTTCCACACATACCTCTGCGCTGCGCGGCTGCMAAGATGTCA-----CCA	5575
Qy	1959	AsnAspSerTYrMetCysArgAsnGIYSerThrIlaGIuArgSerLeuGIYHisArgGIY	1978
Db	5576	CGAACAA-----CCAGAGGTGAGCTGGGTGAGAGGGA	5608
Qy	1979	TrpGIYLeuProLYrAlaGIuSerGIYSerIleLeuSerValHisSerGlnProAlaAsp	1998
Db	5609	GGCTTCTCCCTGAACTCAGACAGAGTCTGTCATCTGTTGGGTGACACGTCGAGTCT	5668
Qy	1999	ThrIserCysIleLeuGIuLeuProLYrAspValHisTYrLeuLeuGlnProHisGIYAla	2018
Db	5669	CGAGGA-----CCSCAACAGCTGTG	5686
Qy	2019	ProThrTrpGIYAlaIleProLYs-----	2026
Db	5687	CCACACTGTG-----CCGCAAGACAGACAGGATGAGTGAACCCACTGAGCCAT	5737

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Oy      2027 ----LeuProProGlyArgSerProLeuAlaGlnArgProLeuArgAlaAla  2045
Db      5738 GCGGTGGAGACCTGGGGCGAAGCTTCTCCCTTCT -CTCTACGAGCCCTCTGCCGG  5796
Oy      2046 ILeArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGlu  2065
Db      5797 ATCCAGAGAACTTCTCT ---GTAGAGTGAAGAGATCCCAT -----TCAACC  5841
Oy      2066 ValSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSerIle  2085
Db      5842 CTGTCGGGTCTGCTGCTGAACATGACA-----  5868
Oy      2086 GlnValGlnGlnArgSerGlyIleGlnSerIleValSerIleHisIleArgLeuProAla  2105
Db      5869 -----GCACTCAAGACCCCAAGTCTTCT  5895
Oy      2106 ProCysProGlyLeuGlnProSerTrpAlaIleAspProGluThrArgSerSerLeu  2125
Db      5896 CCC-----CGAATGCTTCAAGC-----  5913
Oy      2126 GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu  2145
Db      5914 -----CTCTCTGCCCATGCCAGCGAGTTCTTCCACCTG  5949
Oy      2146 ProLeuPhePro-----ArgAspLeuIleGlySerGlySerValGluThrGlnSerCys  2163
Db      5950 CAGTGTCTCCGACGAGAAAGGCCAGAAAAGGACACTGCACGTGAACCTCCCAAGA  6009
Oy      2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgHisSerIleAlaValSerCys  2183
Db      6010 TTGGCGCTG-CAGGGCTCTGGGCACTC-----CTGGGTACCAAGGTCAACTGT  6059
Oy      2184 Leu-----AspSerGlySerGlnProArgLeuCysProSerProSerSerLeu  2199
Db      6060 ACCCTCTCCGGGACGAGCACCGGGAGGAGACACGCGCTGAGACGCGAGCCACAG-CTC  6118
Oy      2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProIleValSerLeuSerProProSer  2219
Db      6119 GCGGGGACGCTCGACGACACGCTCGAGGACAGCTGACCTGAGCGACAGCCCCGGCG  6178
Oy      2220 IleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----ProGly  2237
Db      6179 -----TGCCTGGGGCGCCCGCGCGCTGCTCAGAGACCCGGGC  6217
Oy      2238 ValCysLeuArgArgAlaProAlaSerAspSerIleAspProSerValSerSerPro  2257
Db      6218 CGGCTGTCCCCCGCCCTCGCGCCCGCTGAGCTCGGGGCGGCGCTTCAAGCT  6277
Oy      2258 LeuAspSerThrAlaAlaSerProSerProIleValSerPheThrIleuSerLeuSerGlyLeu  2277
Db      6278 GCGGGGCGCTGCGGCGCATCGCGCAACACAGCAGCGGGGCTTCCACAGCCGGGCTG  6337

RESULT 14
US-09-935-541-3
; Sequence 3, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McSivern, Joseph G.
; TITLE OF INVENTION: 1-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND US$S
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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NAME/KEY: CDS  
LOCATION: (192) .. (6755)  
US-09-935-541-3

Alignment Scores:  
Pred. No.: 0 Length: 6855  
Score: 5420.00 Matches: 1228  
Percent Similarity: 61.97% Conservative: 235  
Best Local Similarity: 52.01% Mismatches: 500  
Query Match: 45.06% Indels: 402  
DB: 9 Gaps: 63

US-09-611-257a-24 (1-2287) x US-09-935-541-3 (1-6855)

QY 12 ThrProbleuAArglySerAlaArgProSerSerAspPro----- 25  
DB 207 TCCCCCGCTTCCTCATCTGACGACCCCGCAGCGCTGACGAGAGTACACGAGAGCAG 266  
QY 26 ProGlyProArgLeuAlaArglyTyrThrArgArgMetGluArgAlaProArgSer 45  
DB 267 CCGGACCCCGG----- 278

QY 46 ArgAspSerProValAlaSerArgSerSerThrCysProGlyProGlyAlaAlaGly 65  
DB 279 -----AGCCCCCATCTCCCGCCAGCGCTGAGAGAGCTGATGAGAGCT----- 326

QY 66 AlaGlySerThrGluArgAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85  
DB 327 -----GATCCT-----CATGTCCACAC 344

QY 86 ProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgProArgSerTyr 105  
DB 345 CCGAGACTGGCGCTTATGCTTCTTCTGCTGACAGACACACAGCCCCCGGAATCG 404

QY 106 CysLeuArgThrValCysAsnProTyrPheGluArgValSerMetLeuValLeuLeu 125  
DB 405 TGCATCAAGATGGTGTGCAACCCGTGGTTGAATGTGTCAAGATGCTGTGATCTGCTG 464

QY 126 AspCysValAlaThrLeuGluMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145  
DB 465 AACGCTGTGACATCTGCAATGACACGCCGTGCGACACATGACCTGCTCGACCGC 524

QY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165  
DB 525 TGCAGATCTCTGACAGCTTGTGATGACTTATCTTTATCTTTGTCAGAGAGATGCTG 584

QY 166 ValIysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsn 185  
DB 585 CTCAGATGGTGGCCCTGGGGATTTTGGCAAGAGTACCTCGGGGACACATGGAGC 644

QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205  
DB 645 CGCCTGATTTCTTCATGTCATGACAGGAGATGTCAGTACCTCCGAGACTTCAGAAC 704

QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225  
DB 705 ATCAACCTGTCAAGCATCCGCAACCGTGGCTCTGAGGCCCTCAAGCATCAACCGC 764

QY 226 ValProSerMetCargIleLeuValThrLeuLeuAspThrLeuProMetLeuGlyAsn 245  
DB 765 GTGCCCGATGTGGGATCTCTGTGAACCTCTCTCTGACACACTGCCCATGTGGGGAAAT 824

QY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTyr 265  
DB 825 GTCTGTGTCTGTCTTGTCTTGTCTTCTTATCTTGTGACATAGGTGTGAGCTCTGG 884

QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGlyLysAsnPheSerLeuProLeuSerVal 285  
DB 885 GCGGGCTGTGTGGTAAACCGCTCTCTGAGAGAGAACTTCAACATACAGAGGAGATGTG 944

QY 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305  
DB 945 GCCTTGGCCCCATATCTACAGCGGAGAGAGATGATGATGCCCTTCACTCTCTCTG 1004

QY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325  
DB 1005 TCGGGGACATGGAGTAAATGGGCTGCCATGAGATCCCCCGCTCAAGAGACAG----- 1058

QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrArgSer 339  
DB 1059 ---GGCCGTGAGTGTGCTGTCCAAAGACAGCTGTACAGACTTTGGGCGGGCGCCAG 1115

QY 340 SerSerAsnThrThr-----CysValAsnThrAsnGlnTyrTyrThrAsnGlySerAla 357  
DB 1116 GACCTCAATGCCAGCGCTGTGTCACTGAACCTGTACTCAATGTGTGCCGACG 1175

QY 358 GlyGluHisAsnProPheLeuGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTyrPle 377  
DB 1176 GCGAGCGCCAAACCCCAAGAGGTGCCATCACTTGAACAATCGTATCTTGANT 1235

QY 378 AlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAsp 397  
DB 1236 GTCATCTTCCAGATGATCACTGTGAGAGGCTGGAGATGATGATGATCACTGATGAT 1295

QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417  
DB 1296 GCTCACTCTTACAACTTCATCTTCACTTCATCTGCTTATATAGTGGCTTCTTC 1355

QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437  
DB 1356 ATGATTAACCTGTGCTCTGTGTCACTAGGACCCAGTTCCGAGACCAAGACGAGAG 1415

QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457  
DB 1416 CACCGCTGATGTGGAGCAGCGGAGCGCTACCTGTCC---TCCAGACGCGTGGCCAGC 1472

QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuTyrTyrLeuValTyrIleLeuArg 477  
DB 1473 TAGCCGAGCCTGGGACAGCTTACAGAGAGATCTTCAGATGATGTGCCAATCTCGCC 1532

QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497  
DB 1533 AAGCCAAAGCC-----CCGCCCTGGGCTGTACAGAGCCCTGGAG 1574

QY 498 SerSerProValAlaArgSerGlyGluProGlnProSerGlySerCysThrArgSer 517  
DB 1575 AGC----- 1577

QY 518 HisArgArgLeuSerValHisIleLeuValHisIleHisIleHisIleHisIleTyr 537  
DB 1578 ---CGCGCCAGGCGCTG----- 1592

QY 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557  
DB 1593 -----GCGCCGAG----- 1601

QY 558 AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly 577  
DB 1602 -----GCCCGGCCCGCCGCAAACTGGGCC----- 1628

QY 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597  
DB 1629 -----CAGGCCAAG-----GAGGCC 1643

QY 598 ValArgCysGlnAlaProProProArgCysProSerGlnAlaSerGlyArgThrValGly 617  
DB 1644 CCGCACTACAGCTGTGCCGCAATAGACCCCTCGAGTGC----- 1685

QY 618 SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys 637  
DB 1686 -----ACGCCCAAC----- 1697

QY 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657  
DB 1698 ---CTGTGTGAG-----CCATCCCGCCAGCGTGGCTTCC----- 1730

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QY 658 ProGlyProPheSerMetMetHisLeuLeuLeuGluThrGlnSerThrGlyAlaCys--- 676
Db 1731 -----GATCCCGCCACCTGGCTTGGCTGACG 1757
QY 677 HisSerSerCysValHisSerSerProCysSerValHisAspSerGlyAlaCysGlyPro 696
Db 1758 CATAGAGACGGCCGGCCCTCGAGGCTGGGACAGCACCGACTGGGCGAGAGAGGCTCG 1817
QY 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Db 1818 GGCTCC-----GGAGGCTCGGCTGGTGGCGAGCAGAGCGCG----- 1853
QY 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
Db 1854 -----GATGGGAGACGGGGCGC-----CGAGACGCGAGGAGCAGAGCCTCTCAGAA 1898
QY 737 LeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
Db 1899 CTGGGGAGAGAGAGAGAGAGAGAGAGAGAG-----GCCGATGGGGCG 1940
QY 757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774
Db 1941 GTCGCGCTGTCGGGGAGTGTGGGGAGACGGAGACCAAGCTGCGGCGCATGCTGGAC 2000
QY 775 SerLysTyrPheGlyArgGlyTyrIleMetIleAlaIleLeuValAspThrLeuSerMetGly 794
Db 2001 AGCAAGTACTTCAACCGGGGCATCATGATGGCATCTCGTCAACACCGTCAGCATGGGCG 2060
QY 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
Db 2061 ATCAGACGCCACGAGCAGCCGAGAGAGCTGACCAATCTGGAGATTCGAAATGTGATC 2120
QY 815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPheGly 834
Db 2121 TTCACAGCAGCATTTGGCTTGGAGATGATCTGAAAGCTGGCGCATTTGGGCTGTTCAC 2180
QY 835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrpGlu 854
Db 2181 TACCTGCTTAACCCCTTACAACTCTTCGACAGCATCATTTGCATCATCAGATCTGGGAG 2240
QY 855 IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874
Db 2241 ATCGTGGGCGAGCGGACGCTGGCTGTGCTGGCTCGGACCTTCGCGCTGTGGCGGTG 2300
QY 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetCysThr 894
Db 2301 CTGAAACTGGTGGCTTATGCTGCTGCTGCGGCGCCGACGCTGCTGCTCATGAAGACC 2360
QY 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIle 914
Db 2361 ATGACAAACGTGGCACCTTCTGCATGCTGCATGCTTCATCTTCATCTTCAGCATC 2420
QY 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGlyLysArgAsp---GlyAspHisLeu 933
Db 2421 CTGGGAATGCAATATTTTGGCTGCAAGTTCACGCTCCGACGAGACCTGGAGACCGGGTG 2480
QY 934 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953
Db 2481 CCCGACAGGAAGACTTTCGACTCCCTGCTGGGCACTGTCACAGTGTTCAGATTCCTC 2540
QY 954 ThrGlnLysAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 973
Db 2541 ACCCGAGGAGACTGGAACGTCGTTCTCTCAATGCAATGCGCATGCTCCACTTCCCGGGCC 2600
QY 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993
Db 2601 TCCCTCTACTTGTGCTCTCAATGCACTTGGCACTATGCTCTTCAACCTGCTGGTG 2660
QY 994 AlaIleLeuValGlyGlyPheGlnAlaGluLysAspAlaThrLysSerGluSerGluPro 1013
Db 2661 GGCATCTCTGTGAGAGGCTTCCAGCGGAGAGGTGAAGCCAAATCGCTCTCAATCGGACGAG 2720
QY 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023

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Db 2721 GACCAGACTCATTCGAACATGAAGAAGATTGATAGCTCCAGGAGGCTTCGACAGACG 2780
QY 1024 GlyAspArgLysValArgLeuAlaLeuValAlaLeuGlyGluHisValGluLeuValGly 1043
Db 2781 GGAGATCCCAAG-----CTGTGCCCAATCCCATGACCCCAATGAGGACATGCCACCCC 2834
QY 1044 SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrProMetSer 1059
Db 2835 AGTCTC-----CCACTGGGTGGGACCTTAAAGTCTGCTGGGCTGGGACCTGCC-- 2885
QY 1060 HisProLysSerSerSerThrGlyValGlyAlaLeuGlyLysArgArgArgThr 1079
Db 2886 ---CCCGACTCTCACTGACCGGAGCCGACCCCATGCTGTGGCTGGCTGCCAAGAGC 2942
QY 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSer 1099
Db 2943 AGTGTCAATGCTCTA-----GGAGAGATGAGCATATGACAGCGCTCTGTCCAGC 2993
QY 1100 AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerThrPheArgArgSer 1119
Db 2994 TCCCGAGCTCTTAACGAGGCAATGGGCGGAGCGGCGGCGGCTGGAGCGCATGCTCC 3053
QY 1120 SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyLysArg 1139
Db 3054 AGCTGGAAC-----AGCTCAAGACCAAGACCGCGCTGGGCGGAGCAT 3095
QY 1140 ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluSerSerGlu 1158
Db 3096 GAGTCCCTGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3155
QY 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3156 GAGGAGCGCGCGCGCGCGCGCACCCCTGACACCCCAACCCCAACCATTCATCAGCGG 3215
QY 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181
Db 3216 CCCCATCTGGCGGACCGCCACCGCCACCGCCGAGCGCTGTCCCTGCACAAAGGGAG 3275
QY 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201
Db 3276 TCGGTGACCTCGCGCGAGCGGTGCTCCGCGGTGGGCCCAACCCCGGCGCGCTGGAG 3335
QY 1202 SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
Db 3336 GCGGACAGCGCGCGCGCGCGCATGAGAGACTGCAATGAGCAGATGCCAGC-----ATC 3389
QY 1220 AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAspAspGlu 1238
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QY 1239 GlyAsnLeuSerLysGlyLysArgIleGlnAlaTrpValArgSerArgLeuProAlaCys 1258
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Db 3510 TGCAGAGTCCCGAAGACTGTGCTGTACTCTTCTCTCCCGAAGACAGGTTCCGGGCTC 3569
QY 1279 LeuCysHisArgIleIleThrHisLysMetPheAspHisValIleValIleIlePhe 1298
Db 3570 CTGTGTACAGCAATATATGGCCACAAACTCTTCACATGACGTCGCTGCTGCTGCTGCTT 3629
QY 1299 LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg 1318
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Dh 3750 AAGTAGTCTCGGTGGGCTGTACTTCGGGAGAGGCGTACCGACGACGTGGAA 3809  
QY 1359 ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer 1378  
Dh 3810 GTGCTGATGCTTTCTTCTTCTTCCTGCTCATCATCGTGGTCTCCGGGCTCA 3869  
QY 1379 AspSerGlyThrIysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 1398  
Dh 3870 GCCGGGGAGCCAAAGATCTTGGGGGTCTCCGAGTCTTGGGCTCTGGCCACCTTAAGC 3929  
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Dh 3930 CCCCTGGTGTCAATCAGCCGGGCGCGCGCTGAAGCTGGTGGAGACATCATCTCC 3989  
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Dh 3990 TCCCTCAAGCCCAATCGCAACATCGTGTATCTGCTGTCTTTCATCATCTTGGC 4049  
QY 1439 IleLeuGlyValGlnLeuPheIysGlyLysPhePheValCysGlnGlyIleAspThrArg 1458  
Dh 4050 ATCTGGAGATGACGCTCTTCAAGGCGAATTTCTACACATGTCTGGGCGTGCACCCGC 4109  
QY 1459 AsnIleThrAsnIysSerAspCysAlaGlnIleSerTyraArgTyrValArgHisIysTyr 1478  
Dh 4110 AACATCAACAACCGCTCGACTGCGATGGCCGCAACTAACCGCTGGTCCATCAAAATAC 4169  
QY 1479 AsnPheAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuIleAspIysAspGly 1498  
Dh 4170 AACCTTCACAACCTGGGCGAGGCTGTGATGCTCTTGTCTGGATCCAAAGATGT 4229  
QY 1499 TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet 1518  
Dh 4230 TGGGTGAACATCATGTCATGACATGACATGCTGTCTGTCTGACCAAGACCTGTGACC 4289  
QY 1519 AsnHisAsnProTyrMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe 1538  
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QY 1539 ValLeuAsnMetPheValGlyValValValGlnAsnPheHisIysCysArgGlnHisGln 1558  
Dh 4350 GTGCTCAACATGTTGTGGGTGTCTGGTGAAGAACTTCCAAAGTCCGCGACACAG 4409  
QY 1559 GlnGlnGlnIleValArgArgArgGlnGlnIysArgLeuArgLeuGlnIysArg 1578  
Dh 4410 GAGGCTGAAGAAGCAGCGCGCGGTGAGAGAAAGCGGTGGCGCTGGAGAAAGACGC 4469  
QY 1579 ArgSerIysGlnIysGlnMetAlaGlnIleGlnCysIysProTyrTyrSerAspTyrSer 1598  
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QY 1599 ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1618  
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QY 1619 GlyValIleGlyLeuAsnValValThrMetAlaMetGlnHisTyrGlnGlnProGlnIle 1638  
Dh 4569 TTGATCATCTGCTCAACGTGTGTCACCATCTCCCTGAGACATCAATCAGCCACGTCC 4628  
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Dh 4629 CTGAGACACACCCCTCAAGTACTGCAACTATATATGTTCCACACTGTCTTGTGGTGAAGCT 4688  
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QY 2018 AlaProThrTrpGlyAlaIleProIysLeuProPro----- 2029  
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 2237 GlyValCysLeuArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSer 2256  
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 Db 6254 GGCAGGCTGTCCCGCGCGCTGCGCGCGCTGAGCCTGCGCGCGCGGCGCTTTCAG 6313  
 2257 ProLeuAspSerThrAlaIleSerProSerProLysLysAspThrLeuSerLeuSerGly 2276  
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 2277 Leu 2277  
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 Db 6374 CTG 6376

Search completed: September 19, 2005, 17:19:14  
 Job time : 3522.34 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame.pln.p2n model

Run on: September 18, 2005, 17:44:07 ; Search time 14386.6 Seconds  
(without alignment)  
6050.997 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028

Sequence: 1 MLPRHVRVCVTRPPLRGSAR.....KKDTLSLSGLSDPTMDPZ 2287

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgr2\_1/USPRO\_pool/US09611257/runat\_15092005\_134301\_25185/app\_query.fasta\_1.4878  
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Database :  
EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_g981:\*  
9: gb\_g982:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1719.5	14.3	6636	3	BC043482 Mus muscu
2	1698	14.1	6035	3	BC051413 Mus muscu
3	1406	11.7	990	4	B1905383 603167426
4	1385.5	11.5	939	4	B1736618 603361089
5	1343	11.2	1076	4	BM479323 AGENCOURT
6	1300	10.8	1064	4	BM451648 AGENCOURT
7	1293.5	10.8	5666	4	AY416501 Mus muscu
8	1275	10.6	879	7	CF548658 AGENCOURT
9	1256.5	10.4	793	6	CA319705 UT-M-FWO-

10	1230.5	10.2	5943	9	AY416499
11	1198	10.0	715	7	CF745071
12	1197	10.0	810	5	B0709095
13	1195.5	9.9	952	7	CF584866
14	1190.5	9.9	4675	3	AK083220 Mus muscu
15	1187.5	9.9	771	5	B0058818
16	1185	9.9	736	4	B1160856
17	1182	9.8	711	5	EM950154
18	1172	9.7	777	5	B0708898
19	1163.5	9.7	957	4	BG298038
20	1162.5	9.7	777	6	CA945335
21	1141	9.5	973	2	BF783704
22	1140.5	9.5	828	2	BF069929
23	1136.5	9.4	784	7	CF742232
24	1135	9.4	690	6	CB840838
25	1112	9.2	6822	9	AY406058
26	1111	9.2	6813	9	AY406056
27	1103.5	9.2	845	6	CA327685
28	1102.5	9.2	773	4	B1249987
29	1096	9.1	676	4	B1917129
30	1088.5	9.0	727	5	BQ443110
31	1088	9.0	710	7	CR576255
32	1079.5	9.0	647	6	CB518482
33	1075	8.9	667	7	CF531859
34	1074.5	8.9	731	7	CN534628
35	1067	8.9	707	7	CN216936
36	1061.5	8.8	708	5	BQ179746
37	1059	8.8	693	5	BM949227
38	1055.5	8.8	803	6	CB245297
39	1034	8.6	843	5	BQ180375
40	1032.5	8.6	710	5	B0704267
41	1018.5	8.5	684	5	B0262763
42	1012	8.4	772	6	CB524738
43	1011	8.4	652	2	BB660642
44	1009	8.4	640	6	CB056097
45	997.5	8.3	658	5	BQ109588

## ALIGNMENTS

RESULT 1 BC043482	LOCUS	BC043482	6636 bp	mRNA	linear	HTC 19-NOV-2003
DEFINITION	Mus musculus calcium channel, voltage-dependent, alpha 1F subunit, mRNA (CDNA clone IMAGE:5369391), containing frame-shift errors.	ACCESSION	BC043482	VERSION	BC043482.1	GI:28175783
KEYWORDS	HTC.	SOURCE	Mus musculus (house mouse)	ORGANISM	Mus musculus	
AUTHORS	Struhsberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhac, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Uedini, T.B., Tothiyaki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Touchman, J.W., Green, E.D., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.	TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			

JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 6636)
AUTHORS	Stranberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (09-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada <a href="mailto:info@cgsc.bc.ca">info@cgsc.bc.ca</a> Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letitia Hsiao, Martin Krzyzanski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Nees, Pavan Pandoh, Anna-Liisa Prabhun, Parvaneh Saeedi, Jacqueline Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasha van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
Series: IRAX Plate: 86 Row: 0 Column: 1  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9624972  
This clone has the following problem: frame shifted.

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    location/Qualifiers
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Alignment Scores:	
Pred. NO.:	1.32e-107
Score:	1719.50
Percent Similarity:	40.38%
Best Local Similarity:	26.28%
Query Match:	14.30%
9B:	3
	Gaps: 95
	Length: 6636
	Matches: 658
	Conservative: 353
	Mismatches: 810
	Indels: 691
	Gaps: 95

US-09-611-257A-24 (1-2287) x BC043482 (1-6636)

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		:::	:::	:::	:::
Db	147	AGAAAGAGACCCACGACACAAACACAAAGACT	GTGGGGGGTGGCCAGTCTCAGAGATCA	206	
Qy	90	ProValValPhePheTyLeuSerGlnAspSerArg	ProArgSerTrpCysLeuArgThr	109	
Db	207	CCTCGAGGCTCTTCTGCTGCTCACCTTACTAT	CCATTCGTCGGCTCTGCATCAGCATT	266	
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Db	267	GTA-----	-----	GAGTGAAGCCTTTTGATTTCTCATCTTCGAC	CAATCTTTGCCAACTGC 320
Qy	128	ValThrLeuGlyMetPheArgProCys-----	-----	GluAsp-----	----- 138

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Db	441	CCACCAGCCAGACCCCAACCCTCCGGGGCTTACCTTACTCTTGGTCTGGCAAA	500
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Oy	149	uglnalpheAsp-----Aspheilephe-	157
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Db	981	ACTCGAGCTATTCTCTCGAGCGAAAGCACAAAGACATGCTACTTC-----	1023
Oy	281	uProLeuSerValAspLeuGlnuProTyrTyrGlnThcGluAsnGluAspGluSerProPh	301
Db	1024	-----CTGGGATCTATATAGAA-----GCAGAGAGAGGCCATCACTC--	1062
Oy	301	eIleCysSerGlnProArgIuAsnGlyMetArgSerCysArgSerValProThrLeuArg	321
Db	1063	-----TGTGCATCT-----	1071
Oy	321	gGlyGlnGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSe	341
Db	1072	-----TCTGGCTCTGGCGCTTATCATCACTGAAC-----	1101
Oy	341	rAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAs	361
Db	1102	-----CATACGAGTGCAGCGGGCGCTGGCCAGG	1130
Oy	361	nProPheGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheG	381
Db	1131	ACCCACAGCGTGGCATCAAGAACTTCGACAAATTTTCTTCCCATGCTAACTGCTTCCA	1190
Oy	381	nValIleThrLeuGlnGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPh	401
Db	1191	GTCATATTCATGAGAGCTGGAACAAGTCTCTTACATGATGCAAGATGCCATGGGGTA	1250
Oy	401	e---TyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAs	420

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QY      221  gAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuPr  241
Db      861  GCTAGTGTCTGGGATCCCGAGTCTGCACATATGTCTCAATTCCATCATGAAGGCGCTTGT  920
QY      241  oMetLeuGIYAsnValLeuLeuLeuCysPhePheValPhePheIlePheGIYIleValGI  261
Db      921  GCCCGCTGTGCACATTTGCCCTGTGGTGCTCTTGTATTATCATTTTAAGCGCATCATCGG  980
QY      261  YValGIleuLeuTrpAlaGIYLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLe  281
Db      981  ACTGAGACTATTCTCCGACGAACAGACAAAGACATGCTACTTC-----  10233
QY      281  uProLeuSerValAspLeuGluuProTyrTyrGIlnThrGluAsnGluAspGluSerProPh  301
Db      1024  ---CTGGAGATCTATATAGAA-----GCAGAGAGAGAGCCCATACCT--  10624
QY      301  eIleCysSerGIlnProArgGluAsnGIYMetArgSerCysArgSerValProThrLeuAr  321
Db      1063  -----TGTCACATCT-----  10711
QY      321  gGIYGIuGIYGIYGIYGIYProProCysSerLeuAspTyrGIuThrTyrAsnSerSerSe  341
Db      1072  ---TCTGGCTCTGGCGCTTTCATCACACTGAC-----  11011
QY      341  rAsnThrThrCysValAsnTrpAsnGIuTyrTyrThrAsnCysSerValaGIYGIuHisAs  361
Db      1102  -----CATACCGAGTGC CGCGGCGCTGGCCAGG  11300
QY      361  nProPheYsGIYAlaIleAsnPheAspAsnIleGIYTrAlaTrpIleAlaIlePheGI  381
Db      1131  ACCCAACGCGTGGCATCACGAACCTTGCACAAATTTTCTTCTCCATGCTAACTGCTTCCA  11900
QY      381  nValIleThrLeuGIuGIYTrpValAspIleMetTyrPheValMetAspAlaHisSerPh  401
Db      1191  GTGATTTACATGGAAGCGTGGACAGACGTCTCTACTGATGCAAGATGCCAGGAGGTA  12500
QY      401  e---TyrAsnPheIleTyrPheIleLeuLeuIleIleValGIYSerPhePheMetIleAs  420

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[illegible]

QY	321	gGlyGluGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSer	341
Db	1072	-----TCTGGCTCTGGCGCTTCATGCACACTGAAC-----	1101
QY	341	rAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHis	361
Db	1102	-----CAATCCGAGTGCCTGGCGGCGCTGCGCAGG	1130
QY	361	nProPheLeuGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheG	381
Db	1131	ACCCACACGCTGGCTACGAACTTCGCAATTTTCTTGGCCATGCTTAACTGGTTCCA	1190
QY	381	nValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPh	401
Db	1191	GTGATTTCCATCGAAGGCTGGAACAGCTCTTACTGATGACGAGATGCAATGGGGTA	1250
QY	401	e---TyrAsnDheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAs	420

[illegible]

Qy	261	YValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLe	281
Db	981	ACTCGAGCTATTCTCGACGAATGACCAAGACATGCTACTTC-----	1023
Qy	281	uProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPh	301
Db	1024	---CTGGAGTCTGATATGGAA-----GCAGAGAGAGACCCTACTCT--	1062
Qy	301	eileCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuAr	321
Db	1063	-----TGTCATCTT-----	1071
Qy	321	gGlyGlnGlyGlyGlyGlyProProCysSerLeuAspTyrGlnThrTyrAsnSerSer	341
Db	1072	-----TCTGGCTCTGGCGCTTCATGCACCTGAAC-----	1101
Qy	341	rAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHis	361
Db	1102	-----CATACCGAGTGGCGGCGGCGTGGCCAGG	1130
Qy	361	nProPheIleGlyAlaIleAsnPheAspAsnIleGlyTyrAlaIlePheIleAlaIlePheG	381
Db	1131	ACCCAGACGTTGCATCAGAACTTCGCAAAATTTTCTTTCGCATGCTACTGGTTCCA	1190
Qy	381	nValIleThrLeuGlnGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPh	401
Db	1191	GTGATTTTCATCGAAGCTCGACAGACGTCTTACTGATGACGATGACGATGCGGGTA	1250
Qy	401	e---TyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAs	420

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QY      221  gAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuPr  241
Db      861  GCTAGTGTCTGGGATCCCGAGTCTGCACATATGTCTCAATTCCATCATGAAGGCGCTTGT  920
QY      241  oMetLeuGIYAsnValLeuLeuLeuCysPhePheValPhePheIlePheGIYIleValGI  261
Db      921  GCCCGCTGTGCACATTTGCCCTGTGGTGCTCTTGTATTATCATTTTAAGCGCATCATCGG  980
QY      261  YValGIleuLeuTrpAlaGIYLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLe  281
Db      981  ACTGAGACTATTCTCCGACGAACAGACAAAGACATGCTACTTC-----  10233
QY      281  uProLeuSerValAspLeuGluuProTyrTyrGlnThrGluAsnGluAspGluSerProPh  301
Db      1024  ---CTGGAGATCTATATAGAA-----GCAGAGAGAGAGCCCATACCT--  10624
QY      301  eIleCysSerGlnProArgGluAsnGIYMetArgSerCysArgSerValProThrLeuAr  321
Db      1063  -----TGTCACATCT-----  10711
QY      321  gGIYGIuGIYGIYGIYGIYProProCysSerLeuAspTyrGIuThrTyrAsnSerSerSe  341
Db      1072  ---TCTGGCTCTGGCGCTTTCATCACACTGAC-----  11011
QY      341  rAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerValaGIYGIuHisAs  361
Db      1102  -----CATACCGAGTGC CGCGGCGCTGGCCAGG  11300
QY      361  nProPheYsGIYAlaIleAsnPheAspAsnIleGIYTrAlaTrpIleAlaIlePheGI  381
Db      1131  ACCCAACGCGTGGCATCACGAACCTTCGACAAATTTTCTTCTCCATGCTAACTGCTTCCA  11900
QY      381  nValIleThrLeuGIYGIYTrpValAspIleMetTyrPheValMetAspAlaHisSerPh  401
Db      1191  GTGATTTACATGGAAGCGTGGACAGACGTCTCTTACATGATGCAAGATGCAGGAGGTA  12500
QY      401  e---TyrAsnPheIleTyrPheIleLeuLeuIleIleValGIYSerPhePheMetIleAs  420

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Db	741	GTTCAGCGCTGCTGTTGGAAACAAGACCTCGGGCGGCCAGAGATGCCCGCATCTAGAGG	800
Qy	204	-----GlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArg	221
Db	801	AAAGCCAGAGAGGCTTCGATGTAAAGGACACTCGGGGCACTTTAGGGGTGTACAGACTCTTAAG	860
Qy	221	GAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuP	241
Db	861	GCTAGTGTCTGGGGTCCCGAGTTCTGCACATAGTCTCAATTCCATCAAGAAGCGCTTGT	920
Qy	241	oMetLeuGIYAsnAlIleuLeuLeuCysPhePheValPhePheIlePheGIYIleValGI	261
Db	921	GCCGCTGCTGCACATTGCCCTGTTGGAGCTCTTGCTATTATCATTTAAGGCATCATCGG	980
Qy	261	YValGIleuLeuTrpAlaGIYLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerI	281
Db	981	ACTGAGATTAATCTCTCGACGAATGACACAAAGACATGCTACTTC-----	1023
Qy	281	uProLeuSerValAspLeuGIYProTYrTYrGlnThrGluAsnGluAspGluSerProPh	301
Db	1024	-----CTGGGATCTGATATGAA-----GCAGAGGAGGAGCCATCACT--	1062
Qy	301	eIleCysSerGIuProArgIuAsnGIYMetArgSerCysArgSerValProThrLeuArg	321
Db	1063	-----TGTGCATCT-----	1071
Qy	321	gGIYGIuGIYGIYGIYGIYProProCysSerLeuAspTYrGIuThrTYrAsnSerSerSe	341
Db	1072	-----TCTGGCTCTGGCGCTTATGCACACTAAC-----	1101
Qy	341	rAsnThrThrCysValAsnTrpAsnGIYTYrTYrThrAsnCysSerAlaGIYGIuHisAs	361
Db	1102	-----CATACCGAGTGCAGCGGCGCTGCGCAGG	1130
Qy	361	nProPheIYAsGIYAlaIleAsnPheAspAsnIleGIYTYrAlaIleTrpIleAlaIlePheGI	381
Db	1131	ACCCAAACGGTGGCATCAGAACTTCGACAAATTTTCTTTCGCATGCTCACTGGTTCCA	1190
Qy	381	nValIleThrLeuGIYGIYTrpValAspIleMetTYrPheValMetAspAlaHisSerPh	401
Db	1191	GTCGATTAACATGGAAGCTGGAAGACGTCCTCTATCGATGACGAGATGCCATGGGGTA	1250
Qy	401	e---TYrAsnPheIleTYrPheIleLeuLeuIleIleValGIYSerPhePheMetIleAs	420

[illegible]

OY	146	-----Cys---ArgIle-Le	149
Db	501	AGCAACCTTAACCTGTGCTTACAGTCAACCA	CGGGGTCTGACCCCTCCCGAAATAAT 560
OY	149	uGlnAlaPheasp-----	AspPheIlePhe-- 157
Db	561	CGAGGCCCTTCACGCCCGCCCGCTGCTCCGCCCT	CAGAAACAGGTAGAATATCGTGTCT 620
OY	158	-AlaPhePheAlaValGluMetValValLysMetValAla	LeuGly--IlePheGlyLy 176
Db	621	GGTATTTTTCACCGTGGAGACAGGTGCTCAAGATG	TGCTTATGCGTGTGCTTCATCC 680
OY	176	slycCysTyrLeuGlyAspThrTPAspAsnGleuAsp	PhePheIleValIleIleIleaglyme 196
Db	681	CAGCGCCCTAATATTCGACATGGCTGGAACCTG	CTGACTATCATTCGTGTGGGGCT 740
OY	196	tLeuGlyTyrSerLeuAspLeu-----	203
Db	741	GTTCAGGGGTGTGCTGGAAACAAGACCTGGGGCGG	CCAGAGATCCCGCATACTGAGG 800
OY	204	-----GlnAsnValSerPheSerAlaValArgTh	ValArgValLeuArgProLeuAr 221
Db	801	AAAGCCAGAGAGCTTCGATGTAAAGACATCGCGG	CAATTAGGTGTATGACACTTAAAG 860
OY	221	gAlaIleAsnArgValProSerMetArgIleLeuVal	ThrLeuLeuLeuAspThrLeuPr 241
Db	861	GCTAGTGTCTGGGTCCCGAGTCTGCACATATGCT	CAATTCATCATGAAGGGCTTGT 920
OY	241	oMetLeuGlyAsnValLeuLeuLeuCysPhePheVal	PhePheIlePheGlyIleValG1 261
Db	921	GCCGCTGTGACATMGCCCTGTGGTGCTCTTGTG	TATATCATTTAACCGCATATCCGG 980
OY	261	yValGlnLeuTrpAlaGlyLeuLeuAlaGAsnArg	CysPheLeuProGlnAsnPheSerLe 281
Db	981	ACTGAGCTAATCTCTCGACGAATGCACAAAGAC	ATGCTACTTC----- 1023
OY	281	nProLeuSerValAspLeuGluProTyrTyrGln	ThrGluAsnGluAspGluSerProph 301
Db	1024	-----CTGGAGATCTATATGAA-----	GCAGAGAGAGGCCATCACCCT-- 1062
OY	301	eIleCysSerGlnProArgGluAsnGlyMetArgSer	CysArgSerValProThrLeuAr 321
Db	1063	-----TGTCACATCT-----	1071
OY	321	gGlyGluGlyGlyGlyGlyProProCysSerLeuAsp	TyrGluThrIleAlaIlePheG1 341
Db	1072	-----TCTGGCTCTGGCGCTTATGCACACTAAC-----	1101
OY	341	rAsnThrThrCysValAsnTrpAsnGlnTyrTyrThr	AsnCysSerAlaGlyGluHisAs 361
Db	1102	-----CATACCGAGTGC	CGCGGGCGCTGGCCAGG 1130
OY	361	nProPheGlyGlyAlaIleAsnPheAspAsnIleGly	TyrAlaThrIleAlaIlePheG1 381
Db	1131	ACCCAAACGGTGGCATACGAACTTGCAAAATTTT	CTTTGCTGCATGCTAACTGTGTCCA 1190
OY	381	nValIleThrLeuGluGlyTrpValAspIleMetTyr	PheValMetAspAlaHisSerPh 401
Db	1191	GTGATTTTACATGAGAGCTGGAAGACGTCTCTA	TCATGATGCAAGATGCCATGGGGTA 1250
OY	401	e---TyrAsnPheIleTyrPheIleLeuLeuIleIle	ValGlySerPhePheMetIleAs 420

[illegible]

Db	321	GTGGCATTGGGGGTATATATATCCCTTCCCTGAGAGCACTCCAACTGCTAAACCAAC	380
Qy	139	-----IIeAla	140
Db	381	TTGGTAGAGCTTACCCCATCCCAACAGACTGAGTCCCTTAAAGCTACAGATTAAA	440
Qy	141	CysaspserGlnArg-----	145
Db	441	CCACCAGCCAGACCCACCCCTCGGGGGCTACCTACTTCACTTGGTCTGGCAAA	500
Qy	146	-----Cys---ArgIle-Le	149
Db	501	AGCAACCTTAACCTGTGCTACGACTGACCCACGGGGTCTGACCCCTCCCGAAATAAT	560
Qy	149	uGlnAlaIleAasp-----AaspIleIlePhe--	157
Db	561	CGAGGCGCTTACGCGCCCGCCCTGCTCCGCCCTCAGAAACAGGTAGAAATACGTTCCT	620
Qy	158	-AlaPhePheAlaValGluMetValValIySmetValAlaLeuGly--IlePheGlyLy	176
Db	621	GGTATTTTTCACCGTGAACAGTGTCTCAAGATGTGATCGCTTAAGGCTGGTCTTCATCC	680
Qy	176	slvsCysTyrluenglYasphrTrpAsnaArgLeuAaspPhehelIleValIleAlaGlyMe	196
Db	681	CAGCGCTTAATTTGGCAATGGCTGGAACTGTCTGACTCATCATGTCGTGGTGGGCT	740
Qy	196	tlEuGlutYserIleuAaspLeu-----	203
Db	741	GTTACAGCGTGTGTTGGAAACAAGACTGTGGCGGCCAGAGATGCCCGCATCTGAGAG	800
Qy	204	-----GlnAsnValserPheSerAlaValArgThrValArgValLeuArgProLeuAr	221
Db	801	AAAGCCAGAGAGCTTCGATGTAAAGGACACTGCGGGCATTTAGGGTCTACGACCTTAAG	860
Qy	221	gAlIleAsnArgValProserMetArgIleLeuValThrIleuLeuAspThrLeuPr	241
Db	861	GCTAGTGTCTGGGGTCCCGAGCTGCACATAGTCTCAATTCCATCAGAAAGGCGTTGT	920
Qy	241	omeLeuGlYAsnAlaIleuLeuLeuCysPhePheValPhehelIlePheGlyIleAlaG	261
Db	921	GCGCGTGTGCACATGCGCTGTGGTGTCTTCTGTATATCATTTACGACCATCATCGG	980
Qy	261	YValGlnIleuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerIe	281
Db	981	ACTGAGAGTATCTCTCGAGCAATGCAACAAGACTGTACTTC-----	1023
Qy	281	uProLeuSerValAspLeuGluIuProTYrTYrGlnThrGluAsnGluAspGluSerProPh	301
Db	1024	-----CTGGAGATCTATATGAA-----GCAAGAGAGAGACCATCACTC--	1062
Qy	301	eIleCysserGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuAr	321
Db	1063	-----TGTGCATCT-----	1071
Qy	321	gGlyGluGlyGlyGlyProProCysSerLeuAspTYrGluThrTYrAsnSerSerSe	341
Db	1072	-----TCTGGCTCTGGGCGTTCATGACACTGAAC-----	1101
Qy	341	rAsnThrThrcysValentTrpAsnGlnTYrTYrThrAsnCysSerAlaGlyGluHisAs	361
Db	1102	-----CATACGAGTGGCGGGCGCTGGCCAGG	1130
Qy	361	nProPheGlyAlaIleAsnPheAspAsnIleGlyTYrAlaTrpIleAlaIlePheG	381
Db	1131	ACCACAGCGTGGCTACAGAACTTCGACAAATTTTCTTCCCATGCTAACTGTCTTCCA	1190
Qy	381	nValIleThrIleuGluGlyTrpValAspIleMetTYrPheValMetAspAlaHisSerPh	401
Db	1191	GTGATTTTACATGAGAGCTGACAGACGTCTCTACATGATGACAGATGCCATGGGGTA	1250
Qy	401	e---TYrAsnPheIleTYrPheIleLeuLeuIleIleValGlySerPhePheMetIleAs	420

[illegible]

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Db 1251 TGAGCTGCTTGGGTACTTTGTGAGCCTTGTGATCTTTGGCTCTTTGTCTTCA 1310
Qy nLeuCyLeuValValIleAlaThrGlnPheSerGlyThrLySGlnArgIleuSerGln 440
Db 1311 CTTTGCTTGGTGAATCTTAAAGCGGGAGCTTCCAAAGAAAGAAAGAAAGCAAGACG 1370
Qy 440 uMetArgIleGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerG 460
Db 1371 AGGTGACTTTCAGAAAGCTTCGG-----GA 1394
Qy 460 uProGlySerCysSerGlyGlnGluLeuLeuLysTyrLeuValTyrIleLeuArgValAla 480
Db 1395 GAAGCAGACAGATGAGAAAGACCTTGGGGCTGACTGATGACATCAACAGCGCTGAGGA 1454
Qy 480 ArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerPr 500
Db 1455 GTTAGACTTTCATACCCCTCA-----GTAGACGGCAACTTGGCTTCT----- 1497
Qy 500 oValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgAr 520
Db 1498 -CTTGCTGAAGAGGAGCG-----CGGGCCATCGTAG 1529
Qy 520 gLeuSerValHisIleValHisIleHisIleHisIleHisIleHisIleHisIleHis 540
Db 1530 G-----CAACTCAA 1538
Qy 540 yAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnG 560
Db 1539 TTCTGGCCCGCGCTTC-ATTCT-----AGCCCTGAGTGT----- 1571
Qy 560 ySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProPro-- 579
Db 1572 ----ATTGCCCTCTGAACCAAGCAAGCGCTGACGCCACCTTA-GGCTTTGCCCAAA 1626
Qy 580 ----ArgGlyAlaGluSerValHisSerPheThrHisAlaProCysHisIleuGluPr 597
Db 1627 TCTGGATCAGGGCAGAGATCTCAACCAATTCAGATACAAAGATC-CAACTAGTTCC 1665
Qy 597 oValArgCysGlnAlaProProProArgCysProSerGlyAlaSerGlyArgThrValG 617
Db 1686 T-----TGTCCCTTAGATTGAC----- 1704
Qy 617 ySerGlyValValTyrProThrValHisThrSerProProGluIleLeuLysAspLy 637
Db 1705 ----CTAATTCGCCACCAAGCACTTCTTCAG----- 1734
Qy 637 sAlaLeuValGlnValAlaProSerProGlyProProThrIleuThrSerPheAsnIlePr 657
Db 1735 ----TTCACTATCTCCCCACA--GGGCCCACTGTCAAGCTGACGTAACAATAGAG 1784
Qy 657 oProGlyPro-----PheSerSerMetHisIleuLeuGluThrGlnSerThrG 674
Db 1785 GCGCGGACGCGTCCGAGCTTACG-----CACTTAATCTGCTCCACACACTCCACAG 1838
Qy 674 yAlaCysHisSerSerCysLyHisSerSerProCysSerLyAlaAspSerGlyAlaCy 694
Db 1839 CAGC---CAGCGCAGCTCCAGCAGATGACATGCTCCATGACAGACAC----- 1887
Qy 694 sGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyLupProGluSerAlaAs 714
Db 1888 ----CTGGAGATGAGATGAAAGAGA-GGGGA 1915
Qy 714 PHis-----ValMetProAspSerAspSerGlyAlaValTyrGluPheThrG 730
Db 1916 CCAATGGCTAGCTGTACAGCTGCTC-----AAACA 1945
Qy 730 nAspAlaGlnHisSerAspLeuArgAspPro-HisSerArgArgGlnArgIleuSerLeuG 750
Db 1946 AGATTATGAAAACAAAGATCTG-----CCGCCATCTCCGCCAGCAACCGGGGTCTC- 1998
Qy 750 lYProAspAlaGluProSerSerValLeuAlaPheTPrArgLeuIleCysAspThrPheA 770
Db 1999 ----CGTGACGCTGC-----C 2011
Qy 770 rGlyIleValAspSerLyTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnT 790
Db 2012 GCCGGCCCGTCAAGTCAACCGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2071
Qy 790 hLeuSerMetGlyIleGlyTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluI 810
Db 2072 CGTTGACCAATGCTTCAGACACACATGGGACGCTTTGTGGCTTCTACCCAGACCAAGAG 2131
Qy 810 lSerAsnIleValPheThrSerPheAlaLeuGluMetLeuLeuLysLeuValT 830
Db 2132 ATGCCAACAAGTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2191
Qy 830 yGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAsp-----G 845
Db 2192 TGGGCCCTCTGTCTACGTGCTGCTTTCCTTTCACCGCTTTCCTGCTGCTGCTGCTGCTG 2251
Qy 845 lValIleValValIleSerValTPrGluIleValGlyGlnGlnGlyGlyLeuSerV 865
Db 2252 GGGGCATCTGAAACCACTTGTGGAGGTGGGGCCATGACGCTTGTGGCATCTCAG 2311
Qy 865 AlLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuG 885
Db 2312 TGCTCCGATGTGATGCTCTCTCAGATCTTCAAGGTACCAAGCACTGGGCACTCCCTGA 2371
Qy 885 lArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeu 905
Db 2372 GCATCTGGTGGCATCTTGTCTCAATTCATGAAAGTCAAGCTGCTGCTGCTGCTGCTGCT 2431
Qy 905 eMetLeuPheIlePheIlePheSerIleLeuGluIleMetHisIlePheGlyCysIlePheA 925
Db 2432 TCTTTCTTTCATCATTCATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2491
Qy 925 lAserGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTPrA 945
Db 2492 ACTTTGACAG-----ACCACACCAAGAGAGCACTTGTATACCTTCCCCCAAG 2542
Qy 945 lAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnG 965
Db 2543 CCTCTCCATCTGCTTTCATGATCTGATCTGATGAGATGGAAGCTGTGATGATGATGATG 2602
Qy 965 lYMetAlaSer-----ThSerSerTrpAlaIleLeuTyrPheIleA 979
Db 2603 GTATCATGCGCTACGCGTGGCCCTTCTTCCAGAGATGCTGCGTGGCTTATTTCTCA 2662
Qy 979 lAlaMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluG 999
Db 2663 TCTCTTTCATCTGTGGCACTACATCTGCTGAAAGTGTCTTTCGCAATTGGCGTGATA 2722
Qy 999 lYPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProS 1019
Db 2723 ACCTA---GCCAGCGGGGATGACAGCACTCCAAA----- 2754
Qy 1019 eValAlaAspGlyAspArgLysArgLeuLysArgLeuAlaLeuValAlaLeuGlyGluHisA 1039
Db 2755 ----GAAAGAGGAGAGAGAGAG----- 2772
Qy 1039 lAgIleuArgLysSerLeuLeuProProIleIleHisThrAlaAlaThrProMetS 1059
Db 2773 ----AGCAGTGAAGAA 2785
Qy 1059 eHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgT 1079
Db 2786 ACCCTCCAAAGAGAAACAAAGTATTTGTTG----- 2814
Qy 1079 hRerSerSerGlySerAlaGluProGlyAlaAlaHisIleGluMetLysCysProProS 1099
Db 2815 ----CTGTGTGAGAGATGAGAGCAAG-----G 2842
Qy 1099 eAlaArgSerSerProHisSerProTrpSerAlaAlaAspSerTrpThrSerArgArgS 1119
Db 2843 GTGCAAGAAAGTGA----- 2856
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QY	1119	erSerArgAsnSerLeuGlyValGalaProSerLeuLysValGArgSerProSerGlyGlu	1139
Db	2857	-----GGAGCGACACCGAGCATG-----	2874
QY	1139	rgArgSerLeuLeuSerGlyGluGlyGlnGlnSerGlnAspGlyGluGlnSerSerGluG	1159
Db	2875	-----GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2914
QY	1159	luaPArgAlaSerProIaGlySerAspNHisArgHisArgGlySerLeuGluArgGlu	1179
Db	2915	AGGAAGAGGAAGAAATGCTCAGGA-----CATGTGGAATCTTGTGAGAGAAGTA-	2961
QY	1179	lalySerSerPheAspLeuProAspThrLeuGlnVal-ProGlyLeuHisArgThrAla	1198
Db	2962	-----GTACCCAAAGAGAAAGTGTTACCATCTCCGAAGGACAGTCCCT	3004
QY	1199	SerGlyArgSerSerAlaSerClnHisGlnAspCys-AsnGlyLysSerAlaSerGlyArg	1218
Db	3005	TCCTTCT---GCCCTTAGCCAAACCAACCCGTAGTGTGTGGAAATCCAGTACGGAGGACA	3061
QY	1218	gLeuAlaArgThrLeuArgThrAspAspProGlyLeuAspArgLysAspAspAspArgL	1238
Db	3062	ACAGCGCGGGAGACCCCTAGAACTACCCAGAGGACAGT-----	3098
QY	1238	uGlyAsnLeuSerLysGlyGluArg-IleGlnAlaThrPvalAlaXSerArgLeuProAlaC	1258
Db	3099	-----GGCCACAGATGATCCCTTGATGATCCCGAAGAAACACCAATACC	3142
QY	1258	ysCyArgGluArgAspSerTrpSerAlaTyr-IlePheProProGlnSerArgPheArg	1277
Db	3143	TGGTT-----TCTACTCACTGCTTTTCTCACTCCAGGCTTGG	3184
QY	1278	LeuLeuCySNI.sargIleIleThrHisLysMetPheAspHisValIleValIleIle	1297
Db	3185	AAGGCTTCACACACTCATATCATCCATATCTTCAACCACTCATCTTCACTGTTGATC	3244
QY	1298	PheLeuAsnCySileThrIleAlaMetGluArgProLysIleAspProHisSerAlaGlu	1317
Db	3245	ATCTCACTAGTATGATGTCCTCGGCTGCTGAGAACCCC---ATCCAGACTCATCTCTCCGA	3301
QY	1318	ArgIlePheLeuThrLeuSerAsnTrpIlePheThrAlaValPheLeuAlaGluMetThr	1337
Db	3302	AACCATATTCGGAGATATTGATTATTCCTTCACTCCATATTCACCTGTGGAATTTCTA	3361
QY	1338	ValLysValIleAlaLeuGlyLTrpCySphGlyGlnAlaTyrLeuLysSerSerTrp	1357
Db	3362	CTCAAGATGACAGTGTGGGGCCCTCTCGACCGAGGCTCTTTGCGCGTACGTGGTTC	3421
QY	1358	AsnValIleuAspGlyLeuLeuValIleuLieserValIleAspIleLeuValSerMetVal	1377
Db	3422	AATCGTTGGATCTCTTGTGGTCAAGTGTGTCCTCATCTCTCTCGGATCCAC-----	3475
QY	1378	SerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuAlaGluLeuArgThrLeu	1397
Db	3476	-----TCCAGTGCACATCAAGTGTGGAAGATTCTCCAGTCCCTCGAGTCTCG	3523
QY	1398	ArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValIleGluThrLeuMet	1417
Db	3524	CGGCTCTCCAGCCATCAACAGACCCAAAGGACTCAAGACATGTGTGTGTGTGTGTC	3583
QY	1418	SerSerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePhe	1437
Db	3584	GTGGCGATCCGGACCATCGGAACAATCATGATTGTACACACCCCTTGTCACTTCATGTTT	3643
QY	1438	GlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThr	1457
Db	3644	GCTCGCATTTGGTGTTCAGCTGTCAAGGAGAAATTTACAGTGTGCATGTAGAGGCCAAA	3703
QY	1458	ArgAsnIleThrAsn-----LysSerAspCysAlaGlu	1468
Db	3704	CACACCTCGAAAGAAATGCAAGGCTCTTCTCTCATTAACCTGATGAGAGTGTGTACGA	3763
QY	1469	AlaSerTyrArg-----TrpValArgHisLysTyrAsnPheAspAsnLeuGlyGln	1485

Db	3764	CTTTGGTCCGGAGCGGCTCTGGGCAACAGTCA	TTTTAACTTTGACAAAGCTCTTTCA	3823
Oy	1486	AlAlemSeSerleuPheValIleuAlaSerLysAspGlyTrpValAspIleMetTyrAsp	1505	
Db	3824	GCATATAGGCGCTGTTCACGTCTCTACCTTTGAAAGCTGGCGCTCTATACAG	3883	
Oy	1506	GlyLeuAspAlaValAlaArgInGlnProIleMetAsnIleAsnProTrpMetLeu	1525	
Db	3884	GCATAGATGCAAACCGAAGATGAGAGGCCCTTATCTCAATTACCAAGTGGAGATATCA	3943	
Oy	1526	LeuTyrPheIleSerPheIleuIleValAlaPhePheValIleuAsnMetPheValGly	1545	
Db	3944	GTAATCTTCAATGTCTACATCAATCAATCAATCGCTTCTCAATGATGAACATCTTTGGGC	4003	
Oy	1546	ValIleValAlaIleAsnPheIleLysCysArgInHisGlnGluGluAlaArgArg	1565	
Db	4004	TTTGTTATCATCATTC-----CGTCCGACGGAGAGACAGATACCAAAAC	4051	
Oy	1566	ArgGluGluLysArgIleuArgArgIleuLysLysArgArgSerLysGluLysGlnMet	1585	
Db	4052	TGNGAA-----CTGGACAAGAACAGCCCGCAGTGTGTGAATATGCC	4093	
Oy	1586	AlaGluAlaGlnCysLysProTyrTyrSerArgPyrSerArgPheArgLeuValHis	1605	
Db	4094	CTCAAGCTCAGCAGCTCCGCGGATACATCCCTAAGATCCTCATACATACCGGTGGC	4153	
Oy	1606	HisLeuCysThrSerHisTyrLeuAspLeuPheIleTrnGlyValIleGlyLeuAsnVal	1625	
Db	4154	GCCACTGTACCTCTCTGCGCTTGTAGATACCTCATGTTCTTGCTCATCTGCTCAACGC	4213	
Oy	1626	ValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIle	1645	
Db	4214	GTGGCCCTAGCCATGACGACATATGAACAGACTGCTCCCTTAACTATGACCATGACATC	4273	
Oy	1646	CysAsnTyrIlePheThrValIlePheValPheGlnSerValPheLysValAlaPhe	1665	
Db	4274	CTCAACATGGTCTTCACTGGCTCTTCAACATTCAGATGAGTGCTCAAAATATAGCGCTTT	4333	
Oy	1666	AlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValIleu	1685	
Db	4334	AAACCAAGATTAATCTTTGCAGATGCGCTGGAATAGCTTTGATGCTCTCATTTGTAGTGGC	4393	
Oy	1686	SerIleMetGlyIleThrLeuGluGluIle-----GluVal	1697	
Db	4394	AGTGATGTGCATGCCCGTCACAGAAATCAATACGAGGCAATCTTGGCGAAGATTCA	4453	
Oy	1698	AsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValIleuArgIleAla	1717	
Db	4454	GAGACAGCTCCGCGATATCTATCAAGTCTTTCGCTCTCCGATGATAGGCTG---	4510	
Oy	1718	ArgValIleuLysLeuLysMetAlaValAlaGlyMetArgAlaLeuIleHisIleHisValMet	1737	
Db	4511	-----GTCAAGTCTTGAGTAAGGTGAGGGGATCCGACACTGCTTGGACATTCATC	4564	
Oy	1738	-----GlnAlaLeuProGlnIleValAlaAsnLeuGlyLeuLysPheMetLeuPhe	1754	
Db	4565	AAGCTTTCCAGGCTTTGCGCTATGG-----GCACTTCTCATGCAATGATATTC	4615	
Oy	1755	PheIlePheAlaAlaLeuGlyValAlaLeuPheGlnAspLeuGluCys--AspGluThr	1773	
Db	4616	TTGATCTATGACAGTCAATGCGATGCGAGATGTTGGCAAGGTGGCTCTTCAGAGCGGACG	4675	
Oy	1774	HisProCysGlnLysLeuLysArgHisAlaThrPheArgAsnPheGlnMetAlaPheLeu	1793	
Db	4676	CAG-----ATAATGGAACAACAATTCCTCAAGACTTTCGCGAGGCTGTGCTG	4733	
Oy	1794	ThrIleuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMet-----LysAspPro	1811	
Db	4724	CTTCTGTTCAGGTGCGCCACTGTGTAGAGCGCTGCAAGAGATATGCTAGCGACGCTTCA	4783	
Oy	1812	SerArgAspCysAspGlnGlnSer-----ThrCysTyrAsn	1823	

Db 4784 GGAATGATGTGACCTGAGTGTGACTTTGGCCCAAGAGAAATTACCTGT---GGT 4840  
 Qy 1824 ThrValIleSerProIleTyrPheValSerPheValIleThrAlaGlnPheValIleVal 1843  
 Db 4841 AGCAGTTTGGCATCGTCTCATCATCAAGCTTCTTTATGCTGTGCTTCCGATTATA 4900  
 Qy 1844 AsnValValIleValIleMet----- 1851  
 Db 4901 AATCTCTTGTGGCTGAATCATCATGATTAATTGATTACTTAACCAAGAGATGGTCTATC 4960  
 Qy 1852 -----LysHISLeuGluGlnSerAsnIleGluAlaIleGluGlu 1868  
 Db 4961 CTGGAGCCCAACCACTGATGAATTC---AAGAGATCTGGTGTAAATGACCCCGGA 5017  
 Qy 1869 AlaGluLeuGluLeuGlu-----MetLysThrLeuSerProGln 1881  
 Db 5018 GCCAAGGCGCGCATCAAGCACTTGATGTGTGCTGCTGAGACCGCATCCAGCCCCA 5077  
 Qy 1882 -----ProHISer----- 1884  
 Db 5078 TTGGGATTTGGAAAGCTATGCCCCACACCGAGTGCCTGCAAGAGCTGTGCAATGAT 5137  
 Qy 1885 ---ProIleuGlySerProPhe-----LeuTrpProGlyVal 1895  
 Db 5138 GTGCCCTTCAACTGAG-TGGACAGTGAATTCACGCTACACTCTTGGCTGTGGCG 5196  
 Qy 1896 GluGlyValAsnSerThrAspSerProIleProGlyAlaProHISThrIleHisIle 1915  
 Db 5197 GACATCCCTGAAGTCAAGACAGAGAGAACTGGATCAAGCCCAAGAGAGCTTGGAT 5256  
 Qy 1916 GlyAlaIleSerGlyPheSerLeuGluHisProThrMetVal-----ProHISProGlu 1933  
 Db 5257 GGTATCATAAAAAGATCTGAAGCGGATTAAGCAAAATTTGGATGAGGCTCATCCCTCC 5316  
 Qy 1934 -----GluValProValPro---Leu 1939  
 Db 5317 TCCCGATGAGGAGGAGTCACTGTGGAAAATTCTATGCCACATTCCTGATCCAAAGATA 5376  
 Qy 1940 GlyProAsnLeuLeuThrValArgIleSerGlyValSerArgThrHisSerLeuProAsn 1959  
 Db 5377 TTTCCGAAATTCGGGAGAGAGAAAGAAAGGGCTACTAGAGAGAGAGC---CCCAAC 5433  
 Qy 1960 AspSerTrpMetCysArgAsnGlySerThrAlaGluArgSer----- 1973  
 Db 5434 AAGACATCTCTGCTCCAGCGCTGTGAAGAGCCTGAGAGACTTGGGCTCCAGAT 5493  
 Qy 1974 -----LeuGlyHisArgGlyTrpGlyLeuProGlyAlaGln 1985  
 Db 5494 CCGTCAAGCCCTCACTATGACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5553  
 Qy 1986 SerGly-----SerIleLeuSerValHisSerGln 1995  
 Db 5554 GGAGGCTGAG 5613  
 Qy 1996 ProIle-----AspThrSerCysIleLeuGlnLeuProGlyAsp 2008  
 Db 5614 CCAGCCCAATCTCGATGAGAACTAGAGATTTC-CGGTGTCTCTACTGTTAAGAGAAAC 5672  
 Qy 2009 ValHisTrpLeuLeuGlnProHisGlyValProThrTrpGlyAlaIleProGlyLeuPro 2028  
 Db 5673 TTCCAGATTTCTCTCAACCTGGGCGGAGTGAATGATGGC-----TGGCTCCCA 5723  
 Qy 2029 ProProGlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaIleAlaIleArgThr 2048  
 Db 5724 ACTCCAGC---AGCCAGCTGAGTACAGCGCTGCTCCCAACCAACACA----- 5768  
 Qy 2049 AspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSerGluValSerGly 2068  
 Db 5769 -----GGAGAAAGCTCTCGGGG 5783  
 Qy 2069 ProSerCysProLeuThrArg-----SerSerSerPheTrpGlyGlySer 2083  
 Db 5784 TTTTCATGTTCATATCCCGAGAGAGAGAGAGATATTACCTCAAGGAACTCAAGGGCAGG 5843

Qy 2084 SerIleGlnValGlnGlnArgSerGlyIleGlnSerIleValSerIleHisIleArgLeu 2103  
 Db 5844 ACAATCAGATGAGGAG 5900  
 Qy 2104 ProIleProCysProGlyLeuGluProSerTrpAlaIleAspProProGluThrArgSer 2123  
 Db 5901 -----CGGGAATC-----CTTGAAACCAAGCTC 5924  
 Qy 2124 SerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGln 2143  
 Db 5925 TTTTACCACCTCACTCG-TCCCAAGCAACAGTAAAGGGCAGCAGATGCGACCGCAGCT 5983  
 Qy 2144 GluGluProLeuPheProArgAspLeuGlyLysCysTrpSerValGluThrGlnSerCys 2163  
 Db 5984 TTGCTGCCCCCAACGCGCTGAGGTCCGAAGCCCTCTCTGACCATTCAG-----TGT 6034  
 Qy 2164 ArgArgArgProGlyPheThrPheLeuAspGluGlnArgHisSerIleAlaValSerCys 2183  
 Db 6035 CTCCAAAGCCAGGAGC-----AGTTGT 6055  
 Qy 2184 LeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeu----- 2199  
 Db 6056 GAAGATTT---ACCTATCCCAAGCACTACCATCGGACGAGCACTCAGACCAAGCAG 6111  
 Qy 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProGlyLysLeuSerProPro--- 2218  
 Db 6112 GGCCTCAGGGTTCCTGGGAGGCCCCCTCTCTCAGAGGGTGCAGCTGTATATGCCCTCTGT 6171  
 Qy 2218 ----- 2218  
 Db 6172 GTTGTGAGAGAAATCAACAGTGGTGAAGATTCCTTGGCAAACTTGGCGCCCACTGCG 6231  
 Qy 2219 -----SerIleSerIleAspProProGluSerGlnGlySerArgProPro----- 2233  
 Db 6232 TACCTTCACTGTCTGCAAGTGCCTGAGGCTCATCCGAATCCAGCAAGAGAGAG 6291  
 Qy 2234 ---Cys-----SerProGlyValCysLeuArgArgArgAlaProIleAspSerIle 2250  
 Db 6292 CAGTGTGAGAGAGTGTGTGAGAGGCTGTGCATCTCCGAGGGCTTGTCTTTGCCCA 6351  
 Qy 2251 AspProSerValSerSerPro-----LeuAspSerThrAlaIleAspSerProPro 2267  
 Db 6352 AGACCAAGATTTGTGCGCTTGGCCCAAGCAGAGATTCAGATGCATGATCACTGACCT 6411  
 RESULT 2  
 BC051413 6035 bp mRNA linear HTC 19-NOV-2003  
 DEFINITION Mus musculus calcium channel, voltage-dependent, alpha 1F subunit,  
 mRNA (cDNA clone IMAGE:6493332), containing frame-shift errors.  
 ACCESSION BC051413  
 VERSION BC051413.1 GI:30802106  
 KEYWORDS Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 REFERENCE  
 AUTHORS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
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 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S.,  
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 Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D.,





[illegible]

Dd	3213	GTCAACAGTATTTTAACCTTGAACACAGCTCTTTACACCAATGATGGCCCTGTCACGTG	3212
Oy	1494	Alaserlyasrpgiyltrvalaerllemetyræbrgiyleuæra avalgiyvalær	1513
Dd	3273	TTCACTTTGAAGGCTGGCTGGCTGCTCTATTAACAGGCGCTTAGATGCAACGCGAAGAT	3332
Oy	1514	GlnlnlProlllemetAaenh aænrProtrmetleuæuylzrphel eserPhenleu	1533
Dd	3333	GAGGGCCCTATCTCAATTACATTCACATGTGAGATATCAATATTTCTCATTTGCTCATATATC	3392
Oy	1534	llvalAlaPhePheValleuæmetPheValgiyvalValgiuaænrhen ævæ	1553
Dd	3393	ATCATGCGCTTTCTTCATGATGACATATCTTTGGGGCTTTGTATACACATTC-----	3446
Oy	1554	Cysarglmhiæglngluglugluglualatrgærglugluglylsargleuærgatg	1573
Dd	3447	-----GGTGCCAGGGAGAGAGCAAGTACCAAAATCTGTGA-----	3482
Oy	1574	leuglulylvsarlgatserlysglulysglImetæ aqlualaglnCyvlærProtyr	1593
Dd	3483	CTGACAAAGAACCGACGCCAGTGCTGTGGAATATGCTCCAAAGCTGACGCACTCGCGCA	3542
Oy	1594	TyrserærryrsærgærpheærgleuæValmhiæleuCystrærhætyrleu	1613
Dd	3543	TACATCCCTTAAGATCCCTCATCACTACCCGCTGTGGGCGCACTGAACTCTGCGCTTT	3602
Oy	1614	AsrleuphehellæthrglvalllæglyleuænaVal thrmætalæmetGlnh ætyr	1633
Dd	3603	GAGTAACTCATGTTTCTGCTCATCTCTGCTCAACAGGAGGCGCTTACCATGACACATAT	3662
Oy	1634	GlnlnlProGlnllleleuærpGlualæuyls leCyææntyr lephæthValle	1653
Dd	3663	GAAACAGACTGCTCCCTTTAACTATGACATGACATCTCCAAACAGTGCCTCACAGGCTC	3722
Oy	1654	PheVal phegiuserVal phey leuæVal aæphæ aærhæærgærpheGlnær	1673
Dd	3723	TTCAACCATTTGATGATGCTGCTCAAAATATGCGCTTTAAACCAACGACTTACTTTGCAAT	3782
Oy	1674	ArgTræpænglneuaærpLeuæ a leValleuæuser lemetGly lethleuGlu	1693
Dd	3783	GCGTGAATACGTTTGAATGCTCATGTTGATGAGGAGTGAATGCAATGCGAGCTGCTG---	3839
Oy	1694	Glu legluValænuæserleuPro-- leænrProthrlle æarg lemetærgv	1713
Dd	3840	---ACAGAAAGCAATAGACAGCTCCGCGCATATTCACAGCTTTGCGCTCTTCGAG	3896
Oy	1713	alleuærgylle æargValleuæyleuæuylsmætalæVal G metærgalæleu	1733
Dd	3897	TCATGAGGCTG-----GTCAAGCTCTGAGTAAGGCGAGGAGGATCGCACACTGC	3947
Oy	1733	euh ætrhValmet-----GlnAlæuProGlnValGlyænuæluglyleuærp	1750
Dd	3948	TTCTGGAATTCATCAAGCTCTTTCAGAGCTTGGCGCTTATGTS-----GCACTTCTCA	3998
Oy	1750	heætleuæleuphePhe lePhe a æleuGlyValGlyleuPheGlyærpæleuGluC	1770
Dd	3999	TAGCAATGATATCTTCATCATCATGCACTATTCAGTGCATGCAAGATGTTTGGCAGAGTGCTC	4058
Oy	1770	ys---æærgluthh æProCyæseluælugleuGlyægh æ æthPhæærgæsnhæg	1789
Dd	4059	TTTCAGAGCGGACGACAG-----ATTAATGCAACAAACAAATTTCCAGACTTTC	4106
Oy	1789	lymætalæPheleu thleuPheærgValser thrglyæærpæænrTræpængly leæmet	1808
Dd	4107	CGCAGGCTGCTGCTCTCTGTTCAAGGTGTGCGACTGætgAGGCTGGCAGAGATTAATGC	4166
Oy	1809	-----lyæærpProserærgæærpCyæærglngluser-----	1819
Dd	4167	TAGCAGAGCTTCCAGAAATGATGTGACCTGATGCTGCACTTGGCCACAGGCGAGAAAT	4226
Oy	1820	---thryætyræænthVal ææserPro letyrPheValserPheValleu thærlæg	1839
Dd	4227	TTACTCTG---GGTGAAGTTTTGCGCATGCGTACATTCATCACTGCTTTATGCTCTGTG	4283

Qy	1839	lnphveValleuValAenValValleValleMet	-----	1851
Db	4284	CCCTTCGATTTAAATCTCTTGTGGCTGAATCAAGTAACCTTGATTTACCTAACCA	-----	4343
Qy	1852	-----	-----	1864
Db	4344	GAGATGTGTCATCTCTGGAGCCCAACCACTTGATGAATTC	-----	4400
Qy	1864	lualagUleuGlualagUleuGlUleuU	-----	1877
Db	4401	AATGTGACCCCGGAGCCAGGCGCATCAAGCACTTGATGTGTGGCTGCTAGAC	-----	4460
Qy	1877	hrluserProGln	-----	1884
Db	4461	GCATCCAGCCCCCATTTGGGATTTGGAAAAGCTATGCCACACCGATGGCTCGAAGAGAC	-----	4520
Qy	1885	-----	-----	1891
Db	4521	TGCTGGCAATGATGTGCTCTCAACTCAGA	-----	4579
Qy	1891	eutPrProGlyValGlUclYValnsertThrsarserProlyuValAprohIst	-----	1911
Db	4580	TTTGCCCTGGGCGACATCTCTTAAGTCAAGCAAGAGGAACCTGGATCAAGCCAAC	-----	4639
Qy	1911	hrtPrAlnAilEglYAlAlaIaserGlyPheserUleuGlnIarothrmetVal	-----	1929
Db	4640	CAGAGAGCTGGAGATGTGATCAAAAAGATCTGGAAGGGATAAAGCAAAATGTGGAT	-----	4699
Qy	1930	--ProhIarProGln	-----	1936
Db	4700	GAGGTCACTCCCTCCCGATGAGAGAGGTCACTGGGAAAATTCTATGCCACATTC	-----	4759
Qy	1936	roValPro	-----	1955
Db	4760	CTGATCCAGATTTATTTCCGAAATTCGCGAAGAAAGAAAGGGGCTACTGAGAA	-----	4819
Qy	1955	IsaserUeProAvnAarPserUmetCyvArGaemGlySerThrlagUarGer	-----	1973
Db	4820	GAGGC	-----	4876
Qy	1974	-----	-----	1981
Db	4877	TTGGGTCTGAGATCTCGAACCTCCTATGACACTGAGAAAGAAAGAAAGAGAA	-----	4936
Qy	1981	eupProLYAlagInsery	-----	1991
Db	4937	GAGGACAGTGGGTCAAGAGGCTGAGGAAGAAGAGAGCTGAACCAACCCAGCAATCAAA	-----	4996
Qy	1991	ervalhIseGelnProAla	-----	2004
Db	4997	GACTCCATGACTCCCAAGCCCAATCTGATGAACTGTAGAAATTT	-----	5055
Qy	2004	lnUeProLYaerValhIerUleuGlnProhIeGlyAlAProthrtPrGlyAlaI	-----	2024
Db	5056	TGTTAAGAGAACTTCCAGATTTCTCTCACTAGGGCCGAGATGATGATGGCC	-----	5111
Qy	2024	leProLYaerProhProGlyAraserProleuAlagUarXProleuYarGlnA	-----	2044
Db	5112	-----	-----	5163
Qy	2044	laAlaIlearGThrsarPserUeArValGlnGlyUleuGlySerArgUlarUeUeUs	-----	2064
Db	5164	CA	-----	5166
Qy	2064	erGlyValserGlyProserCyvProUeUthrtArg	-----	2079
Db	5167	GAGAAAGCTCTGGGTTTCACTATCTCCAGAAAGAAAGATATTCAGCTCAAGG	-----	5226
Qy	2079	hePrGlyGlySerSerIleGlnValGlnGlnArGerGlyUleGlnserUyValserU	-----	2099
Db	5227	AACTCAAGGCGAGCAATCAAAATAGAGAACAGAAAGTCTCTGACTGACTCTGACTT	-----	5286

Oy		2099	yshsi1lea7gleuProAlaProCySerProGlyIleuGIuPProSerThralalabAspProp	21139
Db		5287	GGAAGACCAAG-----CCGGACATC-----	-C 5307
Oy		2119	roGIuThrArgSerSerLeuGIuleuAbspHrGIuleuSerTrPIleSercLyAspLeuL	21399
Db		5308	TTCGAAACCAGTCTTTTACCACCTCACCTGG-TCGCCAGCAAACGTMAAACGGGCACATG	5366
Oy		2139	eUProSerSerGIuGLuPProLeuBheProArGaAPLeuLYeLYeCySTyISerValG	21599
Db		5367	TGCCACGCCCGCATGTTTGCTGCTCCCCCAGCGCTGAGAGTCGGAAGCCTCTTCACCATTC	5426
Oy		2159	IuThrGIuInserCYsARgArGrPrGolyPhetRpleuAbspGIuInArGrArHiseri	21799
Db		5427	AG-----TGCTCTCCAACGCCACGGGC-----	5446
Oy		2179	leaIAValserCYsLeuAbspSerCIysSerGIuPProArGrLeuCyPProSerProSererL	21999
Db		5447	-----AGTTGGAAGAATT---ACCTATCCCAGGCACCTACATCGGACGACGC	54949
Oy		2199	eu-----GIYGIYGIuPProLeuGIYGIYProGIYSerArGrProLYeLYeLYeL	22159
Db		5495	TCAGAGCAACAAGAGGCTCAGGGTTCCTGGGACACCCCTCTCAGAAAGGTCGACTGCTA	55549
Oy		2215	eUSeRProPro-----	2218
Db		5555	TATGCCCCCTGTGTGTGTGAGAGAACTCAAGTGGGTGAGAGATACCTTGCAAACTT	56149
Oy		2219	-----SerIeSerIleaspProProGIuSerGIuIySerarGP	22329
Db		5615	GGCGGCCCACTGCGTACCTTCACCTGTGTCAGAGTGCCTGAGCTCATCCGAATCCAGC	56749
Oy		2232	roPo-----Cys-----SerProGIYValCYsLeuArGrArGrAlaProA	2246
Db		5675	CACCGCAAGAGGGGCACTGTCTGAAGATTGGTGTGAGAGGTGTGTCATCTCGAAGGCTTA	57349
Oy		2246	laSerAspSerLYasPProSerValSerSerPro-----LeuaspSerThralaA	22639
Db		5735	GGTCTCTTTGCCCAAGACCCACGATTTGTGGCCTTGCCCAAGCAGAGATTGACAGATGCA	57949
Oy		2263	laSerProSerPro 2267	
Db		5795	TGTCACTGCAGCCCT 5808	
<b>RESULT 3</b>				
LOCUS	B1905383		990 bp	mRNA linear EST 16-OCT-2001
DEFINITION	603167426F1 NCI_GCAP_Lu33 Mus musculus cDNA clone IMAGE:5255383 5' , mRNA sequence.			
ACCESSION	B1905383			
VERSION	B1905383.1	GI:16167866		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
TITLE	Nih-MGC http://mgc.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999)			
	Contact: Robert Strussberg, Ph.D.			
	Email: rgs@phs-fda.nhl.nih.gov			
	Tissue Procurement: Gilbert Smith, Ph.D.			
	cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima			
	Bonaldo, Ph.D.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: NCI-GCAP clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LMNL at:			
	http://image.llnl.gov			
	Plate: LMML1645 row: d column: 08			
	High quality sequence stop: 911.			
FEATURES	Location/Qualifiers			

source

1. .990

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:5255383"

/tissue\_type="pooled lung tumors"

/lab\_host="DH10B (phage-resistant)"

/clone\_1lib="NCI\_CGAP\_Lu33"

/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5'] TGTACCAATCTGAAGTGGAGGCGGCGCTCTGTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.: 3,84e-87 Length: 990

Percent Similarity: 1406.00 Matches: 293

Score: 90.77% Conservative: 2

Best Local Similarity: 90.15% Mismatches: 22

Query Match: 11.69% Indels: 9

DB: 4 Gaps: 2

US-09-611-257a-24 (1-2287) x B1905383 (1-990)

QY 1823 AsnThrValIleSerProIle-TyrpheValSerpheValIleThrAlaGlnpheValIle 1842

DB 1 AAGACCGTATCTACCCATGTAATCTGTCCTGAGTCAAGCCCACTTGTGCT 60

QY 1842 uvaIaasnValaIleAlaValIleuMetLysHisIleuGluGluSerAsnLysGluAlaIary 1862

DB 61 GGTCAACGTGTGATAGCCGTGTGATGAAGCACTGGAAAGAGCAACAAAGAGCCAA 120

QY 1862 sgluGluAlaGluLeuGluAlaGluLeuGluLeuMetLysThrLeuSerProGlnIleP 1882

DB 121 GGAGGAGGCGGAGTGGAGCGGAGCTGGAGCTAGAGATGAAGACACTCAGCCCGCAGCC 180

QY 1882 oHisSerProLeuGluSerProPheLeuTPPProGluValGluGluValAsnSerThraS 1902

DB 181 CCACTCCCGCTGAGGAGCCCTTCTGCTGAGGCTGGAGGAGTGAATGAGCCCTGA 240

QY 1902 pSerProLysProGluValaProHisThrThraIaHisIleGluValaAala---SerGlyPh 1921

DB 241 CAGCCCTAAGCTGGGGCTCCACACACAGGCCCACTTGGAGCAGGCTTCAGGCTT 300

QY 1921 eSerLeuGluHisProThrMetValProHisProGluGluValaProValaProLeuGluYp 1941

DB 301 CTCCTTGGAGCACCCACGATGTGACTCTCACTGAGGAGGAGCCAGTCCCTTAGAGCC 360

QY 1941 oAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspS 1961

DB 361 AGACTGCTGACTGTGAGAGAGTCTGTGTCAAGCCGAGCACTCTCTGCCCAATAGAG 420

QY 1961 rTyrmecCyarsArgAsnGlySerThrAlaGluArgSerLeuGluValaArgGlyTyrpLys 1981

DB 421 CTACATGTGCGCAATGGAGAGCACTGCCGAGAAATCTCTTGAACACAGAGGCTGGGGGCT 480

QY 1981 uProLysAlaGlnSerGlySerLeuSerValHisSerGlnProAlaAspThrSerCy 2001

DB 481 CCCCAGAGCCCACTGAGGCTCCACTTGTGTCTCACTCCCAACAGCAGACACCAAGCTG 540

QY 2001 sIleleuGlnLeuProLysAspValHisTyrlleuLeuGlnProHisGluValaProThrTr 2021

DB 541 CATCTTAAGCTTCCCAAGATGACACTATCTGCTCCACCTCAAGGGGCTCCACCTG 600

QY 2021 pGlyAlaIleProLysLeuProProProGluYArgSerProLeuAlaGlnArgProLeuX 2041

DB 601 GGGCGGCATCCCTAAACTACCCCACTGAGCGCTCCCTCTGAGCTCAGAGGCTCTCAG 660

QY 2041 gArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAs 2061

DB 661 GGGCAGGAGCAAAAGATGAGTCACTCCCTGAGCTGAGAGGCTGGGGTGAAGGAGAA 720

QY 2061 pleuLeuSerGluValaSerGlyProSerCyProLeuThrArgSerSerPheTrp-G 2081

DB 721 CTTGTTGTCAAGGTGAGTGGGCTCTCTGCTGACCCCTCC-TCACTCTTCTGGGG 779

QY 2081 lGlySerSerIleGluValGlnIArgSer--GlyTlIeGlnSerLysValaSerLys- 2099

DB 780 GGGGTTCAGAGCTCATGTGCGCAGCAGCGCTCCGCGAGCCAGAGCAAAAGTCTCAAGG 839

QY 2100 HisIleArgLeuPro-AlaProCyPro-GlyLeuGlu-ProSerTrpAlaLysAspPro 2118

DB 840 CACATCCGCTCCAGGCGCTTGGCCGAGGCTGAAACCAAGCTGGGCAAGGACCTC 899

QY 2119 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2138

DB 900 AAGAGAACCGAAAGCAGTTAACTTGACCCGGAGCTGAAGTGGATCAGGGGAACTC 959

QY 2139 Ieu 2139

DB 960 TTG 962

RESULT 4

B1736618

LOCUS

DEFINITION 60361089P1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:5367862 5',

ACCESSION B1736618

VERSION B1736618.1 GI:15713631

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE NIH-MGC <http://mgc.mci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)

Tissue Procurement: The Cepko Laboratory

cDNA library Preparation: Life Technologies, Inc.

cDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>

Plate: LHM11936 row: b column: 23

High quality sequence stop: 853.

Location/Qualifiers

1. .939

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:5367862"

/tissue\_type="retina"

/lab\_host="DH10B (phage-resistant)"

/clone\_1lib="NIH\_MGC\_94"

/note="Organ: eye; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally, oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 9.39e-86 Length: 939

Score: 1385.50 Matches: 282

Percent Similarity: 92.48% Conservative: 1



Best Local Similarity: 92.16% Mismatches: 18  
 Query Match: 11.52% Indels: 8  
 DB: 4 Gaps: 2

US-09-611-257A-24 (1-2287) x B1736618 (1-939)

QY 1950 G1YVALSERARGTHIRHISERLEUPROBANAAPSERTYRTHETCYARGANGLYSERTHR 1969  
 DB 3 GGGTCTCAGCCGACACACTCTCTGCCAATGACAGCTACATGTCTCCCAATGGAGACT 62  
 QY 1970 A1AG1UARSERLEUG1VH1SARG1YTRPQ1YLEUPROLYSALAGINSERGL1SERILE 1989  
 DB 63 GCCAGAGATCTCTTGAACACAGGGGCTGGGGGCTCCCAAGCCAGTCAAGCTTCATC 122  
 QY 1990 LEUSERVAH1ISERGINPROIALAAPTHTSERCYH1LEUGINLEUPROLYSAPVA1 2009  
 DB 123 TTGTCTTCACTCCCAACGAGACACAGACGCTGATCTTCAAGCTTCCCAAGATGCA 182  
 QY 2010 H1STYRLEUGINPROH1SGLYALPPTHRTTRPQ1YAL1EPOLYBLEUPRO 2029  
 DB 183 CACTATCTGCTCCAGCTCATGGGGCTCCCACTGGGGGCGCATCTCTAAACTACCCCA 242  
 QY 2030 PROGLYARSERPROLEUALAG1NARGPROLEUARG1NAL1A1A1EARGTHRASP 2049  
 DB 243 CTTGGCCGCTCTCTCTGCTCAGAGGCTCTCAGGGCCAGGACGACATAGGACTGAC 302  
 QY 2050 SERLEUAPVALG1NG1YLEUG1YSERAG1UAPLEUUSERGL1VALSERGL1PRO 2069  
 DB 303 TCCCTGACGCTGCGGCTGGTGAAGCGGGAACCTGTTGTGACAGGTGAGTGGGCC 362  
 QY 2070 SERCYAPROLEUTHRARGSERSESRPHETRPQ1YGLYSERSE11EGL1NVALG1N 2089  
 DB 363 TCCGCTCTGACGCTCTCTCTCATCTTCTGGGGCGGGTGAACATCCAGTCCAGACAG 422  
 QY 2090 ARSERGL1Y1EG1N1SERLYSVALSERLYSH11E1AROLEUPROIALAPROCYAPROGLY 2109  
 DB 423 CGCTCCGACGCGAGACGACATCTCCAGACATCCGCTTGCACGCTTGGCCAGGC 482  
 QY 2110 LEUG1UPROSETRPAL1ALYASAPPROPROGL1UTHRARGSERSE11EUG1LEUASP1TH 2129  
 DB 483 CTGGAACCCAGCTGGGCGAAGACCTCTCAAGACCAAGACCACTTAGCTGACACG 542  
 QY 2130 GLULEUSERTPL1ESERGLYAPLEUUPROSESERGINGL1UUPROLEUPHETRO 2149  
 DB 543 GAGCTGAGCTGATTTCAAGACCTCTCTCCAGCTCAGGAAGAACCTCTTCCCA 602  
 QY 2150 ARGASP1EULYSYRYSERYSERVALG1UTHRG1N1SERCYARGARGATGPROGLY1PHE 2169  
 DB 603 CGGACTTGAATAATGCTACAGTGTAGAGGCCCAAGAGCTGCCGCGAGGCTGGGTCC 662  
 QY 2170 TRYPLEUAPGLUG1NARGARGH1SER11EAL1-VALSERCYLEUAPSPSERGLYSERGL 2189  
 DB 663 TGGCTAAGACGACAGAGACACTCCATCGCTTGTCACTGCTTGGACAGGGCTCCCA 722  
 QY 2189 NPROIALEUCYAPROSETRPROSETRSERLEU-G1YGL1NPROLEUG1YGL1PROGLYS 2209  
 DB 723 GCCCGGCTAGTCAAGCCCTCAAGGCTCGGGGGGCAACCTCTGGGGGCTTGGGGA 782  
 QY 2209 ERARGPROLYSVALYBLEUSERPROBOSER11ESER11EAPPROPROGL1USERGIN 2229  
 DB 783 GCCGGCTTAAGAAAACTCAG-CCACCAATATCTCATAGACCCCGGAGACCA---G 838  
 QY 2229 IYSERARGPROCYSESERPROGL1YVALCYLEUARGARGAL1APRO-ALASERASP 2248  
 DB 839 GACCTCGGGCCCATGCACTCT-GGCGTCTGCC-AGGAGGAGG---CCGGGCGAAGGAC 893  
 QY 2249 SERLYSAPPRO 2252  
 DB 894 TCGAAGGATCTCT 905  
 RESULT 5  
 BM479323  
 LOCUS BM479323 1076 bp mRNA linear EST 05-FEB-2002

DEFINITION AGENCOURT\_6418725 NIH\_MGC\_67 Homo sapiens cDNA clone IMAGE:5502230  
 5', mRNA sequence.  
 ACCESSION BM479323  
 VERSION BM479323.1 GI:18528365  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1076)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
 Plate: LLM412140 row: a column: 15  
 High quality sequence stop: 692.  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:5502230"  
 /tissue\_type="retinoblastoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1ib="NIH\_MGC\_67"  
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 Kb. Library constructed by Life Technologies."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,06e-82 Length: 1076  
 Score: 1343.00 Matches: 281  
 Percent Similarity: 87.23% Conservative: 6  
 Best Local Similarity: 85.41% Mismatches: 19  
 Query Match: 11.17% Indels: 23  
 DB: 4 Gaps: 4  
 US-09-611-257A-24 (1-2287) x BM479323 (1-1076)  
 QY 1458 ARGASN11ETHRANLYSSEARAPCYA1AG1UALASERTYRARGTRPVALARGH1SLYS 1477  
 DB 3 AGGAACATCAACCAATTAATCGACTGTGCCAGGCGACGATTAACGGTGGGTCCGACCAAG 62  
 QY 1478 TYRASNPHASPNLEUG1YGN1ALEUMESERLEUPHEVAL1EUAL1ASERTLYASP 1497  
 DB 63 TACAACCTTACCAACCTTGGCCAGGCCCTGATATCTCTGTCTTGGCTTCACAGAT 122  
 QY 1498 G1YTRVALASPL1EMETRYRASPGLYLEUASPAL1VAL1YVALASPG1NGL1PRO1LE 1517  
 DB 123 GGTGGGTGACATCATGTCATGATGGGCTGAGTGTGGGCTGGACGAGGCCCATC 182  
 QY 1518 METASNH1SAPNPROTPMETLEULEURYRPH1LESERPHLEULEU11EVAL1ALPHE 1537  
 DB 183 ATGAACCAACAACCCCTGAGTGTGCTGTACTTCATCTCGTCTCGCTCATTTGGGCTTC 242  
 QY 1538 PHEVAL1EUSNMETPHEVAL1G1YVAL1VAL1EUAL1ASPNPHE1SLYSYCYARG1NH1S 1557  
 DB 243 TTGTCTGAACATGTTGTGGGTGTGTGGTGAAGACTTCCACAAGTCTCGGACGAC 302  
 QY 1558 G1NGL1UG1UG1UAL1AARGARGTGLUG1LYSARGLEUARG1RGL1UG1ULYS1YS 1577  
 DB 303 CAGGAGGAAGAGAGGCGCGGCGGAGGAGGAGGAGGCTTAAGAACTGAGAAAAAG 362

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QY 1578 ArgArgSerIySGluysGlnMetAlaGlnCysAluSerProThyTyrSerAspTyr 1597
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Db 363 AGAAGG-----AAAGCCAGGCAACCTTACTACTCCGACTAC 401

QY 1598 SerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIle 1617
    |||||
Db 402 TCCCGGCTTCCGGCTCTCGTCCACCACTGTGTGCACGACGACACTGAGCCCTTTCATC 461

QY 1618 ThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGln 1637
    |||||
Db 462 ACAGGTGTATCGGGCTGGAACGTGTCACCATGATGAGCATGACATACAGAGCCCGAC 521

QY 1638 IleLeuAspGlnAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGlu 1657
    |||||
Db 522 ATTCTGATGAGGCTGTGAAGATCTGCACTACATCTTCACTGTCACTTTGCTTGGAG 581

QY 1658 SerValPheIyLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGln 1677
    |||||
Db 582 TCAGTTTCAAACTTGTGGCTTGGTTCCGTCCGTTCTCCAGGACAGGTGGAAACAG 641

QY 1678 LeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluVal 1697
    |||||
Db 642 CTGGAAGCTGGCCATGTGTGCTGTGCATCATGAGGATCAGCGTGAAGAAATCGAGGTC 701

QY 1698 AsnLeuSerLeuProIleAsnProThrIleIleArgIle-MetArgValLeuArgTrpAla 1717
    |||||
Db 702 AAGGCTTGGTGGCCATCAACCCCAACATCATCCGATCATAGAGGTGTGCGCATTCG 761

QY 1717 AatGValIleuYsLeuLeu-LysMetAlaValGlyMet-ArgAlaLeuLeuHisThrVal 1736
    |||||
Db 762 CCGAGTGTCAAGCTGCTGTAATAATCGTGTGGCATGCGCGCTGTGACACCGTG 821

QY 1737 MetGlnAla--LeuProGlnValGlyAsnLeuGlyLeuLeuPheMet-----LeuLeuP 1754
    |||||
Db 822 ATCCAGCCCTCTCTCCCTCCCGTGGGGAACCTGGGAGCTTTTCTCCAGCGCTTGTGTT 881

QY 1754 hePheIlePheAlaIleuGlyVal-----GluLeuPheGlyAspLeuGluCysAspG 1772
    |||||
Db 882 TTCATCCCTCGCGCTCTCTCGGCGCGGTGACAGCTTTTGTGAGAA----- 928

QY 1772 LuThrHisProCysGlu 1777
    |||||
Db 929 -----CCTTGCAAG 937

RESULT 6
LOCUS BM451648 1064 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT 6394764 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5493169
5', mRNA sequence.
ACCESSION BM451648
VERSION BM451648.1 GI:18500688
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1064)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph. D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12116 Row: h Column: 02
High quality sequence stop: 657.
Location/Qualifiers
1. .1064

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5493169"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 67"
/notes="Organ: eye; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:
Pred. No.: 1,02e-79 Length: 1064
Score: 1300.00 Matches: 275
Percent Similarity: 78.89% Conservative: 9
Best Local Similarity: 76.39% Mismatches: 20
Query Match: 10.81% Indels: 56
DB: 4 Gaps: 6

US-09-611-257A-24 (1-2287) x BM451648 (1-1064)

QY 1475 ArgHisIySyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAla 1494
    |||||
Db 1 CGGCACAGATACAACTTTGACAACTTGCCAGCGCCCTGATGCTCCTGCTTGGCC 60

QY 1495 SerIyAspGlyTyrPheValAspIleMetCysArgGlyLeuAspAlaValGlyValAspGln 1514
    |||||
Db 61 TCCAAAGATGTGTGGTGTGACATCATGTACATGAGTGGCTGTGATGCTGTGGGCGTGACAG 120

QY 1515 GlnProIleMetAsnHisAsnProThrPheLeuLeuTyrPheIleSerPheLeuLeuIle 1534
    |||||
Db 121 CAGCCCATCATACACCAACCCCTGATGCTGCTGTACTTCACTTCTGCTGCTCATTT 180

QY 1535 ValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPheHisIyCys 1554
    |||||
Db 181 GTGGCTTCTTGTCTGTGAAACATGTTGTGGGTGTGTGTGTGAGAACTTCCAAAGTGT 240

QY 1555 ArgGlnHisGlnGluGluGluGluAlaArgArgArgGluGluLysArgLeuArgLeu 1574
    |||||
Db 241 CGCAGACACCAAGAGAAAGAGAGGCGCGCGGAGAGAAAGCGCTTACGAAGACTG 300

QY 1575 GluLysIyAsArgSerIySGluysGlnMetAla----- 1586
    |||||
Db 301 GGAATAAGAGAGAGAGTAAAGAGAGAGATGCTGATCTTAATCTGACATGTAAATT 360

QY 1587 -----GluAlaGlnCysLysProTyrTyrSerAsp 1596
    |||||
Db 361 GCTTCCGAGCTCAGCAGCGCTGCGTCAGAAAGCCAGTGCAAACTTACTACTCCGAC 420

QY 1597 TyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPhe 1616
    |||||
Db 421 TACTCCGCTTCCGCTCTCTCGTCCACCACTTGTGTACACAGCACTTACCTGACCTTTC 480

QY 1617 IleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnPro 1636
    |||||
Db 481 ATCAAGGTGTATCGGGCTGACCTGTGACCATGCGCATGAGACATCACAGAGAGCC 540

QY 1637 GlnIleLeuAspGlnAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPhe 1656
    |||||
Db 541 CAGATTCTGATGAGGCTCTGAAAGATCTGCAACTCATCTTCACTGATCTTGTCTTGG 600

QY 1657 GluSerValPheIyLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsn 1676
    |||||
Db 601 GAGTCAGTTTCAAACTTGTGGCTTGTGCTTCCGTGGTCTTCCAGAGACAGGTGAGAC 660

QY 1677 GlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGlu 1696
    |||||
Db 661 CAGCTGAGCTGTGACATGTGTGCTGTCCATCATGAGGATCAGCTGAGAGAAATCCAG 720

QY 1697 ValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgTrp 1716
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Db 721 GTCAACGCTCGCTGCCCATCAACCCACCATCATCCGCATCATGAGGCTGCCCAT 780  
 Qy 1717 A1aargValLeuYsLeuLeuYsMeLa1aValGlyMeLaArgAlaLeuLeuHis-ThrVa 1736  
 Db 781 GCCCGAATGTGAAGCTGCGTGAATGCTGTGGGATGCGGGGCTGCTGGACAACCGG 840  
 Qy 1736 lMet-GlnAlaLeuProGlnValGlyValLeuGly---LeuLeuPheMeLeuLeuPheP 1755  
 Db 841 GATGCCAGGCTGCTGCCAGGTGGGGAACCTTCCCTCCAGGTGGTGGGTT 900  
 Qy 1755 he---lIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGlnThrH 1774  
 Db 901 TTCACCTTGGCCAGCTCTGGGGCC-----GGGAACTCTTTGT----- 941  
 Qy 1774 lAsProCysGluGlyLeuGlyArgHisAlaThrPheArgAspPheGlyMeLaIaPheLeuT 1794  
 Db 941 ----- 941  
 Qy 1794 hrLeuPheArgValSerThrGlyAspAsnTrpAsnGlylIleMeLysAspProSer 1812  
 Db 942 -----GAGAACCGTGGATGGG---GACMAAGAACCCAC 974

RESULT 7  
 AY416501 5666 bp DNA linear GSS 17-DEC-2003  
 LOCUS Mus musculus SCN8A gene, VIRTUAL TRANSCRIPT, partial sequence,

ACCESSION AY416501 GI:39772461  
 VERSION AY416501.1  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 5666)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios

TITLE Science 302 (5652), 1960-1963 (2003)  
 JOURNAL 14671302

REFERENCE 2 (bases 1 to 5666)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.

FEATURES  
 Location/Qualifiers  
 1..5666

gene  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
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 /gene="SCN8A"  
 /locus\_tag="HCM5911"

ORIGIN  
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 Pred. No.: 4,33e-78 Length: 5666  
 Score: 1293.50 Matches: 533  
 Percent Similarity: 36.60% Conservative: 538  
 Best Local Similarity: 22.39% Mismatches: 757  
 Query Match: 10.75% Indels: 755  
 DB: 9 Gaps: 83

US-09-611-257a-24 (1-2287) x AY416501 (1-5666)

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 Qy 45 SerArgAspSerProValAlaSerArgSerSerThrCysProGlyProGlyAlaAla 64  
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 Qy 65 GlyAlaGlySerThrGluYsAspProGlySer-----AlaAspSerGlu 79  
 Db 121 GATGCGAGCCACCGGAGGACGATGAAGACAGCAACCCGCAACCAACGATGACTGGAG 180  
 Qy 80 Ala-----GluGlyLeu----- 83  
 Db 181 GCGGGAGAGATTGGCTTTCATCTACGGGGACATCCCGCAGGCTGGTGGGCTTCCC 240  
 Qy 84 -----ProTyr----- 85  
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 Qy 86 -----ProAlaLeuAlaProValValPheMetYrLeu 96  
 Db 301 AAAACTCTCTTCAGATTTCAGCGCCACTCGCTTGG-----TACATTCTA 345  
 Qy 97 SerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGlu 116  
 Db 346 AGTCTCTTTAACTGTATAGAAAGAAATAGCTATTAAATTTGTATACATTCATTCACG 405  
 Qy 117 ArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCys 136  
 Db 406 ATGATCATCTATGCGACACATCTGACCACTGTGTATTCATGACTTTTATTAACCTGCC 465  
 Qy 137 GluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIle 156  
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 Qy 157 Phe---AlaPhePheAlaValGluMetValValIleMetValAlaLeuGlyIlePheGly 175  
 Db 493 TTCACAGGGATTACACATTGTAATCATCTGTGTAATAATCATGCCACAGAGTTTC 546  
 Qy 176 LysIleCys-----TyrLeuGlyAspThrTrpAsnArgLeuAspPhePhe 190  
 Db 547 -----TGCATAGACGGCTTCACCTTCTTACGAGACCCGCGAATCGTTAGACTTCAGT 600  
 Qy 191 IleValIleAlaGlyMetLeuGluTrpSerLeuAspLeuGlnAsnValSerPheSerAla 210  
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 Qy 271 AsnArgCysPheLeu---ProGluAsnPheSerLeuProLeuSerValaAspLeuGluPro 289  
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 Qy 290 TyrTrpGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsn 309  
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Qy      677  IsSerSerCysLysIleSerSerProCysSer----- 687
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Qy      688  -----LysAlaAspSerGlyAlaCysGlyPro----- 696
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Qy      712  eAlaAspHisValMetProAspSerAspSerGlnAlaValTyrGlnPheThrGlnAsp 732
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Db      1937  ACATGGGCGGCTCGCTGCTGAGGACACACTGAGTGAGATTAAAG----- 1983
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Qy      732  lAGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAla 752
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Db      1984  -----A 1984
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Qy      752  sPAlaGlnProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLys- 771
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Qy      772  --IleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrL 791
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Qy      791  eu----- 791
      |||::|||
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Qy      791  ----- 791
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Qy      911  lPheSerIleLeuGlnMetHisLeuPheGly-----CysLysP 924
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Db	2792	TTATTTCTGGGCTTCCTTCAG------	2814
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Db	2815	-----CTCTTCAAGCCACACAAAT	2833
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Db	2834	CTGGCGGCGCACAGACGACGAGGGGAATGA------CAACTCGAGATATG	2881
QY	1022	LYaPrgLYAspArgLYeLYaTrgLeuAlaLeuValAlaLeuGLYGLuIhIsalIaGLuLeuA	1042
Db	2882	GTGATCCCGATCCAAGAGAGCGGT-----GGCTCGGGCCA------	2916
QY	1042	rgLYsSerLeuLeuProProIeuiIeIhIsThrAlaAlaThrProMetSerhIsProL	1062
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QY	1142	euleuSerGLYGLuGLYGLuIuSerGLYAsnArgGLuGLuIuSerSerGLuIuAspArgA	1162
Db	3102	-----GACGATACCAAGCTCCACAGAA------	3122
QY	1162	IaSerProAlaGLYSerAsnPhIsArgHIsArgGLYSerLeuGLuArgGLuAlaLYsSerS	1182
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QY	1261	luArg------AspSerTrpSerAlaTYrIlePheProProGLuIuSerA	1275
Db	3244	TCACATCGAGAGAGACTAGCAAGTGTGTG-----TGATATC-----	3281

Oy		1275	rgRheAqgLeuLeyCyhiIaXgiIeIethrHslvlySmcPReasPhlValValLeuV	1295
Db		3282	--CTGCGAAAAACCTGGTTCCTCATTTGTGAAGACAATGGATTGTGAACCTTCATCACTT	3339
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Db		3340	TCAATGATTCTCCTCAGACAGTGAGACCCTGGCTTCGAGACATCTACATTGAGCAGA	3399
Oy		1315	eRaLaGuArgIlePheLeuThrLeuSerAntYrlIephThAlaValAPheuaIag	1335
Db		3400	AGACCAATCCGATCACATCTGGAGATATCGGACAAGGCTTCACCTCATCTTCATCTCG	3459
Oy		1335	IumctThValvsValValAlaleuclYlrPrpySpheGlygluAlaETyrLeuarGs	1355
Db		3460	AGATGTGCTCAATGAGACACTATGAGCTTCGTC-----AA GTTCTTCAACA	3507
Oy		1355	eRserTPraenValLeuAspGlYleuLeuValleuIlEservAlIeaSPIleuValS	1375
Db		3508	ATGCCTGGTGTGCTTGGATTCCTCTCATTTGTGGCTNNNNNNNNNNNNNNNNNNNNN	3567
Oy		1375	eRmetValSerAspSerGIYthrIlylleuGIymetLeuArgValleuArgLeueuA	1395
Db		3568	NNN	3627
Oy		1395	rghTrLeuArgProLeuArgValIlEservAlaGInglyLeuLeuValValGIur	1415
Db		3628	NNNNNN-----NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTGTGTGAAC	3678
Oy		1415	hrlEuMetSerSerLeuLyProIIegIyaNIleValIlleCyseCysalaPhePeI	1435
Db		3679	CCTTGGTGGCGCATCCCTCCATCATGAACGCGTGGTGATGTCTCATCTTCTGGC	3738
Oy		1435	IeIlePheGlyIleLeuGIYValGlnleuPheLySGIlyLysPhePheValCYsgIInLyG	1455
Db		3739	TGATTTTCAGATCATATGGCGCTTAACCTGTTTGTGGGAATAATACCACTAGCTTCAACG	3798
Oy		1455	IuaSPthrArg-----AbnIlleThraSNlySerAspCYalaclu-	1468
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Oy		1469	-----AlaserYrArgrtTPrrValArgHlslyVeTyCPAsnPheAspAnlt	1483
Db		3859	TCATGAGAGGCCAACACACAGAGATCCGATGGAAAGAACGTCAACATCACTTCACAAAGC	3918
Oy		1483	eugIGlnAlaLeuMetSerleuPheValleuAlaserLySaSPGIYTriValAspIlem	1503
Db		3919	TCGGGGCAGGCTACTCTGGCTTCCTTCCAAGCGACACTTCCAAAGCGCTGAGTAGACATCA	3978
Oy		1503	eTYrAspGIYleuAspAlaValGIYValAspGIngnIProIleMetAsnHIsanProt	1523
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Db		4039	ACATGTACATCTACTCTGTGTCACTTCATCACTTCGCTCCTTCTTCAACCTCAACCTGT	4098
Oy		1543	heValGIYValValValGIuAsnPhelHlslyScySarGlnHIselnGIuGIuGIuGlua	1563
Db		4099	TCATCGGTGTATCATGACACATTTCAATCAACAGAAAGAAAAAGTTGGAGAGTCAGACA	4158
Oy		1563	Ia---ArgArgArgGIuGIuLYrArgLeuArgArgLeuGIuLYrLYrArgRserLySG	1582
Db		4159	TCTTCATGACAGAGAAACAGAAAGAAAGTACACAGCGCATGAGAGAGCTAGGCTCAAGA	4218
Oy		1582	IuLYrGIuMetAlaGIuAlaGIncyLySPoLYrTYrSerAspTYrSerArgPheargL	1602
Db		4219	AGCCACAG-----AA GCCCATCCCCGACCTTTGAACAAATTCAAAG	4266
Oy		1602	euleuValIHlsHlsLeuCyethrSerHlsIstYrLeuAspLeuPheIleThClYalIlleg	1622
Db		4261	GGATTGTCTTGAATTTGTGTGTCGGAACAAGCCTTCGACATCGTATCATGATGCTCATCT	4320
Oy		1622	IYleuAsnValValThrMetAlaMetGlnHlsIstYrGIngnIProGlnIlleuAspGIua	1642

Db	4321	GCCTTAACATGTGATACCATGTATGTGTGAGACAGACACACAGAGACAGATGTGAGAACAA	4380
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Db	4381	TTCTCTACGTGATTAATATGTGCTTTCGTCATCTTTCACCTGGAGAGTGTGTCTCAAAA	4440
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Db	4495	TGGTGGTCATTTCTCCATTTGTGGAAATGTTCTGGCTGATATGATTTGAGAACTATTC-	4553
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Oy	1816	spGlnGlu-----SerThrCysTyrAsnThrValllleSerProI	1829
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Db	4954	TCTTCTTCGTGAGCTACATCATCATCTCTTCGTGATGGTGSTGAACATGTACATTGCCA	5013
Oy	1849	alleuMetLysNllleGluGlnLeuSerAsnLysGluAlaLysGlu-----GluAlaG	1866
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Db	5074	ACTTCGACACTTTCTATAG-----	5093
Oy	1886	euglySerProPheLeuTrpProGlyValGluGlyValAsnSerThxAspSerProIuYp	1906
Db	5094	-----ATCTGGAGAAAGTTGAT-----	5111
Oy	1906	roGlyAlaProHlisThrAlaHlisGly-----AlaAlaSerGlyPheS	1922
Db	5112	-----CCGATGACCCACCAAGTTTCATCGAGTACTGTAACTGGCCGACATTGGCCGACG	5163
Oy	1922	erleuGlnHlsProHlmetValProHlsProGlnGluValaProValProleuGlyProA	1942
Db	5164	CCCTTGACACATCCGCTCGAGATCCCAAGCCCAACACACATCATGAGCTC--ATCGCATGG	5220
Oy	1942	spLeuLeuThrValArgLysSerGlyValaSerArgThrHlisSerleuProAsnAspSerT	1962
Db	5221	ACCTGCCCATGTG-----AGCGGA---GATCGAATCATCTGCTG-----GACATCC	5265
Oy	1962	yrMetCysArgAsnGlySerThrAlaGluArgSerleuGlyNlsArgGlyTrpGlyLeuP	1982

Db	5686	TTTTTC-----GCTTACCAAGGAGTCTCGGGAGACAGTGCG-----	5305
Oy	1982	rolYsAlAgInSerGIySeRIleuSeVaHIseRgInProAlAsePTHeSeCYeI	2002
Db	5304	-----GAGTTGACATCCTGCGGCAGACAGATGACAGACGCTTCC	5343
Oy	2002	IeLeuGInLeuProLYsAsPvAlHISyRTleuNeuGInPRoHISglYAlAProThrTrPg	2022
Db	5344	TGGCGTCCAATCCTTCCAAAGTGTCTTAAC-----	5372
Oy	2022	lYalAIleProLYsLeuProProGIlyARgeSerProleuAlAglNArgProLeuARgA	2042
Db	5373	-----GAGCTTATCACAGACCATCTTCGCGCGCA	5400
Oy	2042	rGlnAlAAlAleArGThrAsPSerleuApVAlGInglyLeuSeraGlUasPl	2062
Db	5401	AGCG-----	5405
Oy	2062	euleuSerGIuValSerGIyPro-SerCyAProleuthrArgSerSerPheTrPGly	2081
Db	5406	-----GAAGAGGTCTTCGAGTGTCTTTCGACGCGTCTTACAGGGGACACCTGCTTAGGC	5460
Oy	2082	GlySeSerIleGInValGInGInArgSer-----GlyIleGInSerLyS	2096
Db	5461	GGGGCTTCA-----TTGCGAAGAAGTACTCTTCCAAACAAGCTCGAGAAATGAGGCCACC	5514
Oy	2097	VAlserLyshIsIArGLeuProAlAProCyAProGIlyLeuGInProSerTrPAIAlYS	2116
Db	5515	ACCGAGAGAAGAACAGACACCCCCGTCACAGCTCTCCCTCTTACGACGCGTGA	5574
Oy	2117	AsPProProGIuThraArgSerSerleuGluAsPhrUlAuSerTPIlleSerGIy	2136
Db	5575	CNAAGCCCAGCANAGAACACAGC-----AGCGGG	5604
Oy	2137	AspleuNeuProSerSerGInGInGluProLeuPheProARgAspleuLYsLys	2154
Db	5605	CAGAGAAAGCAGAGGAAAAGAG-----CCAGAGGACGAAAAAGAG	5646
RESULT 8			
LOCUS	CF548698	879 bp	mRNA linear EST 22-SEP-2003
DEFINITION	AGENCOURT_15594508 NICHD_XGC_Brln Xenopus laevis cDNA clone		
VERSION	CF548698		
KEYWORDS	CF548698.1 GI:3488530		
SOURCE	EST.		
ORGANISM	Xenopus laevis (African clawed frog)		
AUTHORS	Xenopus laevis		
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;		
COMMENT	Xenopodinae; Xenopus; Xenopus. 1 (bases 1 to 879) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgabbs@remail.nih.gov Tissue Procurement: CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LLM14738 row: j column: 24 High quality sequence spot: 646. Location/Qualifiers 1..879 /organism="Xenopus laevis" /mol_type="mRNA"		
FEATURES			
Source			

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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

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## ORIGIN

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Alignment Scores:
Pred. No.:      4,09e-78      Length:      879
Score:          1275.00      Matches:      250
Percent Similarity: 91.19%      Conservative: 19
Best Local Similarity: 84.75%      Mismatches:  17
Query Match:    10.60%      Indels:      9
DB:              Gaps:      2

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US-09-611-257A-24 (1-2287) x CF548698 (1-879)

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QY 1517 LLEMERASHISAENPOTRPMETLEULEUTYRPHLESESPHELEULEULEVALALA 1536
DB 61 GTGATGATTAACAACCTTGATCTGTATATTTCATCTCATTTTGGCTGATTGGCA 120
QY 1537 PHEPHEVALLEUAMETPHEVALGLYVALVALAGLUANPHEHSLYSCYARGLN 1556
DB 121 TTTTGTGCTCCACATGTTGTGGTGTGGTGAGAACTTCATTAATGCGCGCAG 180
QY 1557 HIEGLNGUGUGUVALAARGARGGLUGLUYARGLEUARGARGLEUGLUYS 1576
DB 181 CATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 1577 LYSARGARGSERLYSGULYGLMEALAGLUAGLUCYLYSPROYTYRSEASAP 1596
DB 241 AAGGAGAGG-----AAGGCCAGGTAAACCTTACTATTCCGAG 279
QY 1597 TYSERARGPHEARGLEULEUVALHISHILEUCYSTRSERHSTRYLEUASPLEUPHE 1616
DB 280 TATTCTCACCTTCGGCTCTCATCATCAGATCGTACATCATATTGGAATTTGTTT 339
QY 1617 ILEPHRGYVALILEGLYLEUASVALAVALHMETALMETGLHISTYRGLNGLNPRO 1636
DB 340 ATTACTGGGGTCATGATTAATGTTATCACTATGGAATGAGACATATCAGCAACC 399
QY 1637 GINILEUAPGLUALALEULYELCYASANTYRILEPHEHTRVALILEPHEVALPHE 1656
DB 400 CAGGATATTGTTGAAGCTCTAAATCTGTATTAACATCTTACCCTCATTTTGGTACTG 459
QY 1657 GLUSERVALPHELYSLEUVALALEPHEALAPHEARGARGPHEPHEGLNAPARGTPRASN 1676
DB 460 GAATCTGGGTGCAAAATGATAGCTTTTGGCTCCGGCCATCTTTTAAAGACAGGTGGAC 519
QY 1677 GINLEUAPLEUALALEUULEUSERTILEMETGYLLETTRLEUGLNUILEGLU 1696
DB 520 CAGTTGGATCTGGCCATGTTCTTCTCCATCATGAGAACACATGGAAGAAATTGAA 579
QY 1697 VALANLEUSERLEUPROILEASNPROTHRILELEARGLILEMETARGVALLEUARGLILE 1716
DB 580 GTCAATGATCACTGCCCATTTACCAACATCAATCCGAATTAAGAGGCTCTTGCGAGTT 639
QY 1717 ALAARGVALLEULYGLEULEULYMECALAVAGLYMETARGALALEUULHISTHYAL 1736
DB 640 GCTCGGGGTCTGAAGTTATTAAGATGCGACATCGGTATGCAAGCCCTGCTGATACGGTT 699
QY 1737 METGLNALALEUPROGLNVALGLYASNLEUGLYLEUAPHEMETLEULEUPHEPHEILE 1756
DB 700 CTGCAAGCGCTTTCTCAAGTGGGGAATCTCGGCTGCTTTATAGCTCTGTTCTTTTAA 759

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QY 1757 PHEALALEUUGLYVALGILEUPHEGLYASPLEUGLUCYSASPLGUTHRHISPROCVS 1776
DB 760 TTTTCCGCTCTGGAGATGTAACCTTTTGGTACTTAAAGACATGATCCATCCCTGT 819
QY 1777 GLU-GLYLEUGLYARGHISALATHRPHARGAAN---PHEGLY 1789
DB 820 GAAAGGCTTGGACGACTTCCACTTTTCAAGAAATTTTCGG 862

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RESULT 9
CA319705
LOCUS
DEFINITION
CA319705
ACCESSION
CA319705
VERSION
CA319705.1
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
793 bp mRNA linear EST 09-JUL-2003
UI-M-FW0-cca-d-09-0-UI-r1 NIH_BMAP_FW0 Mus musculus cDNA clone
IMAGE:6816826 5', mRNA sequence.

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@ds-rfemail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNI at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.

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## FEATURES

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Location/Qualifiers
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/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FW0"
/note="Organ: Brain; Vector: pYX-Aac; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction. Ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Aac vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGACAGCAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemlin Chih, Ph.D.,
program coordinator."

```

## ORIGIN

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Alignment Scores:
Pred. No.:      6.7e-77      Length:      793
Score:          1256.50      Matches:      241
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Best Local Similarity: 91.63%      Mismatches:   9
Query Match:    10.45%      Indels:      11
DB:              Gaps:      1

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QY	1464 SerAspCyAlaGluAlaSerTyrArgTTPValArgHisLysTyrAsnPheAspAsnLeu 1483
DB	63 TCCGACTGCTCGAGGCGAGTTACCGGTGGGTCCGGACAGTACATTTGACAACTTG 122
QY	1484 GlyAlaAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTTPValAspIleMet 1503
DB	123 GGCAGAGCTCTATATGTCCTGTTGTGTGGCTCCAGAGATGGCTGGGTGACATCAG 182
QY	1504 TyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTTP 1523
DB	183 TATGATGAGACTGATCTGTGGAGTGAGACAGACCCATCATGTGAACCAACCTTGG 242
QY	1524 MetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPhe 1543
DB	243 ATGCTCTCTACTTCACTCTCTCTCTCTCATCTGAGCTTCTTCTTGAACATGTT 302
QY	1544 ValGlyValValGluAlaGluAsnPheHisLysCyArgGlnHisGlnGluGluGluAla 1563
DB	303 GTGGGGGTGGTGGTGAAGAACTTCCATTAAGTGCAGGACAGACAGAGAGAGAGCGG 362
QY	1564 ArgArgArgGluGluValArgLeuArgLeuGluLysLysArgArg----- 1579
DB	363 CGCGCGCGGAGAGAGAGAGCACTMAAGAGCTCGAGAAAAAGAGGAATCTAATGTTG 422
QY	1580 -----SerLysGluLysGlnMetAlaGluAlaGlnGlnCysLysPro 1592
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DB	483 TACTACTCTGACTACCTCGGCTTCGCGCTCTCTGTCACACACTGTGTACAGCCACTAC 542
QY	1613 LeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHis 1632
DB	543 CTGGACCTCTTCACTCACTGTGTGCATCGGGCTGAATGGTCAAGTGCATGACCAAGCAAT 602
QY	1633 TyrGlnGluProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrVal 1652
DB	603 TACACAGACCCCAATCTCTGACGAGGCTCTGAAGATCTGCAACTTCACTTTACCGTC 662
QY	1653 IlePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGln 1672
DB	663 ATCTTTGTCTTGAGTCAATTCANACTTGTGGCTTCGCGCTTCGCGGTTCTTCAG 722
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ACCESSION AY416499	
VERSION AY416499.1 GI:39772459	
KEYWORDS GSS.	
SOURCE Homo sapiens (human)	
ORGANISM Homo sapiens	
REFERENCE 1 (bases 1 to 5943)	
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,	

TITLE		Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	
JOURNAL		Interfing nomenclural evolution from human-chimp-mouse orthologous	
PUBMED		gene trlos	
REFERENCE		Science 302 (5652), 1960-1963 (2003)	
AUTHORS		14671302	
TITLE		2 (bases 1 to 5943)	
JOURNAL		Clark,A.G., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,	
COMMENT		Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
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DB	22 CCACAGAGCCCTGATGATGTTTCAAGCCTTACAC-----CCTGAG 60	DB	346 AGTCCCTTTTAACTGATTAAGAGAAATAGCTATTAATAATTTGATACATTCATTATTGAC 405
QY	45 SerArgAspSerProValAlaSerArgSerThrThrCysProGlyProGlyAlaAla 64	QY	117 ArgValSerMetLeuValIleLeuLeuAsnCyValIThrLeuGlyMetPheArgPro--- 135
DB	61 TCACAGGCAAAATGAGAGGCGCATTTGCTGAGCAAGCTCAAGAAACCAACCAAGGCC 120	DB	406 ATGATCATATATGACATATTTTGAACCACTGTGATTCATGACATTTTAAGTAACCTCCT 465
QY	65 GlyAlaGlySerThrGluLysAspProGlySer-----AlaAspSerGlu 79	QY	136 -----CysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAsp 153
DB	121 GATGCAATCATCGAGAGAGCATGACAGCAAGCCCAAGCCCAACCAAGCCTGGAA 180	DB	466 GACTGCTCGAAGAAATGTC----- 483
QY	80 Ala-----GluGlyLeu----- 83	QY	154 AspPheIlePhe---AlaPhePheAlaValGluMetValIleValMetValAlaLeuGly 172
DB	181 GCAAGGAAGATTTGCCCTTTCATCTACGGGGGACATCCCCCAAGGCTGGTTCAGTTCCC 240		
QY	84 -----ProTyr----- 85		
DB	241 CTGAGAGACTTTGACCCATACATATTGACGCAAAACCTTTGTAGTATTAAACAGAGG 300		
QY	86 -----ProAlaLeuAlaProValPhePheTyrLeu 96		
DB	301 AAAACTCTTTCAGATTAGTTCACAGCGCTGCTTG-----TACATTTTA 345		
QY	97 SerGlnAspSerArgProArgSerTTPCysLeuArgThrValCysAsnProTTPPheGln 116		
DB	346 AGTCCCTTTTAACTGATTAAGAGAAATAGCTATTAATAATTTGATACATTCATTATTGAC 405		



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Db 2307 NNN 2366  
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Db 2367 NNNNGTTTTCACGTGAATTTTCACAGCGAAATGTTCTGAAGCTCATAGCCATGGATCC 2426  
QY 832 opheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVa 852  
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QY 1000 ----- 1000  
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Db 3072 GCAGCGTGAAGCTGATGAGGTGAAG----- 3096  
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Db 3097 ----- 3116  
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Db 3170 -----GTGACTTCCA 3179

QY 1100 LArgSerSerProHisSerProTrpSerAlaAlaSerSerTrp-----ThrSerArgA 1118  
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Db 3392 CCTGGAAGGA---AGCACATTTGATATCAACCGAAGTAGAAGAGGTCCCT----- 3441  
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QY 1269 LpheProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetP 1289  
Db 3557 TC-----CTGCGGAAAACCTGTTCTCTCATCGTGAAGCAACATGGT 3598  
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      1463  ySerAspCyValaglu-----AlaSerTyArgTyrValArgHisL 1477
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      4118  AAAGTGAATGGAAGAACTTATGAGAGGGGAAACAAATACAGAGATGATGGAAGAACTGTA 4177
      |||      ::      ::      ::      ::      |||
      1477  ySfTyAsnProPheAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysA 1497
      |||      ::      ::      ::      ::      |||
      4178  AGATCAACCTTGGACAAATGTGGGGCAGAGATACCTGGCCCTTCCAAATGAGCAACCTTCA 4237
      |||      ::      ::      ::      ::      |||
      1497  spGlyTyrValAspIleMetTyrAspArgLysLeuAspAlaValGlyValAspGlnProI 1517
      |||      ::      ::      ::      ::      |||
      4238  AAGCTGAGATGAGACATGATGATGACCTGATGATCCCGAAGCCGATGAGAGAGCTTA 4297
      |||      ::      ::      ::      ::      |||
      1517  leMetAsnHisAsnProTyrMetLeuLeuTyrPheIleSerPheLeuIleValAlaLar 1537
      |||      ::      ::      ::      ::      |||
      4298  AGTATGAGACAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4357
      |||      ::      ::      ::      ::      |||
      1537  hePheValLeuAsnMetPheValGlyValValAlaGlyAsnProHisLysCysArgGlnH 1557
      |||      ::      ::      ::      ::      |||
      4358  TCTTCACCCCTGAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4417
      |||      ::      ::      ::      ::      |||
      1557  isGlnGluGluGluGluAla---ArgArgArgGluGluGluValArgLysLeuArgLysLul 1576
      |||      ::      ::      ::      ::      |||
      4418  AGTTGGAAGCTCAGACACTTTCATGACCCGAAAGACAAAGAACTACTAATGCCATGA 4477
      |||      ::      ::      ::      ::      |||
      1576  ySfTyAspArgSerLysGluLysGlnMetAlaGlnValGlnCysLysProTyrTyrSerA 1596
      |||      ::      ::      ::      ::      |||
      4478  AAAAGCTGGGCTCAAAAGACGACAG-----AAACCATTCCTCCGCC 4519
      |||      ::      ::      ::      ::      |||
      1596  spTySerArgPheArgLeuLeuValHisLysCysThrSerHisTyrLeuAspLeuP 1616
      |||      ::      ::      ::      ::      |||
      4520  CCTTGAACAAATCCAGAAATCGTCTTGTGATTTGTTCACCTCAGCAAGCCCTTGACATGG 4579
      |||      ::      ::      ::      ::      |||
      1616  heIleThrGlyValIleGlyLeuAsnValAlaThrMetAlaMetGlnHisTyrGlnGlnH 1636
      |||      ::      ::      ::      ::      |||
      4580  TTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4639
      |||      ::      ::      ::      ::      |||
      1636  roGlnIleLeuAspGluAlaLeuLysLysIleCysAsnTyrIlePheThrValIlePheValP 1656
      |||      ::      ::      ::      ::      |||
      4640  GCAAGCAGATGAGAAACATCTCTACGATTAACCTGGCTTTGTATCTTCTTCACT 4699
      |||      ::      ::      ::      ::      |||
      1656  heGlySerValPheLysLeuValAlaPheAlaPheArgArg---PhePheGlnAspArgT 1675
      |||      ::      ::      ::      ::      |||
      4700  GTGAGTGAGCTCAAAATG-----TTTGGCTGAGGCACTACTACTCACTCACTGGCT 4753
      |||      ::      ::      ::      ::      |||
      1675  rPAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnLul 1695
      |||      ::      ::      ::      ::      |||
      4754  GGAACATCTTCGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4813
      |||      ::      ::      ::      ::      |||
      1695  leGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuA 1715
      |||      ::      ::      ::      ::      |||
      4814  TAAATGGAATATCTTT-----GTTTCCCAACCCCTATTCGAGTATCCGATGGGCC 4867
      |||      ::      ::      ::      ::      |||
      1715  rGlnIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisT 1735
      |||      ::      ::      ::      ::      |||
      4868  GTATTTGGCGCATCTTGCATGATCAAAAGCGCAAGGGATTCGTAACCTGCTCTTGG 4927
      |||      ::      ::      ::      ::      |||
      1735  hValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheP 1755
      |||      ::      ::      ::      ::      |||
      4928  CCTTAAATGATGCTCTTGCCTGCTGCTTCAACATCGGCTTCTGCTTCTGCTGCTGCTG 4987
      |||      ::      ::      ::      ::      |||
      1755  heIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisP 1775
      |||      ::      ::      ::      ::      |||
      4988  TCACTTCTCTCATTTTGGATGTCGAATTTTGGATATGTAACACAGAG-----5037
      |||      ::      ::      ::      ::      |||
      1775  roCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrL 1795
      |||      ::      ::      ::      ::      |||
      5038  -----GCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5092
      |||      ::      ::      ::      ::      |||
      1795  euPheArgValSerThrGlyAsnProThrPheArgGlyIleMet-----LysA 1810
      |||      ::      ::      ::      ::      |||

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Db      5093  TGTTCAATACAAACCTCAGCTGTTGGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5152
      |||      ::      ::      ::      ::      |||
      1810  spProSerArgAspCysAspGlnGlu-----SerThrCysTyArg 1823
      |||      ::      ::      ::      ::      |||
      5153  CCCCTACTCTGCAACCTTGAATGAGAAACACCAGGAGTGGCTTTAAGGAGATTTGGGA 5212
      |||      ::      ::      ::      ::      |||
      1823  snThrValIleSerProIleTyrPheValSerPheValLeuThrHisLagIlnPheValLeuY 1843
      |||      ::      ::      ::      ::      |||
      5213  ACCCTCAGTGGGACATCTTCTTGTGTAAGCTACATCATCTCTTCCATATGTTGG 5272
      |||      ::      ::      ::      ::      |||
      1843  alAsnValValIleAlaValLeuMetLysHisLeuGluLysSerAsnLysGlyAlaLysG 1863
      |||      ::      ::      ::      ::      |||
      5273  TGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5332
      |||      ::      ::      ::      ::      |||
      1863  lu-----GluAlaGluLeuGluAlaGluLeuGluLysLeuMetLysThrLeuSerP 1880
      |||      ::      ::      ::      ::      |||
      5333  ACCCTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5370
      |||      ::      ::      ::      ::      |||
      1880  roGlnProHisSerProLeuGlySerProPheLeuThrProGlyValGluGlyValAsnS 1900
      |||      ::      ::      ::      ::      |||
      5371  -----ATCTGGAGAAATTCGAC-----5388
      |||      ::      ::      ::      ::      |||
      1900  erThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGly-----1916
      |||      ::      ::      ::      ::      |||
      5389  -----CCGATGCCACCGAGTTCAATGATGATGATGATGATGATGATGATGATGATG 5422
      |||      ::      ::      ::      ::      |||
      1917  --AlaAlaSerGlyPheSerLeuGlnHisProThrMetValProHisProGluGluValP 1936
      |||      ::      ::      ::      ::      |||
      5423  TGGCAGACTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5482
      |||      ::      ::      ::      ::      |||
      1936  roValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHis 1956
      |||      ::      ::      ::      ::      |||
      5483  AGCTC---ATCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5530
      |||      ::      ::      ::      ::      |||
      1956  erLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGlnArgSerLeuGlyH 1976
      |||      ::      ::      ::      ::      |||
      5531  GCTTG-----GACATCTTTT-----GCCTTCAACAGCGGGTCTGGAG 5572
      |||      ::      ::      ::      ::      |||
      1976  isArgGlyTyrGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnP 1996
      |||      ::      ::      ::      ::      |||
      5573  ATAGCGGG-----GAGTTGACATCTGCGGACAG 5602
      |||      ::      ::      ::      ::      |||
      1996  roAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProH 2016
      |||      ::      ::      ::      ::      |||
      5603  AGATGGAAGACGGTTCGGGATCCCAATCTTCAAAAGTCTTAC-----5649
      |||      ::      ::      ::      ::      |||
      2016  isGlyAlaProThrTyrGlyAlaIleProLysLeuProProGlyArgSerProLeuA 2036
      |||      ::      ::      ::      ::      |||
      5650  -----GAGCCATCA 5659
      |||      ::      ::      ::      ::      |||
      2036  lagIlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyL 2056
      |||      ::      ::      ::      ::      |||
      5660  CAACACATCGCTCGCAAGAG-----5682
      |||      ::      ::      ::      ::      |||
      2056  euGlySerArgGluAspLeuLeuSerGluValSerGlyPro-SerCysProLeuThrArg 2075
      |||      ::      ::      ::      ::      |||
      5683  -----GAGAGAGTATCTGACAGTGTCTGACGGCTGCT---5716
      |||      ::      ::      ::      ::      |||
      2076  SerSerSerPheTyrGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSer 2095
      |||      ::      ::      ::      ::      |||
      5717  ACCGGGACATTTTGGACAGGGCGGGCTTCACTCGCAAAAAGACACTTCTAATACTGG 5776
      |||      ::      ::      ::      ::      |||
      5777  AGATGAGAGCACACACCGGAGAAAGAGAGCACCCCATCTACAG-----5824
      |||      ::      ::      ::      ::      |||
      2116  LysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSer 2135
      |||      ::      ::      ::      ::      |||
      5825  -----CTTCCCTCCGCTTATGACAGTGAACCTTAACCTGAAGAGAAAGACACAGCAG 5878
      |||      ::      ::      ::      ::      |||
      2136  GlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAspLeuLysLys 2154
      |||      ::      ::      ::      ::      |||
      5879  GGG-----CAGAGGAAGAGAAAGGAAGAACCCAAAGACAAAGAGAGAG 5923
      |||      ::      ::      ::      ::      |||

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RESULT 11  
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LOCUS UI-M-GVO-cju-p-15-0-UI.r1 NIH BMAP\_GVO Mus musculus cDNA clone  
DEFINITION IMAGE:30622742 5', mRNA sequence.  
ACCESSION CF745071  
VERSION CF745071.1 GI:37641411  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 715)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.iowa.edu/distribution/mouse1.html>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)  
Seq primer: pyx-5.  
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1..715  
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/mol\_type="mRNA"  
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Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction. Ligated with  
EcoR I adaptor, digested with NotI and then cloned  
directionally into pyx-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is CGACTGCAAT. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the  
Developing Mouse Nervous System", supported by National  
Institute of Mental Health (NIMH), Hemm Chin, Ph.D.,  
program coordinator."

ORIGIN  
Alignment Scores:  
Pred. No.: 6.63e-73 Length: 715  
Score: 1198.00 Matches: 233  
Percent Similarity: 98.73% Conservative: 1  
Best Local Similarity: 98.31% Mismatches: 3  
Query Match: 9.96% Indels: 0  
DB: 7 Gaps: 0  
US-09-611-257a-24 (1-2287) x CF745071 (1-715)  
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DB 3 CACCTTTTGGTGGCAAGTTCGATCGAAGCGGAGTGGGACAGCTTGGCCAGACCGGAG 62  
QY 938 AsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleuThrGlnGluAsp 957  
DB 63 AATTTCACCTCCTGGCTCTGGGCAATTGTCACTGCTTTCAATTCGACTCAGGAAGAC 122

QY 958 TrpAsnIysValIleuTyrAsnGlyMetAlaSerThrSerSerTrpAlaIleuTyrPhe 977  
DB 123 TGGAAATAAAGTCCTTTACACAGGCAATGGCTTCACAGTCATCTTGGGCTGCTTTACTTC 182  
QY 978 IleAlaLeuMetThrPheGlyAsnTyrValIleuPheAsnLeuLeuValAlaIleVal 997  
DB 183 ATCGCCCTCAGACCTTTGGCACTAGCTGCTTTACCTGCTTTCAGCTTGTGGCATTCCTGTG 242  
QY 998 GluGlyPheGlnAlaGluGlyAspAlaThrIysSerSerGluSerGluProAspPheSer 1017  
DB 243 GAGGGTTTCCAGGACAGAGAGATCCACCAAGTGTGAGTACAGACCTGATTTCTTTTCG 302  
QY 1018 ProSerValAspGlyAspGlyAspArgIysIysPheArgLeuAlaLeuValAlaLeuGlyGlu 1037  
DB 303 CCCAGTGTGATGATGATGATGGGACAGGAAGAGCCCTTGCCCTGTGGGAGAA 362  
QY 1038 HisAlaGluLeuArgIysSerLeuLeuProIleuIleIleIleThrAlaAlaThrPro 1057  
DB 363 CACTGGAACTACGAAAGAGCCTTTGGCACTCATCATCCACAGACAGCTGCTACACCG 422  
QY 1058 MetSerHisProIysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArg 1077  
DB 423 ATGTCACTGCCCAAGAGCTCCAGCACAGGTGGGGGAGACACTGGCTCTGCTCGC 482  
QY 1078 ArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisIleGluMetIysCysPro 1097  
DB 483 CGACCCAGAGCAGAGGATCCCTAGCCTGGAAGCTCCATCATCATGATGAATCACCAG 542  
QY 1098 ProSerAlaArgSerSerProHisSerProTrpSerAlaAlaIleSerSerTrpThrSerArg 1117  
DB 543 CCAAGTGGCCGAAAGTCCCGGACAGTCCCTGGAAGCGAGCAAGCAGCTGGACCGACGAG 602  
QY 1118 ArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuIysArgArgSerProSerGly 1137  
DB 603 CCCTCCAGCGGAAACAGCTGGGCGGGCCGCCACCTGGAACGTGAGAGCCCAAGCGGG 662  
QY 1138 GluArgArgSerLeuLeuSerGlyGlyGlyGlnGluSerGlnAspGlyGlu 1154  
DB 663 GAGCGAGGATCCCTGCTGTGTGAAGAGGTCAAGAGACCGAGATGAGAG 713  
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LOCUS BUI709095 810 bp mRNA linear EST 15-JUL-2003  
DEFINITION UI-M-EMO-gaz-e-20-0-UI.r1 NIH BMAP\_EMO Mus musculus cDNA clone  
IMAGE:6419323 5', mRNA sequence.  
ACCESSION BUI709095  
VERSION BUI709095.1 GI:23642225  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 810)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)  
Seq primer: pyx-5.  
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source  
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URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers

FEATURES  
Source

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## ORIGIN

## Alignment Scores:

Pred. No.: 4,62e-71 Length: 4675  
Score: 1190.50 Matches: 407  
Percent Similarity: 43.22% Conservative: 265  
Best Local Similarity: 26.17% Mismatches: 537  
Query Match: 9.90% Indels: 349  
Gaps: 55

US-09-611-257a-24 (1-2287) x AK083220 (1-4675)

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DB 4 GTAGGGAACCTGGTGTCTTCCAAAGAGCTGGAACATTGTGACGATTATGCTCC 63  
QY 830 TyrGlyProheGlyTyrIleLysAsnProLysAsnIlePheAspGlyValIleVal 849  
DB 64 ATGGATCCCTACTATTAATCTTCCAAAGAGCTGGAACATTGTGACGATTATGCTCC 123  
QY 850 TlSerValTyrGluIleValGlyGlnGlyLysLeuSerValLeuArgThrPhe 869  
DB 124 CTCAGTTAATGAGCTGGGCTTGCAAGCGTGGAGGGCTCTCAGTGGCTGCTTTC 183  
QY 870 ArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnLysLeuVal 889  
DB 184 CGATTGCTCCGAGCTTCAAAATGGCCAATGCTGGCCCACTGGAACATGCTGATCAAG 243  
QY 890 ValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIle 909  
DB 244 ATCATTTGGGAATCTCGTTGGCGCCCTGGGCAACCTGACCTGGTGGCCATATTGTC 303  
QY 910 PheIlePheSerIleLeuGlyMetHisLeuPheGly-----Cys 922  
DB 304 TTCACTCTTGGCGCGTGGGAGTACAGCTCTTGGAAAGAGCTACAAGAGTGGTCTGT 363  
QY 923 LysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeu 942  
DB 364 AAGATCGCCGAGAG-----TGCAAGCTCCG---CGCTGGCAGATGAACGACTTC 411  
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DB 412 TTCACCTCTTCTCATCTGCTTCCGAGTGTGTGGGAG---TGATCGAACAACATG 468  
QY 963 TyrAsnGlyMet---AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMet 981  
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QY 982 ThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGluGlyPheGln 1001  
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DB 589 GCACGCAATCTGGCG-----GCCACGGAC 612

QY 1022 GlyAspGlyAspArg-----LysLysArgLeuAla 1031  
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QY 1032 LeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuIleIle 1051  
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DB 706 -----GCACACTTCAACAACGAGGAGCTGATGAATGAACCT 744  
QY 1072 LeuGly-SerGlySerArgArgThrSerSerSerGlySerAlaGluProGly----- 1088  
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QY 1089 -----AlaAlaHisGluMetLysCysProProSerAlaArgSerSerProHis 1105  
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DB 1323 GACCATCGTAACATCTGAGATGAGCAAGTCTTACCTTACCTTCACTTCACTCGGA 1382  
QY 1335 uMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaLysLeuArgSe 1355  
DB 1383 GATGTTGCTCAAAATGACAGACCTATGCTTGTGTC-----AAGTTCTTCAACAA 1430





Db 430 CTGAAGCTGTTGAAGATGGCTGTGGGCATGCCGGCACTGCTGGACACGGTGATGCAGGCC 489

QY 1740 LeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaAla 1759  
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Db 490 CTGCCCCAGGTGGGGAACCTGGGACTTCTTCATGCTATATTATTTCATCTTTCAGCAGCT 549

QY 1760 LeuGlyValGluLeuPheGlyAspLeuGlyCysAspGluThrHisProCysGluGlyLeu 1779  
|||||  
Db 550 CTGGGCGTGAGGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTTGTGAGGGCTTG 609

QY 1780 GlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSer 1799  
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QY 1800 ThrGlyAspAsnTrpAsnGlyIleMetLeuAspProSerArgAspCysAspGlnGluSer 1819  
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QY 1820 ThrCysTrpAsnThrValIleSerProIleTyrPheValSer 1833  
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Db 729 ACCTGCTACAC-ACCGTCACTCACCCCATCTACTTGTC 769

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Job time : 14571.6 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 18, 2005, 16:30:41 | Search time 20656.3 Seconds  
(without alignments)  
5315.550 Million cell updates/sec

Title: US-09-611-257A-37  
Perfect score: 11904  
Sequence: 1 MDEEBDAGABESGQPRSFM.....PKKDVLSLGLSPDADLP 2266

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-UNITS-bits -START=1 -END=1 -MATRIX=D1osum62 -TRANS=human40.cdi -LIST=45  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.\*

- 1: gb\_ba:\*
- 2: gb\_hng:\*
- 3: gb\_in:\*
- 4: gb\_on:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pt:\*
- 10: gb\_ro:\*
- 11: gb\_sls:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vt:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11895	99.9	6801	9	AF227751 Homo sapi
2	11877.5	99.8	6822	6	AR201014 Sequence
3	11877.5	99.8	6822	9	AF227744 Homo sapi
4	11877.5	99.8	7741	6	AR201015 Sequence

5	11872	99.7	6855	9	AF227749
6	11843.5	99.5	6866	9	AF227745
7	11838	99.4	6999	9	AF227750
8	11815.5	99.3	7648	9	AF134986
9	11758.5	98.8	7253	9	AF126965
10	11741	98.6	7274	9	AF126966
11	11741	98.6	7349	9	AF190860
12	11735.5	98.6	6786	9	AF227747
13	11707	98.3	6897	9	AF227746
14	11703	98.3	6921	9	AF227748
15	11251.5	94.5	7030	9	AF134985
16	11246.5	94.5	7030	6	CQ724231
17	11133.5	93.5	7625	10	MMU012569
18	11111	93.3	7129	6	BD224078
19	11111	93.3	7285	6	BD224079
20	11111	93.3	7286	6	AF125161
21	10945	91.9	6942	10	AF290212
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23	10913	91.7	7527	10	BC057399
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25	8977	75.4	5475	6	AB032949
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29	6224.5	52.3	7044	9	HS420779
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32	6215.5	52.2	7898	6	BD087035
33	6215.5	52.2	7898	9	AF073931
34	6214.5	52.2	7898	6	BD087032
35	6211.5	52.2	7762	9	AF051946
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37	5637.5	47.4	6924	6	CQ730788
38	5496.5	46.2	6990	9	AF142567
39	5493	46.1	6911	10	AF068827
40	5492.5	46.1	6816	6	AR175747
41	5492.5	46.1	6816	6	AR352550
42	5484	46.1	6885	6	AR175748
43	5484	46.1	6885	6	AR352551
44	5484	46.1	6885	9	AF393329
45	5432.5	45.6	6740	9	AF129133

ALIGNMENTS

RESULT 1	AF227751	6801 bp	mrna	linear	PRI 06-MAR-2000
LOCUS	AF227751				
DEFINITION	Homo sapiens voltage-dependent calcium channel alpha 1G subunit				
VERSION	AF227751.1	GI:7159274			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Montell, A., Chemin, J., Bourinnet, E., Mennessier, G., Lory, P. and Nargeot, J.				
TITLE	Molecular and functional properties of the human alpha(1G) subunit that forms T-type calcium channels				
JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)				
MEDLINE	20158909				
PUBMED	10692398				
REFERENCES	2 (bases 1 to 6801)				
AUTHORS	Montell, A., Mennessier, G., Bourinnet, E., Lory, P. and Nargeot, J.				
TITLE	Direct Submmission				
JOURNML	Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.) U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France				
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ORIGIN

Alignment Scores:

Prod. No.: 0 Length: 6801  
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Best Local Similarity: 99.96% Conservative: 0  
Query Match: 99.92% Mismatches: 1  
Query Match: 99.92% Indels: 0  
DB: 9 Gaps: 0

US-09-611-257A-37 (1-2266) x AF227751 (1-6801)

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QY 41 ProGlySerAlaAspSerGlyalaglyGlyLeuProTyRProAlaLeuAlaProValVal 60  
DB 121 CCGGACAGCGCGGATCTCCGAGGCGGAGGGGCTGCCGTACCGGCGCTGGCCCCGGTGGTT 180  
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ORGANISM Unknown.  
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AUTHORS Dublin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.  
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 REFERENCE 1 (bases 1 to 6822)  
 Montell,A., Chemin,D., Bourinac,E., Mennessier,G., Lory,P. and Nargeot,J.

TITLE Molecular and functional properties of the human alpha1G subunit  
JOURNAL that forms T-type calcium channels  
MEDLINE J. Biol. Chem. 275 (9), 6090-6100 (2000)  
PUBMED 20158909  
10692398  
REFERENCE 2 (bases 1 to 6822)  
AUTHORS Montell, A., Mennessier, G., Bourinet, E., Lory, P. and Nargeot, J.  
TITLE Direct Subunit  
JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)  
U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France

FEATURES

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ORIGIN

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Db	1741	GGCAGGAGCTGTGGGCAAGCGGAGAGGTATGCCACCTGACACACAGCCCTTCACCGGAG	1800
QY	601	THRIEULYSGIULYVALALEUVALIGIULVALIALASERSESGIUPROPROTHRIEUNHR	620
Db	1801	ACGCTGAAGGAGAGACACTAGTAGAGGTGGCTGCACCTCTGGGCCCCCAACCTACCC	1860
QY	621	SERLEUENILIEPROPROGLYPROTYRSESERMETHISLYSLEULEUGIUTHRGINSER	640
Db	1861	AGCTTCACATCCCAACCCGGGGCCCTACAGCTTCATGACCAAGCTCTGGAGACACAGAGT	1920
QY	641	THRGIALACYGGINSESESCYLSILLESERSESPROCYSEULYVALAASPSEGLY	660
Db	1921	ACAGGTGCTCGCAAAAGCTTTGGCAAGATTCACAGCCCTGCTTGAAGACAGACGTGGA	1980
QY	661	ALACYSGIYPROABPSECYSPROTYRCYVALAARGALAGIYVALAGIYGLIUNVALIGIULEU	680
Db	1981	GCTCTGTGTCCAGACAGCTGCCCTCACTGTGCCCCGGCGGGCGGAGAGTGAAGCTC	2040
QY	681	ALASPARGIUMERPROASPSESESPSESGIUALIYTYRGLUPHETHGLIASPALA	700
Db	2041	GCCGACCGGTGAATATCCCTGACTCAACACGAGGCACTTTATAGATTACACAGAGATCC	2100
QY	701	GLINHISSEARPLEUARGSPROHISERARGARGINARGSEGLEUGIYPROASPARLA	720

Dp	2101	CAGCAGCGCACTCCGGACCCCAAGCCGGCAACGAGCTGGGCCAGATCA	2166
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Dp	2161	GAGCCGAGCTCTGTGCTGGCTTCTGGAGGCTATCTGTGACACTTCGAAAGATTGTG	2222
Qy	741	AspSerIysTyrrpheglIyAargIylIemellalIleleuValasnThrIeusermet	760
Dp	2221	GACAGCAAGTACTTTGGCCGGGGAAATGATGTCCCATCTCGTGCACACACTCAGCAATG	2280
Qy	761	GIylIlegIuTyrrhsIugInProGIuGluuethrasnalaleuGIuIleSerAsnIle	780
Dp	2281	GGCATCGAATRCCACGAGCAACCCGAGAGCTTACCAAGCCCTTAGAAATACGAACTC	2340
Qy	781	ValPhethSerIeuPhealaleuGIumetIeuIeusIleuValTyrgIyProPhe	800
Dp	2341	GTCTTTCACGAGCCTTTTGGCCCTGGAGTGTGTGTGAAGCTGTTGTGTATGTGTCCTTT	2400
Qy	801	GIyTyrrIleIysanProTyrrAsnIlePheAspIyValIleValIleSerValTrr	820
Dp	2401	GGCTACATCAAGAAATCCCTACAACTCTTCATGTGTGTATGTGTATGTGTATGTGTG	2460
Qy	821	GIuIleValGIyngInngIyGIyIleuSerValIleuAgtTrpPharIeumetArg	840
Dp	2461	GAGATCGTGGCCACGACAGGGGGGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2520
Qy	841	ValIeuIysIeuValArgPheIeuProalaleuGIuArgInuArgInuValIaleuMetIys	860
Dp	2521	GTGTGTGAAGCTGTGTGGCTTCTGTCCGGCGGTGCAGGGGAGCTGTGTGTGTGTGTGTG	2580
Qy	861	ThrmetasPhanValalatrPhpeCyemIeIeuIeuIeuIlePheIlePheSer	880
Dp	2581	ACCATGACAACAGTGGCCACCTTCTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2640
Qy	881	IleIeuGIyethIleuPheGIyCyalyAspPheIaseGIuAgsAspGIyAspThrIeu	900
Dp	2641	ATCTGTGGCAATGCAATCTTCTGTGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2700
Qy	901	ProAspArgIysaAsnPhasPserIeIeuIeuTrrPalaIleValIthrValIpheGIuIleIeu	920
Dp	2701	CCAGACCGGAAGATTTTGACTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	2760
Qy	921	ThrgInGIuAspTyrrPaanIysValIeuTyrrAsnGIyMetAlaserThrSerSerTrrPala	940
Dp	2761	ACCCAGAGAGCACTGGAACTGAAGTCTCTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2820
Qy	941	AlaleuTyrrPheIleIaleuMetThrPheGIyAsnTyrrValIleuPheAsnIleuVal	960
Dp	2821	GCCCTTATTTCAATGCCCTCATACCTTGGCAACTACGTGTCTTCAATTTGTGTGTGT	2880
Qy	961	AlalIleuValGIuGIyPheGIuAlagIuGIuIleSerIysArgGIuAspAlaseGIy	980
Dp	2881	GCCATTCTGTGTGAGGGCTTCCAGCGGAGGAATACGAAACGGGAAGATGCGAGTGTGA	2940
Qy	981	GIuIeuSerCyIleGIuIeuProValAspSerGIuGIyIAspPalaAsnIysSerGIu	1000
Dp	2941	CAGTTAAGCTGTATTACGTGCTGTGTGACTCCACAGGGGGAGATGCCMAAGTCCGAA	3000
Qy	1001	SerGIuProAspPhePhePheSerProSerIeuaSpGIyAspGIyAspArgIyIysSerIeu	1020
Dp	3001	TCAAGAGCCGATTTCTTCTCAACCAAGCTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3060
Qy	1021	AlaleuValSerIeugIyGIuIleProGIuIleuArgIyIysSerIeIeuProProIeuIle	1040
Dp	3061	GCTTTGTGTGTCTCGGAGAGCAACCCGAGCTGTGGAGAGAGCTGTGTGTGTGTGTGTGT	3120
Qy	1041	IleIethIrrAlaalatrProIemSerIeuProIysSerThrIserThrGIyIeugIyGIu	1060
Dp	3121	ATTCACACAGGCGGCAACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3180
Qy	1061	AlaleuGIyProAlaserArgIyThrSerSerSerGIySerAlagIuProGIyAlaalale	1080



Db	3181	GGCGTGGGCGCTCGCTCGCGCCGACCAAGACAGCGGGCTGGCAAGACCTGGGGCGGCG	3240
Qy	1081	HisgIumEcLysSerProSerAlaArgSerProHisSerProTyrSerAla	1100
Db	3241	CACGAGATGAAGTCAACGCCCAAGGCCCGGACGCTCTCCGACACACCCCTGGAGGCGTGC	3300
Qy	1101	SerSerTyrThrSerArgArgSerSerArgAnSerLeuGlyAlaProSerLeuLys	1120
Db	3301	AGCAGCTGGACCAAGCAGCGCGCTCCAGCCGGAACAGCCTCGGCGGTGCACCCAGCCTTAAG	3360
Qy	1121	ArgArgSerProSerGlyGlyAlaArgSerLeuLeuSerGlyGlyGlyGlnGlnSerGln	1140
Db	3361	CGGAGAACCCCAAGTGAAGAGCGGGGCGCTCTGTGTGGAGAAAGGCAGAGAGCCAG	3420
Qy	1141	AspGlnGlnGlnSerSerGlyGlyGlyAlaArgAlaSerProAlaGlySerAspHis	1160
Db	3421	CATGAAAGAGAGCTCAAGAAAGAGCGGGCCAGCCTCGGGCAGTGAACATTCGCCAC	3480
Qy	1161	ArgGlySerLeuGlnArgGlyAlaAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
Db	3481	AGGGGCTCCCTGGAGCGGAGGCCAAGAGTTCCTTTGACCTGCAGACACACTCAGAGTG	3540
Qy	1181	ProGlyLeuHisArgThrAlaSerGlyAlaArgGlySerAlaSerGlyHisLeuGlnAspCysAn	1200
Db	3541	CCAGGGCTGCATTCGACCTGCACAGTGCGCGAGGGTCTGCTTGTGAGCACACAGACTGCAT	3600
Qy	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuAlaGlyProAspAspProProLeuAsp	1220
Db	3601	GGCAAGTGGGCTTCAGGGGCGCTGGCGCGGGCCCTGGCGGCTGATGACCCCCACTGGAT	3660
Qy	1221	GlyAspAspAlaAspAspGlyGlyValAnLeuSerLysGlyGlyAlaArgAlaTyrPhe	1240
Db	3661	GGGAGTGAAGCGCGATGACGAGGGGACCACTGACGAAAGGGAACGGGTCGCGCGGTGATC	3720
Qy	1241	ArgAlaArgLeuProAlaCysThrLeuGlnArgAspSerTyrSerAlaTyrPhePhe	1260
Db	3721	CGAGCCCACTCCCTCGCTGCTGCTCGAGCGAGCTCTGGTGCACCTGATCATCTTCCCT	3780
Qy	1261	ProGlnSerArgPheArgLeuLeuCysHisArgGlyLeuThrHisLysMetPheAspHis	1280
Db	3781	CCTCAGTCCAGGTTCCGCTCCTGTGTCAACCGGATCATCACCCACAGATGTTGCACAC	3840
Qy	1281	ValValLeuValIleIlePheLeuAnCysIleThrIleAlaMetGlyArgProLysIle	1300
Db	3841	GGGCTCTTGTATCATCTCTCTTAATGACATCACATCGCATGAGCGCCCCAAATTT	3900
Qy	1301	AspProHisSerAlaGlyAlaArgIlePheLeuThrLeuSerAnTyrIlePheThrAlaVal	1320
Db	3901	GACCCCCACAGCGCTGAAACGCAATCTTCTGACCCCTCCAAATTCATTCACCGCACTC	3960
Qy	1321	PheLeuAlaGlnMetThrValLysValAlaAlaLeuGlyTyrCysPheGlyGlyGlnAla	1340
Db	3961	TTTTCGCTGAAATACAGTGAAGGGTGGGCACTGGGCTGTGGCTTGGGGAGCGAGCG	4020
Qy	1341	TyrLeuArgSerSerTyrAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp	1360
Db	4021	TACCTCGCGAGACAGTTGGAACGCTGTGACGGGCTGTGGTGTCTATCTCCGTATCGAC	4080
Qy	1361	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380
Db	4081	ATTCTGGTGTCCATGGTCTCTGACAGCGGACCAAGATCTTGGCATCTCGAGGTGCTG	4140
Qy	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400
Db	4141	CGGCTGCTGGGACCCCTGGCGCCGCTCAGGGGTGATAGCGGGGCCAAGGGGCTGAAGCTG	4200
Qy	1401	ValValGlyThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys	1420
Db	4201	GTGGTGGAGACCTGATGTCTCATCTGAAACCCATCGGCAACATTTGTATCTGTGCTGT	4260
Qy	1421	AlaPhePheIleIlePheGlyTyrLeuGlyValAlaGlnLeuPheLysGlyLysPhePheVal	1440
Db	4261	GGCTTCTTATCATATTTTCCGCAATCTTGGGGGTGACGCTTCTTCAAGGGAAGTTTTCGTG	4320

QY	1441	CysgInglYgluaPthrIrraGAsnIleThraAsuYsSerAspCYbaGluaIaSerTYr	1460
Db	4321	TGCCAGGCGCAGGATACCAAGGAACATCAACAATTAATCGAGCTGTGCGCGAGGCGAGTTAC	4380
QY	1461	ArgTTrValaArgHIslyrTYrAsnPhaAspAsnLeuIYglInIaLeuMetSerLeuPhe	1480
Db	4381	CGGtGGGTCCCGGCAACAGTACMACTTTTGACAACTTGTGACAGGCCCTGATGTCTCTGTC	4440
QY	1481	ValLeuIaSerLYsAspAGLYTTrpValAspIImetTYrAspGlyLeuAspAlaValGlyY	1500
Db	4441	GTTTTGGCTTCAGAGATGGTGTGGGTGGACATCATATACATGGGCTGGAGTGTGGGCG	4500
QY	1501	ValAspInglInProIImetAsnHIsAsnProTrpMetLeuLeuTYrPheIaSerPhe	1520
Db	4501	GTGGACGAGAGCCCATCATATCAACAACCCCTGGATGTGCTGTACTTCATCTCGTTC	4560
QY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540
Db	4561	CTGCTCATTTGGGCTCTTGTGTCTTGAACAATGTTTGTGGGTGTGGTGTGGAAACTTC	4620
QY	1541	HisLYsCYsArGgInHIsngInglInglInglInuIaArGaArGaArGgInuLYsArGgLeu	1560
Db	4621	CACAAGTGTGGCGACACAGAGAGAAAGAGAGGCCGCGCGCGAGAGAGAACGGCTTA	4680
QY	1561	ArgArGLeuGInuLYsLYsArGArG-----LYsAlaGInCYsLYs	1573
Db	4681	CGAGACTGGAGAAAAGAAAGAAAGTAAGAGAAAGCAAGTGGCTGAAGCCCAATGGCAAA	4740
QY	1574	ProTYrTYrSerAspTYrSerArPheArGLeuLeuValHIsHIsLeuCYrThSerHis	1593
Db	4741	CCTTACTACTCCGACTACTCCGCTCCGAGCTCTCGTCCACCACTTGTGACCAAGCCAC	4800
QY	1594	TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu	1613
Db	4801	TACCTGGACCTCTTATCATCAAGGTGTACTCGGCGTGAACGGTGTACCATGGCCATGGAG	4860
QY	1614	HisTYrGInglInProGInIleLeuAspGluValaLeuLYsIleCYsAsnTYrIlePheThr	1633
Db	4861	CACTRCCAGCAAGCCCAAGTTCGTGATGAGGCTCTGAAGACTCTGCAACTACATCTTCACT	4920
QY	1634	ValIlePheValLeuGluSerValPheLYsLeuValAlaPheGlyPheArGArGpPhe	1653
Db	4921	GTCACTCTTGTCTTGAGAGTCAAGTTTTCAACTTGTGGCTTGTGGTTTCCGTCTTCTC	4980
QY	1654	GlnAspArGTTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr	1673
Db	4981	CAGGACAGGTGGAACCACTGACCTGGCCATCGTGTGCTCATCATATGAGCATACG	5040
QY	1674	LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProTrpIleIleArgIImet	1693
Db	5041	CTGGAGAAATCGAGGTCAACGCTCTGCTGCCATCAACCCACCATATCCGCATCATG	5100
QY	1694	ArgValLeuArGlyleAlaArgValLeuLYsLeuLeuLYsMetAlaValImetArGla	1713
Db	5101	AGGGTCTGGCGATTGGCCCGAGTGTGTAAGCTGTGTAAGAGTGGCTGTGGCATGGCGG	5160
QY	1714	LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet	1733
Db	5161	CTGCTGGACACGGTGTATGACAGGCCCTCGCCCAAGGTGGGGAACCTGGGACTTCTTCACTG	5220
QY	1734	LeuLeuPhePheIlePheAlaAlaLeuGlyValGlyLeuPheGlyAspLeuGluCYsAsp	1753
Db	5221	TGTGTGTTTTCATCTTTTGACAGCTCTGGGCGTGAAGCTCTTTGAGACTTGGAGTGTAC	5280
QY	1754	GluThrHisProCYsGluGlyLeuGlyValArgHIsAlaThrPheArGAsnPheGlyMetAla	1773
Db	5281	GAGACACACCCCTGTGAAGGGCTGGGCGCTATGACACTTTTCGAACTTTGGCATGGCC	5340
QY	1774	PheLeuThrLeuPheArGValaSerThrGlyAspAsnTrpAsnGlyIImetLYsAspThr	1793
Db	5341	TTCCTTAACCTCTTTCGAGTCTCCCAAGAGTACCAATTTGAAATGGCATTTATTAAGACACC	5400

QY	1794	LeuArgAspCysAspGlnGlnIuSerThrCysTyrAsnThrValIleSerProIleTyrPhe	1813
DB	5401	CTCCGGAGCTGTGACAGGAGTCACCTCTACAAACGGTCACTTCGCTTCACTTT	5460
QY	1814	ValSerPheValLeuThrIleGlnPheValLeuValAsnValValIleValLeuMet	1833
DB	5461	GTGTCTTGTGTGACGGCCGACGTTGCTGTAGTCAAGCTGGTGTATGCCGGCTGATG	5520
QY	1834	LysHisLeuGlnGlnIuSerAsnLysGlnValAlaLysGlnGlnValGlnLeuLeu	1853
DB	5521	AAGCACTCGAGAGGACAAAGAGGCGCAAGAGAGGCGCGACGTAAAGCTGTGCTG	5580
QY	1854	GluLeuGlnMetLysThrLeuSerProGlnProHisSerProLeuGlnLysProPheLeu	1873
DB	5581	GAGCTGGAATGAAGACCTCAGCCGCCAGCCCACTCGCACTGGGAGGCCCTTCTC	5640
QY	1874	TyrProGlnValGlnIuLysProAspSerProAspSerProLysProGlnValLeuHisPro	1893
DB	5641	TGGCCCTGGGGGTGAGGGGCCCGACGCCGACAGCCCAAGCTGGGCTGTGACCCA	5700
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DB	5701	GGGGCCCAAGCGAGATCAGCTCTCCACTTTCTCTGAGACACCCCAAGATGACGCCAC	5760
QY	1914	ProThrGlnLeuProGlnLysProAspLeuLeuThrValArgLysSerGlnValSerArgThr	1933
DB	5761	CCACAGAGCTGCCAGAGCCAGACTTACTGACTGTGCGAAGCTTGGGGTCAAGCCAG	5820
QY	1934	HisSerLeuProAsnAspSerTyrMetCysArgHisGlnLysSerThrAlaGlnGlnProLeu	1953
DB	5821	CACCTCTGCGCCAAATACAGACTCATGTGTGCGCATGGAGGACTGCCAGGGGCCCTG	5880
QY	1954	GlyHisArgGlyTyrProLysLeuProLysAlaGlnSerGlnLysSerValLeuSerValHisSer	1973
DB	5881	GGACAGAGGGGCTGGGGGCTCCCAAGCTCAGTGGCTCCCTCTGCTGCTTCACTCC	5940
QY	1974	GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGln	1993
DB	5941	CAGCCAGAGATACAGCTACATCTGCAAGCTTCCCAAGATGACCTCATCTGCTCCAG	6000
QY	1994	ProHisSerAlaProThrTyrProLysThrIleProLysLeuProProGlnLysSerPro	2013
DB	6001	CCCAACAGGCGCCCACTGGGGCAACATCCCAACTGCCCAACAGGACGCTCCCT	6060
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DB	6061	TTGGCTCAAGGGCACTCAGGCGCCAGGAGCAATAGAGCTGACTCTTGGACGTTCAAG	6120
QY	2034	GlyLeuGlnSerArgGlnAspLeuLeuAlaGlnValSerGlnYrProSerProProLeuAla	2053
DB	6121	GGTCTGGGCGAGCGGAGAGCTGCTGGAGAGGTAGTGGCCCTTCCCGCCCTGGCC	6180
QY	2054	ArgAlaTyrSerPheThrProLysGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis	2073
DB	6181	CGGGCTCACTCTTCTGGGGCGAGTCAAGTACCCAGGACAGCAGCACTCCGCAAGC	6240
QY	2074	SerLysIleSerLysHisMetThrProProAlaProCysProGlnLysProGlnProAsnTyrP	2093
DB	6241	AGCAAAATCTCCAAAGACATGAGCCCGCAGCCCTTGGCCCAAGGCCCAAGCACTGAG	6300
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DB	6301	GGCAAGGGCCCTCCAGAGACAGAAACAGTTAGATTGGACACGAGCTGAGCTGGATT	6360
QY	2114	SerGlyAspLeuLeuProProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	2133
DB	6361	TCAGAGAGACTCTCTGCGCCCTGGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG	6420
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DB	6421	AACTGTCTACAGCTGTGAGGCGCAGAGCTGCAAGCGCGGCCAGCTCTGGCTGTGATGAG	6480
QY	2154	GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlnSerGlnProHisLeuGln	2173

DB	6481	CAGAGAGACACTCATGCGGTGACGCTCGACGAGCAAGCGGTCCCAACCCACCTGGGC	6540
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DB	6541	ACAGACCCCTTAACTTGGGGGCGAGCCTCTTGGGGGGGCGCTGGGAGCGCGCCCAAGAA	6600
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DB	6601	AAACTAGCCCGCTGATATCAACATAGACCCCGGAGAGCCAGAGTCTTCGAGCCCCG	6660
QY	2214	ProSerProGlnLysCysLeuArgArgAlaProSerSerAspSerLysAspProLeu	2233
DB	6661	CCCAAGCCTGATATGCTCCGAGAGAGGGGTCCGTCAAGGACTCCAGAGATCCCTTG	6720
QY	2234	AlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSer	2253
DB	6721	GCCTCTGGCCCCCTGAGACGATGCTGCTGCTCCCTCCCAAGAAAGATGTGCTGAGT	6780
QY	2254	LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro	2266
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DEFINITION Sequence 4 from patent US 6358706.  
ACCESSION AR201015  
VERSION AR201015.1 GI:20251903  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 7741)  
AUTHORS Dubin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.  
TITLE DNA encoding human alpha1G-C T-Type calcium channel  
JOURNAL Patent: US 6358706-A 4 19-MAR-2002;  
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Query Match:	99.78%	Indels:	1
DB:	6	Gaps:	1

US-09-611-257A-37 (1-2266) x AR201015 (1-7741)

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QY	21	ArgLeuAsnAspLeuSerGlnAlaGlnLysArgProGlnLysSerAlaGlnLysAsp	40
DB	583	CGGCTCAAGACCTTCTGGGGGCGGGGCGCGGGGCGGGGCTCAGCAAAAAGAGAC	642
QY	41	ProGlnSerAlaAspSerGlnAlaGlnLysLeuProTyrProAlaLeuAlaProValVal	60
DB	643	CCGGGAGGGCGGAGCTCCAGAGCGAGGGGCTGCCGTACCGGCCCTGGCCCGGTGGTT	702
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
DB	703	TTCTTCTACTTACGACAGGACAGCGCGCGAGACTGGTGTCTCCGACGGGTCTGTAC	762
QY	81	ProTyrPheGlnLysGlnIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlnMet	100
DB	763	CCCTGGTTTGAAGCATGAGATGTTGTGATCTTCTCAACTGTGATGACCTGGGCAATG	822

QY	101	PhearGProCySGluAapIleAlaCyAspSerGlnArgCyAargIleuGlnAlaPhe	120
Db	823	TTCCGGCATCGAGCATCGCTGTGACTCCAGCGCTGCGGATCTCGACGGCTTT	882
QY	121	AspAapPheIlePheAlaPhePheAlaValGluMetValValIysMetValAlaLeuGly	140
Db	883	GATACCTTCATCTTGGCTCTTGGCCGTGAGATGGTGTGAAGATGGTGGCTTGGGG	942
QY	141	IlePheGlyValblybCybTybLeuGlyAAsPThrTrpAsnArgLeuAAsPheIleVal	160
Db	943	ATCTTTGGGAAAAAGTGTACTTACCTGGAGACACTTGGAAACGGCTTACTTTTCATCGTC	1002
QY	161	IleAlaGlyMetLeuGlnTybSerLeuAAsPheGlnAsnValSerPheSerAlaValArg	180
Db	1003	ATCCAGAGGAGTGTGAGTACTCGCTGACCTGCAGAACTTCAGCTTCAGCTGTCAAG	1062
QY	181	ThrValArgValIleuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
Db	1063	ACAGTCCCGTGGCTGGCGACCGCTCAGGAGCAATTAAACGGGGTGGCCACAGACGGCATCTCT	1122
QY	201	ValThrLeuLeuLeuAAsPThrLeuProMetLeuGlyAsnValLeuLeuLeuCybPhePhe	220
Db	1123	GTCACGTTGCTGCTGGATACGCTCCATGCTGGGCAACGTCCTGCTGTCTCTTCTTC	1182
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
Db	1183	GTCCTCTTCATCTTCGGCATGTGGCGGTCCAGCTGTGGCAGGGCTGTTCGGAAACCA	1242
QY	241	CybPheLeuProGluAAsPheSerLeuProLeuSerValAspLeuGluAArgTybTrpGln	260
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QY	301	AspTybArgGluAlaTybAsnSerSerSerAsnThrTybCybValAsnTrpAsnGlnTybTyb	320
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QY	321	ThrAsnCybSerAlaGlyGluHisAsnProPheIysGlyAlaIleAsnPheAspAsnIle	340
Db	1483	ACCAACTGCTCAGCGGGGAGACACACCCCTTCAGAGGGCGCATCACTTTGACACACTT	1542
QY	341	GlyTybAlaTrpIleAlaIlePheGlnValIleThrLeuGlnGlyTrpValAspIleMet	360
Db	1543	GGCTATGGCTGGATGGCATCTTCAGAGTATCAACGCTGAGGGCTGGGTGCACATCATG	1602
QY	361	TybPheValMetAspAlaHisSerPheTybAsnPheIleTybPheIleLeuLeuIleIle	380
Db	1603	TACTTTTGATGAGAGTCACTTCCTTCATCAATTTCATCTTCACTTCCTTCATCATC	1662
QY	381	ValGlySerPhePheMetIleAsnLeuCybLeuValValIleAlaTrpGlnPheSerGln	400
Db	1663	GTTGGCTCTCTTCATATCACTGTGCTGTGGTGGATGGACGACGACTTCACAG	1722
QY	401	ThrTybGlnArgGluSerGlnLeuMetArgGlnGlnArgValArgPheLeuSerAsnAla	420
Db	1723	ACCAAGCAGCGGGAAAGCCAGCTGTGGGAGCAGCGTGTGGCTTCGTCCAAAGCC	1782
QY	421	SerThrLeuAlaSerPheSerGlnProGlySerCybTybGlnGlnLeuLeuTybTybLeu	440
Db	1783	AGCACCTCGGCTATCTGTGAGCCCGGACGCTATGAGAGCGTCTCAAGTACTGT	1842
QY	441	ValTybIleLeuArgValAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
Db	1843	GTTGTACATCTCTGTAAAGCAGCCCGACGGCTGAGTCTCTCGGGACGACAGGTGTG	1902
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGlnTrpGlnProSerSer	480
Db	1903	CGGGTTGGGCTGTCAAGACCCAGACCCCTTGGGGGCCAGAGAACCCAGCCACGAC	1962
QY	481	SerCybSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHis	500
Db	1963	AGCTGCTGTGCTCCACCGCCGCTATCGTCCACACCTGGTGCACACACACACACAC	2022
QY	501	HisHisHisHisTybTybIleuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
Db	2023	CATCACACACACTCACCTGTGGCAATGGGACCTCAGAGGCCCCCGGGCCAGCCGGAG	2082
QY	521	IleGlnAAsPArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro	540
Db	2083	ATCCAGACAGGAGTGCATAGGTGCTCCGAGGCTATGCTGCCACACCTTCAGAGCTT	2142
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTybHisAlaAsp	560
Db	2143	GCCCTTCGGGGCCCCCTGTGGTGGAGAGATGTGTGACAGCTTCAACATGGCCAG	2202
QY	561	CybHisLeuGlnProValArgCybGlnAlaProProProArgSerProSerGlyAlaSer	580
Db	2203	TGCCATTAGAGCAGATCCCTGTGCGAGGCCCTCCACAGGTCCTCACTGTGAGGATCC	2262
QY	581	GlyArgThrValGlySerGlyValbTybProThrValHisThrSerProProProGlu	600
Db	2263	GGCAGAGCTGTGGCAGCGGAGAGTATTCACCGTGCACACAGCCCTCCACCGGAG	2322
QY	601	ThrLeuIysGlyValAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
Db	2323	ACGCTGAAGAGAAAGCATAGTAGAGTGGTGCAGGCTGTGGCCCCCAACCTCACCC	2382
QY	621	SerLeuAsnIleProProGlyProTybSerSerMetHisblyLeuLeuGlnTrpGlnSer	640
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QY	641	ThrGlyAlaCybGlnSerSerCybHisIleSerSerProCybLeuIysValaAspSerGly	660
Db	2443	ACAGGTGCTGTCCAAACCTCTTGACAAATCTCCAGCCCTTCTTGAAGCAGACAGTGA	2502
QY	661	AlaCybGlyProAspSerCybProTybCybAlaArgAlaGlyAlaGlyLeuGluLeu	680
Db	2503	GCTGTGTCCAGACACTGCTGCCCTTACTGTGTGCCGGGCGGGGAGGTGGAGCTC	2562
QY	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTybGluPheThrGlnAspAla	700
Db	2563	GCCGACCGTGAATGCTGTCACTCAGACAGGAGGCAAGTTTATGATTCACACAGAGTGC	2622
QY	701	GlnHisSerAspLeuAAsPArgProHisIleSerArgArgGlnArgSerLeuGlyProAspAla	720
Db	2623	CAGCACAGCAGCTCCGGAGACCCCAACGCGGGGGAGAGAGCCTGGGCCACAGATGCA	2682
QY	721	GluProSerSerValIleuAlaPheTrpArgLeuIleCybAspThrPheArgIysIleVal	740
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QY	741	AspSerTybTybPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet	760

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Db	5203	CGAAGACCTGGAGAAAAGAGAAAGATGAAGAGAACAGATGCGTGGACCCAGCTGGCAAA	5262
QY	1574	ProTYrTyrSerAspTYrSerArgPheArgLeuLeuValHisHsileuCYeThrSerHis	1593
Db	5263	CTTAACTACTCGACTACTCCCGCTTCGGGCTCTCGTCCACACTTGTGTGACACAGCCAC	5322
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Db	5233	TACCTGGACCTCTTCATCACAAGGTGTATCGGGGCTGAACGTGTGTACCATGGCCATGGAG	5382
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Db	5443	GTCACTCTTGTCTGGAGTCAGATTTCAAACTGTGGCTTTGGTTTCGTCGGTTCTTC	5502
QY	1654	GlnAspArgTyrPAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr	1673
Db	5503	CAGACACAGTGGAAACCACTGACCTGGCCATTGTGCTGCTGTCAATATGGGATCACG	5562
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Db	5863	TTCTTAACCTCTTTCAGAGCTTCCACAGGTGACATTTGGATGGCATTTATGAAGACACC	5922
QY	1794	LeuArgAspCYeAspGlnGlnSerThrCYeTYrAsnThrValIleSerProIleTYrPhe	1813
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QY	1814	ValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	1833
Db	5983	GTGTCTTTCGTGCTACGCGCCCAAGTTCGTGTAGTCAACAGTGTGTATGCCGTGTGTATG	6042
QY	1834	LysHisLeuGlnGlnLysSerAsnLysGlnAlaLysGlnGluAlaGluLeuGluAlaGluLeu	1853
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QY	1974	GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGln	1993
Db	6463	CAGCCAGCAGATCACACTACATCTTCGACTTCCCAAAAGATGACCTCATCTGCTCAG	6522
QY	1994	ProHisSerAlaProThrTTPGlyThrIleProLysLeuProProGlyValArgSerPro	2013
Db	6523	CCCCACAGCGCCCCAACCTGGGGGACCATCCCAATGCCCCCACAGAGAGCTCCCTC	6582
QY	2014	LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln	2033
Db	6583	TTGGCTCAGAGGGCCACTCAGCGCCGACAGCAATAGAGCTGACTCTCTTGAGAGTTTCAG	6642
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Db	6643	GGTCTGGGCGAGCCGGGAAGACTGTCTGACAGAGGTGAGTGGCCCTTCCCGCCCTGGCC	6702
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Db	6703	CGGGCTACTCTTCTTCTGGGGCACTCAAGTACCAAGCACAGGACGACCTCCGAGCGCAC	6762
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Db	6883	TCAGGAGACCTCTCTGCCCCCTGGGGCGCCAGSAGSAGGCCCATCCCAACGGGACTGAAG	6942
QY	2134	LysCysTyrSerValGlnAlaGlnSerCysGlnArgArgProThrSerTTPLeuAspGlu	2153
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DEFINITION Homo sapiens voltage-dependent calcium channel alpha 1G subunit  
ACCESSION AF227749  
VERSION AF227749.1 GI:7159270  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1 (bases 1 to 6855)  
AUTHORS Montell, A., Chemin, J., Bourinac, E., Mennesier, G., Lory, P. and  
Nargeot, J.  
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ORIGIN

Alignment Scores:  
Pred. No.: 0 Length: 6855  
Score: 11872.00 Matches: 2264  
Percent Similarity: 99.17% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 99.73% Indels: 18  
DB: Gaps: 1

US-09-611-257A-37 (1-2266) x AF227749 (1-6855)

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DB 61 CGGCTCAACGACCTGTCCGGGGCCCGGGGGCCGGCCGGGGTCCAGCAAGAAAAGGAC 120  
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QY 61 PhePheTYRLeuSerGLnAspSerArgProArgSerTYRcySLeuArgThrValCysAsn 80  
DB 181 TTCCTTCACTTGAAGCAGGACAGGACCGCCCGGAGACTGGTCTCCGACGGTCTGTAAAC 240  
QY 81 ProTYRLeuGLuArgTLeuSerMetLeuValLLeuLeuAenCysValThrLeuGLyMet 100  
DB 241 CCTGGTGTGAGCGCATCAGCATGTGTGTCATCTTCACTGCGTGAACCTCGGGCATG 300  
QY 101 PheArgProCysGLuAspLLeAlaCysAspSerGLnArgCysArgTLeuGLnAlaPhe 120  
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QY 121 AspAspPheLLeuPheAlaPhePheAlaValGLuMetValLLeuMetValLLeuGLy 140  
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QY 181 ThrValArgValLeuArgProLeuArgAlaLLeuAanArgValProSerMetArgLLeu 200  
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Qy	321	ThrAnCyvSeraIaGIYgIuHIsAnPbOheIYsgIYalIIsAnPheAspAnIle	340
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Qy	361	TyrPheValMetAspAlaHIsSerPheYrAAsnPheIleTYrPheIleLeuIleIle	380
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Qy	401	ThrIYgIuAlaArgIuSerGlnLeuMetCArgIuGlnAlaArgPheLeuSerAsnAla	420
Db	1201	ACCAAGCGCGGGAAAGCCAGCTGATGGGGAGACGCTGGCGGTTCTGTCCAAAGCC	1260
Qy	421	SerThrLeuAlaSerPheSerGluProGlySerCyTYrGluGluLeuLeuYsTYrLeu	440
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Db	1621	GCCCTCTCGGGGCCCCCTGTGTGGCCAGAGTCTGTGCACAGCTTTCACATGCCAGC	1680
Qy	561	CysHIsleuGluProValArgCyvGlnAlaProProProArgSerProSerGIYAlaSer	580
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Qy	581	GlyArgThrValGIYSerGIYIYsAlYrProThrValHIsThSerProProProGlu	600
Db	1741	GGCAGAGACTGTGGGAGCGGGAGAGGTGTATCCACCGTGACACCAAGCCCTTCCACGGAG	1800
Qy	601	ThrLeuYsGluYsAlaLeuValGluValAlaAlaSerSerGIYProProThrLeuThr	620
Db	1801	ACGCTGAAGAGAAAGGCACTATTAAGGTGGCTGCCACTGTGGGCCCCCAACCTCAAC	1860
Qy	621	SerLeuAsnIleProProGIYProTYrSerSerMetHIsIYsIYsLeuGluThrGlnSer	640
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 LOCUS AF227745  
 DEFINITION Homo sapiens voltage-dependent calcium channel alpha 1g subunit  
 isoform aef (CACNA1G) mRNA, complete cds.  
 ACCESSION AF227745  
 VERSION AF227745.1 GI:7159262  
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 SOURCE  
 ORGANISM  
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 REFERENCE  
 1. (bases 1 to 6966)  
 Montell, A., Bourinet, E., Mennessier, G., Lory, P. and  
 Nargeot, J.  
 Molecular and functional properties of the human alpha(1g) subunit  
 that forms T-type calcium channels  
 J. Biol. Chem. 275 (9), 6090-6100 (2000)  
 MEDLINE 20158909  
 PUBMED 10692398  
 REFERENCE  
 2. (bases 1 to 6966)  
 Montell, A., Mennessier, G., Bourinet, E., Lory, P. and Nargeot, J.  
 Direct Submision  
 Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)  
 U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France  
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ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 6966  
Score: 11843.50 Matches: 2264  
Percent Similarity: 97.59% Conservative: 1  
Best Local Similarity: 97.54% Mismatches: 55  
Query Match: 99.49% Indels: 2  
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US-09-611-257A-37 (1-2266) x AF227745 (1-6966)

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 1 (bases 1 to 6999)  
 Montell, A., Bourinet, E., Mennesier, G., Lory, P. and Nargeot, J.  
 Molecular and functional properties of the human alpha(1g) subunit  
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 J. Biol. Chem. 275 (9), 6090-6100 (2000)  
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 Direct Submission  
 Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)  
 U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France  
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ORIGIN

Alignment Scores:

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US-09-611-257a-37 (1-2266) x AF227750 (1-6999)

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QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAn	80
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DB	241	CCCTGGTTGAGCGCATACAGATGTTGGTATCTTCTCACTGCGGTGACCTTGGGCAAG	300
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	301	TTTCGGGCATGCGAGCAATCGCTGTGACTCCAGGCGTGCAGGATCCGAGGCGCTTT	360
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValIysMetValAlaLeuGly	140
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DB	421	ATCTTTGGGAAAAAGTTTACCTGGGAGACATTGGAACCGGCTTGACTTTTTCATGCTC	480
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180

DB	481	ATCGAAGGAGTCTGGATGACTCGCTGACCTGCAGAAAGTCAGCTTCTCAGCTGCAGG	540
QY	181	ThrValArgValAlaArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
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QY 561 CysHisLeuGluProValIArgCysGlnAlaProProProArgSerProSerGlyAlaAsp 580  
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DB 1741 GCGAGACCTGTGGGACGGGAGGTATACCCAGCTGCACACACCCCTCCACCGGAG 1800  
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Qy      1910 -----MetGlnProHisPro 1914
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 SOURCE  
 ORGANISM  
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 REFERENCE  
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 JOURNAL  
 MEDLINE  
 PUBMED  
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 AUTHORS  
 TITLE  
 JOURNAL  
 1 (bases 1 to 7648)  
 Mitman,S., Guo,J., and Agnew,W.S.  
 Structure and alternative splicing of the gene encoding alpha1g, a  
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 Neurosci. Lett. 274 (3), 143-146 (1999)  
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 2 (bases 1 to 7648)  
 Mitman,S., Guo,J., and Agnew,W.S.  
 Direct Submission  
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 Johns Hopkins University School of Medicine, 600 N. Wolfe Street,  
 Meyer 297, Baltimore, MD 21287-7294, USA  
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ORIGIN

Alignment Scores:

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US-09-611-257a-37 (1-2266) x AF134986 (1-7648)

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QY	61	PhePheTyLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn	80
DB	181	TTCCTTACTTGAGCAGGACAGCCGCCCGGAGCTGGTGTCCGCAAGCTCTGTAAC	240
QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
DB	241	CCCTGGTTGAGGCAACAGATGTGGTATCTCTCACTGCGAGACCTTGGGCATG	300
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	301	TTCGGGCAATGGAGAGCATCGCTGTGACTCCAGAGGCTGGCGAATCCGACAGGCT	360
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DB	361	GATGACTTCATCTTTGCTTCTTGGCCGTGGAGATGGTGTGAAGATGGTGGCGGCG	420
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DB	601	GTAACGTTGCTGTGGATACGCTGCCATGCTGGGCAACGTCCTGCTCTCTCTCTTC	660
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QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyTrpGln	260
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DB	901	GACTATGAGGCTTACCAACAGCTCCAGCAACACCACTGTCTCACTGGAACCAATACATAC	960
QY	321	ThrAsnCysSerAlaGlyGlyLysAsnProPheGlyAlaIleAsnPheAspAsnIle	340
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QY	561	CysHisIleuGluProValArgCysGlnAlaProProProArgSerProSerGluAser	580
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DEFINITION			isoform (CACNA1G) mRNA, complete cds.
ACCESSION	AF126965		
VERSION	AF126965.1	GI:4761538	
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SOURCE			Homo sapiens (human)
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REFERENCE			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS			1 (bases 1 to 7253) Monteill,A., Chemin,J., Bourinnet,E., Mennesier,G., Lory,P. and

TITLE	Nargeot J.
JOURNAL	Molecular and functional properties of the human alpha (1G) subunit
MEDLINE	that forms T-type calcium channels
PUBMED	J. Biol. Chem. 275 (9), 6090-6100 (2000)
REFERENCE	2 (bases 1 to 7253)
AUTHORS	Monteill,A., Mennesier,G., Bourinnet,E., Lory,P. and Nargeot,J.
TITLE	Direct Submission
JOURNAL	Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R.
FEATURES	1142, C.N.R.S., 141 rue de la Cardonille, Montpellier 34396, France
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 7274) Montell,A., Chemlin,J., Bourinnet,E., Mennesier,G., Lory,P. and Nargeot,J.		
TITLE	Molecular and functional properties of the human alpha(1G) subunit that forms T-type calcium channels		
JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)		
MEDLINE	20158909		
PubMed	10692338		
REFERENCE	2 (bases 1 to 7274) Montell,A., Mennesier,G., Bourinnet,E., Lory,P. and Nargeot,J.		
AUTHORS	Direct Submission		
TITLE	Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R.		
JOURNAL	1142, C.N.R.S., 141 rue de la Cardonille, Montpellier 34396, France		
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ORIGIN

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DB	236	CGGCTCAACGACCTGTGGGGGGCGGGGGCGGGCGGGGGCTACGCAAAAAGAC	295
QY	41	ProglyseralaaapsergiuialagluilyleuprotyrproalaleuilaProvala	60
DB	296	CCGGGACCGCGGACTCCGAGCGGAGGGGGCTGCGTACCCGGGCGTGGCCCGGTGTT	355
QY	61	PhepethyleusergiuaapserfargProargsertipyaleuagthvAlaCyasn	80
DB	356	TTCTTCTACTTGACCGACGACGCGCGCGCGAGCTGGTGTCTCCGACCGCTCTGTAA	415
QY	81	ProtrptheigiuaaglliserMetleuValileuenuaenCyvsaIthfleglyMet	100
DB	416	CCCTGGTTTGACCATCAGATGTGTACTCTTCTCACTGGGTACCTTGGGCATG	475
QY	101	PhearpproCysgiuaaspiIealCyasapsergiuargCyvatgyleuGlnalabhe	120
DB	476	TTCCGGCCATCGAGACATCGCCTGTGACTCCACAGGCTCCGGATCTCTCAAGCCTTT	535
QY	121	AspaspheIlephelaphepheaIvaligluetvalValilyvmetvalAlaleuGly	140
DB	536	GATGACTTCATCTTGGCTTTTGGCCGTGAGATGGGTGGAAGATGGTGGCTTGGGC	595
QY	141	IlephegiylvslvCyvtyrleuGlyAsapthrrpnaanaargleuaapPheheIleval	160
DB	596	ATCTTGGGAAAAGTGTACTCGGAGACACTTGGAAACCGGCTTGTGACTTTTCACTGTC	655

QY 1161 IleAlaGlyMetLeuGlnIuTySerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
| | | | |  
Db 656 ATGCAAGGATGCTGGAATCTGCTGCACCTGCACAACTGCTTCTCAGCTGTCAGG 715  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
| | | | |  
Db 716 ACAGTCCGTGTGCTGCACCGCTCAGGGGCATTAACTGGGGTCCGACATGCGCATCTT 775  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlnAsnValLeuLeuLeuCysPhePhe 220  
| | | | |  
Db 776 GTACCTGTGTGTGATAGCTGCTGCATGCTGGGCAAGCTCTGTGCTGTCTTCTTC 835  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
| | | | |  
Db 836 GTCTTTTCATCTTCCGGCATTGTCGGCGTCCAGCTGTGGGCAAGGGTGTGCTTGGAACTCA 895  
QY 241 CysPheLeuProGlnAsnPheSerLeuProLeuSerValAspLeuGlnArgTyTyTyGln 260  
| | | | |  
Db 896 TGCTTCTACCTGAGATTTCAGCTCCCTCCAGCGTGGACTGTGAGCGCTATTACCAAG 955  
QY 261 ThrGlnAsnGlnAspGlnSerProPheIleCysSerGlnProArgGlnAsnGlyMetArg 280  
| | | | |  
Db 956 ACAGAAACAGAGATAGAGAGCCCTTCATCTGCTCCAGCCAGCAGAAACGACATGCGG 1015  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
| | | | |  
Db 1016 TCTTGCAGAAAGCTGCTCCACGCTGCGCGGGAGCGGGGGCGTGCCCATCTTCCGCTCTG 1075  
QY 301 AspTyTyGlnAlaTyArgAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyTyTy 320  
| | | | |  
Db 1076 GACTATAGAGCCCTTAACAAGCTCCACCAACACCACTGTGTCAACCTGGAACAGTCTAC 1135  
QY 321 ThrAsnCysSerAlaGlyGlyGlyIleAsnProPheGlyValAlaIleAsnPheAspAsnIle 340  
| | | | |  
Db 1136 ACCAACTGCTCAGCGGGAGACAAACCCCTTCAAGGGCGCCATCAACTTTGACAACTT 1195  
QY 341 GlyTyAlaTrpIleAlaIlePheGlnValIleThrLeuGlnGlyTyTrpValAspIleMet 360  
| | | | |  
Db 1196 GGTATAGCCCTGATCCGATCTTCCAGGTATCAAGCTGGAGGGGTGGGTCCGATCATCAG 1255  
QY 361 TyrPheValMetAspAlaHisSerPheTyArgAsnPheIleTyPheIleLeuLeuIleIle 380  
| | | | |  
Db 1256 TACTTGTGATGATCTCATCTCTTCAATTTCAATTCATCACTTCACTCCCTCATCATC 1315  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGln 400  
| | | | |  
Db 1316 GTGGGCTCTCTTTCATGATCAACCTGTGCTGTGGTGTGATGTCCACGCACTTCTCAAG 1375  
QY 401 ThrTyrGlnArgGlnSerGlnLeuMetArgGlnGlnArgValArgPheLeuSerAsnAla 420  
| | | | |  
Db 1376 ACCAAACAGCGGGAAGCCAGCTGATGCGGAGCAAGTGTGCGTTCCGTCCAAACGCGC 1435  
QY 421 SerThrLeuAlaSerPheSerGlnProGlySerCysTyTyGlnGlnLeuLeuTyTyTyLeu 440  
| | | | |  
Db 1436 AGCAACCTGCTGCTCTCTCTGAGCCCGGCACTGCTATGAGAGCTGCTCAAGTCACTCG 1495  
QY 441 ValTyTrpIleLeuArgIleValAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVal 460  
| | | | |  
Db 1496 GTTATCACTCTTGTGAAGGAGCCCGAGGCTGTGCTCAGGCTCTCTGAGGAGCAAGGTGAG 1555  
QY 461 ArgValGlyLeuLeuSerProAlaProLeuGlyGlyGlnGlnThrGlnProSerSer 480  
| | | | |  
Db 1556 CGGGTGGGGTGTCTCAGAGCCAGCACTCCGCGGGGCGAGAGACCCAGCCCAACAG 1615  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHis 500  
| | | | |  
Db 1616 AGCTGTCTCTGCTCCACCGCCCTATCTGTCACACCACTGTGTGACCAACCAACCAAC 1675  
QY 501 His 520  
| | | | |  
Db 1676 CATCAACCAACCAACCACTGTGGGCAATGGGAGCTCAAGGCCCCCGGGGCGCAACCGGAG 1735  
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540  
| | | | |

Db 1736 ATCCAGAGACAGGAGATGCCAATGGATGCCGCCGCTCATGCTGCACCAACCTCCAGACT 1795  
| | | | |  
QY 541 AlaLeuSerGlyAlaProProGlyGlyValAlaGlnSerValHisSerPheTyTrpIleAsp 560  
| | | | |  
Db 1796 GCCCTCTCGGGGGCCCCCTGTGTGGCGAGATGTGTGCACAGCTTCTTCACTATCCCAAC 1855  
QY 561 CysHisLeuGlnProValArgCysGlnAlaProProProAspSerProSerGlnAlaSer 580  
| | | | |  
Db 1856 TCCCATTTAGAGCAAGTCCGCTGCAGAGCGCCCTCCAGAGTCCCATTTGAGGATCC 1915  
QY 581 GlyArgThrValGlySerGlyValValTyProThrValHisThrSerProProProGln 600  
| | | | |  
Db 1916 GGCAGAGACTGTGGAGGCGGGAAGGTGATCCACCGGTGCACACCAAGCCTTCCACCGGAG 1975  
QY 601 ThrLeuValGlnValAlaLeuValAlaValAlaSerSerGlyProProThrLeuThr 620  
| | | | |  
Db 1976 AGCTGAAGAGAAAGCACTAGTAGAGGTGTGTGCAGCTTGGGCCCCCAACCTTCAAC 2035  
QY 621 SerLeuAsnIleProProGlyProTySerSerMetHisValLeuLeuGlnThrGlnSer 640  
| | | | |  
Db 2036 AGCTTCAACATCCACCGCGGCTTACAGCTTCCATGCACAGCTCTGGAGACACAGAGT 2095  
QY 641 ThrGlyAlaCysGlnSerSerCysIleHisSerProCysLeuValAlaAspSerGly 660  
| | | | |  
Db 2096 ACAGGTGCTGCGCAAGCTCTTGCAAGATCTCCAGCTTGTGCTTGAAGACAGACAGTGA 2155  
QY 661 AlaCysGlyProAspSerCysProTyTyCysAlaArgAlaGlyGlnValGlnLeu 680  
| | | | |  
Db 2156 GCTGTGTGTCCAGACAGCTGCCCTTCACTGTGCTCCGGGCGGGGAGGGAGGTGAGCTC 2215  
QY 681 AlaAspArgGlnMetProAspSerAspSerGlnAlaValTyGlnPheThrGlnAspAla 700  
| | | | |  
Db 2216 GCCGACCGTGAATCCTGACTGACACAGCAGCGAGGATTATGAATTCAACAGATGCC 2275  
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
| | | | |  
Db 2276 CAGCAACAGGACCTCGGGAGCCCCACAGCCCGCGGCAACGAGCTGGGCCCAATGGA 2335  
QY 721 GlnProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgHisIleVal 740  
| | | | |  
Db 2336 GAGCCAGCTGTGTCTGTGCTGTGAGGCTTAATCTGTACACTTCCGAAGAATTGTG 2395  
QY 741 AspSerTyTyTyPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
| | | | |  
Db 2396 GACAGCAATCACTTTGTGCCGGGAATCATGATGCGCATCTGTGCACACTCAGCATG 2455  
QY 761 GlyIleGlyTyHisGlnGlnProGlnGlnLeuThrAsnAlaLeuGlnIleSerAsnIle 780  
| | | | |  
Db 2456 GGCATCGAATTAACAGAGAGCCCGAGGAGCTTACCAACGCCCTGAAATCAGCAACTTC 2515  
QY 781 ValPheThrSerLeuPheAlaLeuGlnMetLeuLeuValLeuValTyTyTyProPhe 800  
| | | | |  
Db 2516 GTCTTTCACAGCCTCTTGTGCTGGAAGATGTGTGAAAGCTGTGTGTATGTCTCTTT 2575  
QY 801 GlyTyTrpIleValAspProTyArgAsnIlePheAspGlyValIleValValIleSerValTrp 820  
| | | | |  
Db 2576 GGCTACATCAAGAAATCCATCAACATCTTGCATGTGATGCTATGTGTATCAGCGGTGG 2635  
QY 821 GlnIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
| | | | |  
Db 2636 GAGATCGTGGGCAACAGGAGGCGCGCTGTGTGTGCGGACCTTCCGCTGATGTGCT 2695  
QY 841 ValLeuValLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
| | | | |  
Db 2696 GTGTGAAGCTGTGTGCTTCTGTGCGGGGTGTGCAGGGCACTGTGTGTCTCATGAAG 2755  
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880  
| | | | |  
Db 2756 ACCATGAGCAAGTGGCCACTTCTGCATGTGTGATTATGTCTTTCATCTTCACTTCAAC 2815  
QY 881 IleGlnGlyMetHisLeuPheGlyCysIlePheAlaSerGlnArgAspGlyAspThrLeu 900  
| | | | |

Db	2816	ATCCTGGGCATGCATCTTCTGCTGCAAGTTGCTCTGAGCGGAGTGGGACACCTTG	2875	Qy	1261	ProGlnSerArgPheArgLeuLeuCyshIleArgIleIleThrHisIleMetPheAspHis	1280
Qy	901	ProAspArgHisPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	920	Db	3887	CCTCAGTCCAGGTTCCGCTCTGTCACCGGATCATCACCAAGAATGTTGCACAC	3946
Db	2876	CCAGACCGGAGAAATTTGACTCTTCTGCTGCGGCATCGTCACTGCTTTGACATCTG	2935	Qy	1281	ValValLeuValIleIlePheLeuAsnCyshIleThrIleAlaMetGlnArgProIle	1300
Qy	921	ThrGlnGlnAspTrpAsnIleValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla	940	Db	3947	GTTGCTCTTGTCAATCTTCTTAAGTCACTGATCACCATGAGAGGCCCCAATAAT	4006
Db	2936	ACCAGAGAGACTGCAACAAAGTCTCTACCATGTGTAGCTCCAGGTGCTCGGGCG	2995	Qy	1301	AspProHisSerAlaGlnArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal	1320
Qy	941	AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal	960	Db	4007	GACCCCAACAGCGCTGAAGCATCTTCTGACCGCTCTCCAAATTAATCTTACCGCAGTC	4066
Db	2996	GCCCTTATTTCAATGCTTCATGACCTTGCGCAACTACGTGCTTTCATTTGCTGTC	3055	Qy	1321	PheLeuAlaGlnMetThrValIleValAlaLeuGlyTTrpCyshPheGlyGlnAla	1340
Qy	961	AlaIleLeuValGlnGlyPheGlnAlaGlnIleIleSerIleArgGlnAspAlaSerGly	980	Db	4067	TTTCTGCTGTAATATGACAGTAAGTGTGTGCACTGGGCTGGTCTTGGGAGCGAGCG	4126
Db	3056	GCCATTCTGATGAGGCTTCCAGGCGGAG-----	3085	Qy	1341	TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp	1360
Qy	981	GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyIleAspAlaAsnIleSerGln	1000	Db	4127	TACCTGCGAGACGTTTGAACTGTGACGAGGCTGTGTGCTCATCTCCGTCAATGAC	4186
Db	3086	-----GGAGATGCCCAACAGTCCGAA	3106	Qy	1361	IleLeuValSerMetValSerAspSerGlyThrIleIleLeuGlyMetLeuArgValLeu	1380
Qy	1001	SerGlnProAspPhePheSerProSerLeuAspGlyAspGlyAspArgIleIleCysLeu	1020	Db	4187	ATTCTGATGCCATGTGCTCTGACACGCGCACCAAGATCCTGGGCAATGCTGAGGGTCTG	4246
Db	3107	TCAAGACCCGATTTCTTCTCACCCAGCTGATGATGGAGACAGAGAAAGTGTCTG	3166	Qy	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuIle	1400
Qy	1021	AlaLeuValSerLeuGlyGlnHisProGlnLeuArgIleSerLeuLeuProProLeuIle	1040	Db	4247	CGGCTGCTGGGACCTTGGCGCCGCTCAGGGTATCAGCGCGGCGAGGGGCTGAAGCTG	4306
Db	3167	GCTTGTGATGCTCTGGAGAGACCCGAGCTGCGGAAAGCTGCTGCGCCCTCTCATC	3226	Qy	1401	ValValGlnThrIleMetSerSerLeuIleProIleGlyAsnIleValIleIleCysCys	1420
Qy	1041	IleHisThrAlaAlaThrProMetSerLeuProIleSerThrSerThrGlyLeuGlyIle	1060	Db	4307	GTTGATGAGCGGTGATGCTCTCACTGAACCATGAGGCAACATGTAGTACTGCTGT	4366
Db	3227	ATCCACACGCGCGCCACACCATATGCTGCTGCCAAGAGCACACACGCGGCTGGGAG	3286	Qy	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheIleGlyIlePhePheVal	1440
Qy	1061	AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGlnProGlyAlaAla	1080	Db	4367	GCTTCTTCAATCTTTCGCGCATCTGGGGGTGACGTCCTTCAAGGAAATTTTCGTG	4426
Db	3287	GCGCTGGCGCTGCTGCGCGCGCACAGCAGCGGCTGCGAGAGCTCGGGGCGGCGC	3346	Qy	1441	CysGlnGlyGlnAspThrArgAsnIleThrAsnIleSerAspCysAlaGlnAlaSerTyr	1460
Qy	1081	HisGlnMetCysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla	1100	Db	4427	TGCCAGGGCGAGGATATCCAGGAACATACCAATAATTCGACATGTCGCGAGGCGAGTTAC	4486
Db	3347	CACGAGATGAAGTACCGCCCGCCAGCGCCCGAGCTCTCCGACACACCTCGAAGCGCTCA	3406	Qy	1461	ArgTrpValArgHisIleTyrAsnPheAspAsnLeuGlnAlaLeuMetSerLeuPhe	1480
Qy	1101	SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuIle	1120	Db	4487	CGGTGGTCCGACAGTACCACTTGTGACACTTGTGACAGCCCTGATGTCCTGTC	4546
Db	3407	AGCAGCTGACACACAGCGCTCCAGCCGGAACAGCTCGGCGCTGACACCCAGCCTGAAG	3466	Qy	1481	ValLeuAlaSerIleAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
Qy	1121	ArgArgSerProSerGlyIleArgArgSerLeuLeuSerGlyGlnGlnIleSerGln	1140	Db	4547	GTTTGGCTTCCAAAGATGTTGGGTGACATCATATGATGGGTGATGCTGTGGGC	4606
Db	3467	CGGAGAGCCCAAGTGAAGAGCGCGGCTCTGTGTGCGGAGAAAGGCGAGAGAGCCAG	3526	Qy	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
Qy	1141	AspGlnGlnGlnSerSerGlnGlnIleArgAlaSerProAlaGlySerAspHisArgHis	1160	Db	4607	GTCGACAGACGCCATCATGAACCAACCCCTGATGCTGCTGTAATCTTCACTTCCTTC	4666
Db	3527	GATGAAGAGAGAGACTCGAAGAGAGAGCGGCGCACCTCGGCGCAGTACATCTGCGCAC	3586	Qy	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGlnAsnPhe	1540
Qy	1161	ArgGlySerLeuGlnArgGlnAlaIleYsSerSerPheAspLeuProAspThrLeuGlnVal	1180	Db	4667	CTGCTCAATTTGACCTTCTTGTCTGAACATGTTGTGGTGTGGTGTGGAGAACTTC	4726
Db	3587	AGGGGGTCCCTGAGCGGAGGAGCCAGAGATTCTTTGACTGCGACACACTCTCAAGTGTG	3646	Qy	1541	HisIleCysArgGlnHisGlnGlnGlnGlnAlaArgArgArgGlnIleValIleValIle	1560
Qy	1181	ProGlyLeuHisIleArgThrAlaSerGlyIleArgGlySerAlaSerGlnHisGlnAsnCysAsn	1200	Db	4727	CACAAAGTGTGGACACACAG	4786
Db	3647	CCAGGGCTGCAATCCCATGCGCAGTGTGCGAGAGGTCTGCTTGTGAGCACACAGAGCTGCAT	3706	Qy	1561	ArgArgLeuGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle	1573
Qy	1201	GlyIleYsSerAlaSerGlyIleArgLeuAlaArgAlaLeuArgProAspAspProLeuAsp	1220	Db	4787	CGAAGACTGAGAAAAAG	4846
Db	3707	GCGAAGTCCGCTTTCAGGGCGCTGCGCCCGGCGCTTGTGAGTACACCCCTGCTGAT	3766	Qy	1574	ProTyrTyrSerSerPheTyrSerArgArgPheArgLeuLeuValHisIleLeuCysThrSerHis	1593
Qy	1221	GlyAspAspAlaAspAspGlnGlyIleAsnLeuSerIleGlyGlnArgValArgAlaIleTrpIle	1240	Db	4847	CTTAACTACTCCCACTACTCCGCTTCCGCTCTCTGTCACCACTGTGTGACACAGCCAC	4906
Db	3767	GGGGATGACCGCGATGAGAGGGGCACTTGAAGCAAAAGGGGATCCGCGCTGGATC	3826	Qy	1594	TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGln	1613
Qy	1241	ArgAlaArgLeuProAlaCysTyrIleGlnIleArgAspSerTrpSerAlaTyrIlePhePro	1260	Db	4907	TACCTGACCTTTCATCAACAGGTGATCGGGCTGAAGCTGTGACCATGGCAGATGAG	4966
Db	3827	CGAGCCCACTCCCTGCTGCTGCTGAGGAGATCTCTGTGACACCTTAATCTTCCCT	3886				



QY 1614 HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuValIleCysAsnTyrIlePheThr 1633  
| | | | |  
Db 4967 CACTTACAGAGACCCCAAGATTCTGGATTGAGGCTCTAAGATCTGCAACTACATCTTCACT 5026  
QY 1634 ValIlePheValIleuGlnSerValPheValLeuValAlaPheGlyPheArgPhePhe 1653  
| | | | |  
Db 5027 GTCATCTTTGTCTTGGAGTCAAGTTTCAAACTGTGGCCCTTGTGTTCCGTGGTCTTC 5086  
QY 1654 GlnAspArgTTrpAsnGlnLeuAspLeuAlaIleValIleuLeuSerIleMetGlyIleThr 1673  
| | | | |  
Db 5087 CAGGACAGAGGTGAACAGCTGAGCCTGGCCATTGTCTGTCTGCATCACTATGGGCATCAAG 5146  
QY 1674 LeuGlnGlnIleGlyValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet 1693  
| | | | |  
Db 5147 CTGGAGAAATCGAGGTCAACGCTCGCTGCCATCAACCCCACTCATCCGATCAAG 5206  
QY 1694 ArgValIleuArgIleAlaArgValLeuValLeuValLeuValMetAlaValGlyMetArgAla 1713  
| | | | |  
Db 5207 AGGGTCTGGCATTCGCCAGTGTGAAGCTGTGAAGTGGCTGTGGGCAATGGCGGCG 5266  
QY 1714 LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet 1733  
| | | | |  
Db 5267 CTGCTGGAACAGGTGATGACAGGCGCTGCCAGGTGGGAACTTGGGACTTCTTTCATG 5326  
QY 1734 LeuLeuPhePheIlePheAlaAlaLeuGlyValGlyLeuPheGlyAspLeuGlnCysAsp 1753  
| | | | |  
Db 5327 TTGTGTTTTTCACTTTCGAGCTCTGGCGTGGAGCTCTTGGAAACCTGGAGTGTGAC 5386  
QY 1754 GlnThrHisProCysGlnGlyLeuGlyArgHisAlaIleThrPheArgAsnPheGlyMetAla 1773  
| | | | |  
Db 5387 GAGACACACCCCTGTGAGGGGCTGGGCGCTCATGCCACCTTGGAACTTGGCAATGGCG 5446  
QY 1774 PheLeuThrIleuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetCysAspThr 1793  
| | | | |  
Db 5447 TTCTTAACCTCTTTCGAGTCTCCACAGGTGACAAATGGCAATGGCAATGGCAAGGACCC 5506  
QY 1794 LeuArgAspCysAspGlnGlnSerThrCysTyrAsnThrValIleSerProIleTyrPhe 1813  
| | | | |  
Db 5507 CTCGGGAGCTGTGACAGAGAGTCCACTGTTCAACAACGGTCACTTCGGCTATCTTACTT 5566  
QY 1814 ValSerPheValIleuThrAlaGlnPheValIleuValAsnValValIleAlaValLeuMet 1833  
| | | | |  
Db 5567 GTGTCTCTCGTCTGACGGGCCAGTTCGTCGTAGTCAACGTGGTGTATCCCGCTGAGAG 5626  
QY 1834 LysHisLeuGlnGlnLeuSerAsnValAlaValGlnGlnAlaGlnLeuGlnAlaGlnLeu 1853  
| | | | |  
Db 5627 AACCACTTGAGGAGGACCAAGAGGCGCAAGAGAGGCGCAGCTAAGAGCTGAGCTG 5686  
QY 1854 GlnLeuGlnMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu 1873  
| | | | |  
Db 5687 GAGCTGGAAGATGAAGACCTCAACCCCAACCCCACTCGCACTGGGCAAGCCCTTCTCTC 5746  
QY 1874 TrpProGlyValGlnGlyProAspSerProAspSerProIleProGlyAlaIleuHisPro 1893  
| | | | |  
Db 5747 TGGCTCGGGGTCAAGGCGCCCGACAGCCCGCAGAGCCCAAGCCTGGGGCTGTGACCCA 5806  
QY 1894 AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGlnHisProThrMetGlnProHis 1913  
| | | | |  
Db 5807 GCGGCCCAAGCGAGATCAAGCTCCACTTTTCCCTGAGACCCCAAGATGAGGCCCCAC 5866  
QY 1914 ProThrGlnLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThr 1933  
| | | | |  
Db 5867 CCCACGAGCTGCAGAGACCAAGCTTACTGACTGTGCGAAGCTGTGGGTCAAGCCCAAG 5926  
QY 1934 HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGlnGlyProLeu 1953  
| | | | |  
Db 5927 CACTCTCTGCCAATGACAGTACATGTGTCGCGATGGAGCACTGCCGAGGGGCCCCG 5986  
QY 1954 GlyHisArgGlyTTrpGlyLeuProLysAlaGlnSerGlySerAlaLeuSerValHisSer 1973  
| | | | |  
Db 5987 GGACACAGGGGCTGGGGGCTCCCAAGCTCACTAGGCTCCCTCTTGTTCCTTCACTCC 6046  
QY 1974 GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGln 1993  
| | | | |

Db 6047 CAGCCAGAGAGATACAGCTACATCTGCAGCTTCCCAAGATGACCTCATCTGCTCCAG 6106  
QY 1994 ProHisSerAlaProThrTTrpGlyThrIleProLysLeuProProGlyValArgSerPro 2013  
| | | | |  
Db 6107 CCCCAAGGCGCCCAAGCTGGGGGACCAATCCCAATCGCCCCCAAGAGAGCTCCCT 6166  
QY 2014 LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln 2033  
| | | | |  
Db 6167 TTGGCTCAGAGGCTCAAGGCGCAGGAGCAATAGAGATGACTCTCTTGGACCTTCAAG 6226  
QY 2034 GlyLeuGlySerArgGlnAspLeuAlaGlnValSerGlyProSerProProLeuAla 2053  
| | | | |  
Db 6227 GGTCTGGGAGCCGGGAAAGACTGCTGGCAGAGGTGAAGGGGCTCCCGCCCTGGCC 6286  
QY 2054 ArgAlaTyrSerPheTTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis 2073  
| | | | |  
Db 6287 CCGGCTTACTTCTTTCGGGGCCAGTCAAGTACCCAGGACAGACACTCCCGCAGCCAC 6346  
QY 2074 SerLysIleSerLysHisMetThrProProAlaProCysProGlyProGlnProAsnTrp 2093  
| | | | |  
Db 6347 ACAGAGATCTCAAGCACAATGACCCCGCAGCCCTTGCAGAGCCCAAGAACCACTGG 6406  
QY 2094 GlyLysGlyProProGlnThrArgSerSerLeuGlnLeuAspThrGlnLeuSerTrpIle 2113  
| | | | |  
Db 6407 GGCMAAGGCGCTCCAGAGACAGAGCAAGCTTAGAGTTGACACAGGACTGAGCTGATTT 6466  
QY 2114 SerGlyAspLeuLeuProProGlyGlyGlnGlnGlnProProSerProArgAspLeuLys 2133  
| | | | |  
Db 6467 TCAGAGAGACTCTCTCCCTCCCGCGGCGCAGAGAGGCCCCCATCCCAAGGACCTGAG 6526  
QY 2134 LysCysTyrSerValGlnAlaGlnSerCysGlnArgGAspProThrSerTrpLeuAspGlu 2153  
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ACCESSION AF190860  
VERSION AF190860.1 GI:7021332  
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REFERENCE  
1 (bases 1 to 7349)  
Cribbs, L.L., Gomora, J.C., Daud, A.N., Lee, J.H. and Perez-Reyes, E.



TITLE Molecular cloning and functional expression of Ca(v)3.1c, a T-type calcium channel from human brain  
JOURNAL FEBS Lett. 466 (1), 54-58 (2000)  
MEDLINE 20115462  
PubMed 10648811  
REFERENCE 2 (bases 1 to 7349)  
AUTHORS Cribbs, L.L., Gomora, J.C., Lee, J.-H., Daud, A.N. and Perez-Reyes, E.  
TITLE Direct Submission  
JOURNAL Submitted (29-SEP-1999) Physiology, Loyola University Medical Center, 2160 South First Avenue, Maywood, IL 60153, USA  
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Qy	1954	GlyHisAspGlyTrpGlyLeuProIlyAlaGlnSerGlySerValIleSerValHisSer	1973
Dp	6028	GGACACAGGGGCTGGGGGCTCCCAAACTCAGTCAAGGCTCGTGTGTCTCGTTCATCTCC	6087
Qy	1974	GlnProAlaAspThrSerTyrIleLeuGlnLeuProIlyAspAlaProHisLeuLeuGln	1993
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Dp	6268	GGTCTGGGCAACCGGGAAGACCTGTGGCAAGGTAAGTGGGCCCTCCCGCCCTGGCC	6327
Qy	2054	ArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis	2073
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Qy		2154	GlArGrhIshSerIleAlaValaIserCySLeuaApsSerGlySerGlnProhIslaEuGly	2173
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Qy		2194	LyLeuSerProProSerIleThrIleAapProProGluSerGlnGlyProArGlyPro	2213
Dp		6748	AAACTACGCCCGCTAGTATACCAATGACCCCCCGAGGCCAAGTCTCTGGACCCCG	6807
Qy		2214	ProSerProGlyIleCySLeuaAGArGArAlaProSerSerApsSerLyAspProLeu	2233
Dp		6808	CCGAGCCCTGTATCTGCTCCCGAGAGAGGGCTCCGTCCAGGCACTCCAAGATCCCTTG	6867
Qy		2234	AlAsSerGlyProProApsSerMetAlaAlaIserProSerProLySlyAspValLeuSer	2253
Dp		6868	GCCCTGTGCCCCCTGACACATGAGCTGCTCCGCTCCCAAGAAAGATGTGCTAGT	6927
Qy		2254	LeuSerGlyLeuSerSerAapProAlaAspLeuAapPro	2266
Dp		6928	CTCTCCGGTTTATCTTGACCAAGACGACTGAGCCCC	6966
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	ORGANISM	Homo sapiens		
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		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	REFERENCE	1. (bases 1 to 6786)		
	AUTHORS	Montell,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and		
		Nargeot,J.		
		Molecular and functional properties of the human alpha(1g) subunit		
		that forms T-type calcium channels		
	JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)		
	MEDLINE	20158909		
	PUBMED	10692398		
	REFERENCE	2. (bases 1 to 6786)		
	AUTHORS	Montell,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.		
	TITLE	Direct Submission		
	JOURNAL	Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)		
		U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France		
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		PCSDIDSORCRLTQAFDFLTAFRAVENVMVALGFGKCYIGDTNNRLDFIV		
		IADMLRYSLDLDQNVSAVKTVAFLPRLINPVMRLIVTLTLDLTPMLGNVLLIC		



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Qy	501	HisHisHisHisTyrHisLeuGluYAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
Db	1501	CATACCAACCACTACCACTCGGGCAATGGACGGTCAAGGGCCCCCGGGCCAGCCGGAG	1560
Qy	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
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Qy	541	AlaLeuSerArgYValaProProGluYValaGluSerValHisSerPheTyrHisAlaAsp	560
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QY	881	IlLeuEnGlyMetHsIleuPheGlyCySerAspPheAlaSerGluArgAspGlyAspThrLeu	900
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QY	901	ProAspArgIysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	920
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QY	941	AlaLeuTrpPheIleAlaLeuMetThrPheGlyAsnTrpValLeuPheAsnLeuVal	960
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Db	2881	GCCATTCTGGAGGGGCTTCAGCGGAG-----	2910
QY	981	GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyIleAspAlaAsnIysSerGlu	1000
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QY	1001	SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgIysLeuCyLeu	1020
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QY	1021	AlaLeuValSerLeuGlyGluHisProGluLeuArgIysSerLeuLeuProProLeuIle	1040
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QY	1081	HisGluMetIysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla	1100
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Db	5752	CTGACTGTGCGGAAGTCTGGGGTCAAGCCGACGACTCTCTGCGCCCAATGACACTACATG	5811
Qy	1943	CysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyLysProGlyLeuProLys	1962
Db	5812	TGTGGGCAATGGAGCACTGCTCCAGAGGGGCTGGGACACAGGGGGCTGGGCTCCCA	5871
Qy	1963	AlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTrpIleLeu	1982
Db	5872	GCTCACTAGAGGCTCCGCTCTTGTCCGTCACTCCACACGACGATACAGACTACATCTG	5931
Qy	1983	GlnLeuProLysAspAlaProHisIleLeuGlnProHisSerAlaProThrTrpGlyThr	2002
Db	5932	CAGCTTCCCAAGATCACCCTCATCTGCTCCAGCCCAAGCGGCCCACTGGGGCACCC	5991
Qy	2003	IleProLysLeuProProGlyProGlyArgSerProLeuAlaGlnArgProLeuArgArgGln	2022
Db	5992	ATCCCAAACTGCCCCACAGGACCTCTCCCTTGGCTCAAGAGGCGACTCCAGGCGCCAG	6051
Qy	2023	AlaAlaIleArgThrAspSerIleuAspValGlnGlyLeuGlySerArgGlnAspLeuLeu	2042
Db	6052	GACGCAATAGACTACTCTCTTGGACGTTCAAGGCTCTGGGACGCCGGAGAACCTGCTG	6111
Qy	2043	AlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSer	2062
Db	6112	GCAAGGTAGTGGGCTCTCCCGCCCTGGCGCCGGGCTACTCTTCTGGGGCCAGTCA	6171
Qy	2063	SerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetThrPro	2082
Db	6172	AGTACCAAGGACAGAGCACTCCCGACACCAAGAAATCTCCCAAGACACATGACCCCG	6231
Qy	2083	ProAlaProCysProGlyProGlyProAlaSerTrpGlyLysGlyProProGluThrArgSer	2102
Db	6232	CCAGCCCCCTTGGCCAGGCCAGAACCCAACTGGGGGACAGGCGCTCCAGAGACCAAAAC	6291
Qy	2103	SerLeuGlnLeuAspThrGlnLeuSerTrpLysSerGlyAspIleuLeuProProGlyGly	2122
Db	6292	AGCTTAGAGTTGACACGAGAGCTGAGCTGGATTTCAGAGAACTCTCGCCCTCGCGCGAC	6351
Qy	2123	GlnGluGlnProProSerProAlaArgAspLeuLysLysCysTrpSerAlaGlnAlaGlnSer	2142
Db	6352	CAGGAGAGACCCCACTCCCAAGGACCTGAAAGTGTCAAGCTGAGGCGCCAGAC	6411
Qy	2143	CysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAlaValSer	2162
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Qy	2163	CysLeuAspSerGlySerGlnProHisIleuGlyLysThrAspProSerAsnLeuGlyGln	2182
Db	6472	TGCTGGAACAGCGGCTCCCAACCCCACTGGGCAAGACCCCTCTAACTTGGGGGCGCAG	6531
Qy	2183	ProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIleThrIle	2202
Db	6532	CCCTTGGGGGGCTGGAGCCGCGCCCAAGAAAAAACTCAGCCCGCTGATACACACATA	6591
Qy	2203	AspProProGluSerGlnGlyProArgThrProProSerProGlyLysCysLeuAspArg	2222
Db	6592	GACCCCCCGAGAGCCTGCTCCGACCCCGCCCAAGCCCTGTATCTGCTCCCGAGG	6651
Qy	2223	ArgAlaProSerSerAspSerIysAspProLeuAlaSerGlyProProAspSerMetAla	2242
Db	6652	AGGGCTCCGTCGACGACTCCCAAGATCCCTTGGCTCTGGGCCCCCTGACACATGGCT	6711
Qy	2243	AlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAla	2262
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Qy	2263	AspLeuAspPro 2266	
Db	6772	GACCTGGAACCC 6783	

RESULT 13  
AF227746  
LOCUS AF227746 6897 bp mRNA linear PRI 06-MAR-2000

DEFINITION	Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform af (CACNA1G) mRNA, complete cds.
ACCESSION	AF227746
VERSION	AF227746.1 GI:7159264
KEYWORDS	
SOURCE	· Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS	1 (bases 1 to 6897) Monteill, A., Chemin, J., Bourinet, E., Mennesier, G., Lory, P. and Nargeot, J.
TITLE	Molecular and functional properties of the human alpha(1G) subunit that forms T-type calcium channels
JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)
MEDLINE	20158909
PUBMED	10692398
REFERENCE	2 (bases 1 to 6897) Monteill, A., Mennesier, G., Bourinet, E., Lory, P. and Nargeot, J.
AUTHORS	Direct Submission
TITLE	Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)
JOURNAL	U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France
FEATURES	Location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 6897  
Score: 11707.00 Matches: 2241  
Percent Similarity: 96.60% Conservative: 1  
Beet Local Similarity: 96.55% Mismatches: 1  
Query Match: 98.35% Indels: 78  
DB: Gaps: 3

US-09-611-257a-37 (1-2266) x AF227746 (1-6897)

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QY 21 ArgLeuAaAapLeuSerGIyaIaGIyArProGIySerGIaGIuLysAaP 40  
DB 61 CGGCTCAACGACTGTGCGGGGCGGGGGCGGGGCGGGGCTACAGAAAGAGAC 120  
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QY 61 PhePheTyLeuSerGIuaAapSerGIaProArGserTTPCyLeuAaGThrVaI 80  
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QY 81 ProTrpPheGIuaGIyIeSerMetLeuVaIleuLeuAaNCyVaIThrLeuGIyMet 100  
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DB 661 GTCTTCTTCACTTCCGATCGGATCGTGGGCTCCAGGCTGTGGGCAAGGCTTCCGAAACCGGA 720  
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Oy	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheIleGlyTyLeuPheVal	1440
Db	4192	GCCTTCTTCATCATTTTCCGCATCTTGGGGGTGCACTCTTCAAGGAGATTTTTCGGT	4251
Oy	1441	CysGlnGlyGlnLeuAhrThrAhrGAsnIleThrAsnTySerAspCysValIleValIleSerTy	1460
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Db	4612	CGAAGACTGGAGAAAAAG	4671
Oy	1574	ProTyrTySerAspTyTySerArgPheArgLeuLeuValHisIlePheCysThrSerHis	1593
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Oy	1614	HisTyGlnGlnProGlnIleLeuAspGlnAlaLeuValIleCysAsnTyrIlePheThr	1633
Db	4792	CACACACAGAGCCCGCAGATTCTGGATGAGGCTCTGAGATCTGCAACTCACTCACTCACT	4851
Oy	1634	ValIlePheValLeuGlnSerValPheTyLeuValAlaPheGlyPheArgArgPhePhe	1653
Db	4852	GTCATCTTGTCTTGAGACTCAGTTTCAAACTTGTCCTTGGTTTCCGTCCGTTCTTC	4911
Oy	1654	GlnAspArgTTPAsnGlnLeuAspLeuAlaIleValIleLeuSerIleMetGlyIleThr	1673
Db	4912	CAGACAGAGTGAACAGCTGACCTGGCCATTTGCTGCTGCTGCATCATAGGACATCAGG	4971
Oy	1674	LeuGlnGlnIleGlnValAlaAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet	1693
Db	4972	CTGAGAGAGAAATCGAGGTCAAGCCTCGCTGCCATCAACCCCAACATCATCGCATCAAG	5031
Oy	1694	ArgValLeuArgIleAlaArgValLeuLeuLeuLeuTyMetAlaValGlyMetArgAla	1713
Db	5032	AGGGTGGTGGCCATTTGCCCGAGTCTGAAGCTGTGAAGATGGCTGTGGCCATGGCGGGG	5091
Oy	1714	LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet	1733
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Db	5152	TTTGTGTTTTCATCTTTTGACACTCTGGGCGGAGACTCTTTTGAAGACTTGGATGTGAC	5211
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Db	5212	GAGACACACCCCTGTGAGGGCTCGGGCGCTCATGCCACCTTTCGAACTTTGGCATGGCC	5271
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Oy	1814	ValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	1833
Db	5392	GTCGTCTTGCTGTGACGGCCAGTTCGCTAGTCAACAGTGTGATGCGCTGCTGATG	5451
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Oy	1946	GlySerThrAlaGlnGlyProLeuGlyHisIleArgGlyTTPGlyLeuProTyAlaGlnSer	1965
Db	5932	GGGAGCACTGCCAGAGGGGCGCCCGGAGACACAGAGGCTGGGGCTCCCAAGCTCAAGCA	5991
Oy	1966	GlySerValLeuSerValHisSerGlnProAlaAspThrSerTyIleLeuGlnLeuPro	1985
Db	5992	GGCTCGCTTGTCTGTTACTCTCCAGCGAGAGATCAAGCTTAATCTGTGAGCTTCC	6051
Oy	1986	LeuAspAlaProHisLeuLeuGlnProHisSerAlaProThrTTPGlyThrIleProTyS	2005
Db	6052	AAAGATGACCTCATCTGCTCAAGCCCAAGCGGCCCAACCTGGGGGACCATCCCAAA	6111
Oy	2006	LeuProProProGlyValTySerProLeuAlaGlnAhrProLeuAhrArgGlnAlaIle	2025
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Oy	2026	ArgThrAspSerLeuAspValGlnGlyLeuGlyTySerArgGlyAspLeuLeuAlaGlyVal	2045
Db	6172	AGGACTGACTCTTGGACCTTTCAGGGTCTGGGACGCGGAGAAAGACTCTGTGGAGAGGTC	6231
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Qy	2126	ProProSerProArgArgLeuIlySlySlySlySerValGlnAlaGlnSerCysGlnArg	2145
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DEFINITION	Homo sapiens voltage-dependent calcium channel alpha 1g subunit		
ACCESSION	AF227748		
VERSION	AF227748.1	GI:7159268	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 6921)		
AUTHORS	Monteill, A., Chemin, J., Bourinac, E., Mennessier, G., Lory, P. and Nargec, J.		
TITLE	Molecular and functional properties of the human alpha(1g) subunit that forms T-type calcium channels		
JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)		
MEDLINE	20158909		
PUBMED	10692398		
REFERENCE	2 (bases 1 to 6921)		
AUTHORS	Monteill, A., Mennessier, G., Bourinac, E., Lory, P. and Nargec, J.		
TITLE	Direct Subunit		
JOURNAL	Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)		
FEATURES	U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France		
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VERSION AF134985.1 GI:6625656  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1 (bases 1 to 7030)  
AUTHORS Mitten, S., Guo, J. and Agnew, W. S.  
TITLE Structure and alternative splicing of the gene encoding alpha1g, a  
human brain T calcium channel alpha1 subunit  
JOURNAL Neurosci. Lett. 274 (3), 143-146 (1999)  
MEDLINE 20014446  
PubMed 10548410  
REFERENCE 2 (bases 1 to 7030)  
AUTHORS Mitten, S., Guo, J. and Agnew, W. S.  
TITLE Direct Submission  
JOURNAL Submitted (15-MAR-1999) Anesthesiology/Critical Care Medicine, The  
Johns Hopkins University School of Medicine, 600 N. Wolfe Street,  
Meyer 297, Baltimore, MD 21287-7294, USA

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ORIGIN

Alignment Scores:

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Qy 161 IleAlaGlyMetLeuGlyIyRserLeuAspLeuGlnAsnValSerPheSerIleValArg 180  
Dh 481 ATGCGACAGGAGATGCGAGTACTCGCTGAGCTGCAGAACGTCACGCTTCTCAGCTGTAGG 540  
Qy 181 ThrValArgValIleuAspProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Dh 541 ACAGTCCGCTGTGCTGCAACCGCTCAGAGCCATTAAACCGGCTGCCACAGATCGCATCTT 600  
Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValIleuLeuLeuCybPhe 220  
Dh 601 GTACGTTGGCTGGATACGCTGCCATGCTGGGCAACGTCCTGCTGCTTCTTCTTC 660  
Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuThrPalagIyLeuLeuArgAsnArg 240  
Dh 661 GTCTTCTTCACTTTCGGCATCTGCGGCTCGAGCTGAGGCGAGGCTGCTTGGAAACCGA 720  
Qy 241 CybPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGlyArgTyRTrpGln 260  
Dh 721 TGCTTCTTCACTGAGATTTTCAGCTCCCTTGAAGCTTGAAGCTTGAAGCTTATTAACAG 780  
Qy 261 ThrGluAsnGluAspGluSerProPheIleCybSerGlnProArgGluAsnGlyMetArg 280  
Dh 781 ACAGAGAACAGAGATGAGAGGCCCTTCACTGCTCCACAGCCAGCGAGAACGGCATCGCG 840  
Qy 281 SerCybArgSerValProThrLeuArgGlyAspGlyIyGlyIyProProCybGlyLeu 300  
Dh 841 TCCGCGAGAAAGCGTCCACGCTCGCGGCGAGCGGCGGCTGCGCCACCTTGGGCTCTG 900  
Qy 301 AspThrGluIyAlaTyRAsnSerSerSerAsnThrThrCybValAsnThrPasnGlnTyRTrp 320  
Dh 901 GACTATAGAGGCTTACACAGCTCCAGAACACACCTGTGTACACTGAGAACAGTACTAC 960  
Qy 321 ThrAsnCybSerAlaGlyGluIyAsnProPheGlyAlaIleAsnPheAspAsnIle 340  
Dh 961 ACCAAGCTGCTAGCGGGGAGACACACCCCTTCAAGGGCGCCATCACTTGAACAACATT 1020  
Qy 341 GlyTyRAlaTrpIleAlaIlePheGlnValIleThrLeuGlyIyTrpValAspIleMet 360  
Dh 1021 GGCATATGCTGAGATGCGCATCTTCAGGTATCAAGCTGAGGGCTGGTGTGACATCATG 1080  
Qy 361 TyrPheValMetAspAlaHisSerPheTyRAsnPheIleTyRPhelIleLeuIleIle 380  
Dh 1081 TACTTTTGATGATGATGCTCATTTCTTCAAAATTCATCTTCAATCTTCTCATATC 1140  
Qy 381 ValGlySerPhePheMetIleAsnLeuCybLeuValValIleAlaThrGlnPheSerGlu 400  
Dh 1141 GTGGGCTCTCTTCAATCATGATCAACTGCTGCTGGTGGATGGACAGCAAGCATTTCTCAGAG 1200  
Qy 401 ThrIyGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
Dh 1201 ACCAAGACAGCGGAGAAAGCAGCATGATGCGGAGACAGCTGCGGTTCTCTTCCAACGCC 1260  
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCybTyRArgIyIyLeuLeuIyTyRLeu 440  
Dh 1261 AGCACCCCTGAGCTTCTTGTAGCCCGGACGCTGTATGAGAGAGCTCAAGTACTCTG 1320  
Qy 441 ValTyRileuLeuAGlyAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
Dh 1321 GTGTACATCTCTTGTAAAGGACAGCCGAGCTGGCTCAGTCTCTCGGGACAGAGGTGTG 1380  
Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyIyGlnGlnThrGlnProSerSer 480  
Dh 1381 CGGGTGGGCTGTCTACAGACGCCAGCACTCGGGGCGCAGAGAGACCCACAGCAGCAGC 1440  
Qy 481 SerCybSerArgSerHisArgArgLeuSerValHisIleLeuValHisIleHis 500  
Dh 1441 AGTGCTCTGCTCCACCGCGGCTATCGTTCACACACTGTGTGACACACACACACAC 1500

Qy 501 HisHisHisIleTyRHisIleuGlyAsnGlyThrLeuArgAlaProAsnAlaSerProGlu 520  
Dh 1501 CATCACACACACACTACCACTCGGCAATGGACCTCAGGGCCCCCGGGCCAGCCGAG 1560  
Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540  
Dh 1561 ATCCAGACAGGAGATGCCAATGGGTCCCGAGGCTCATGTGACACACACCTTGAGCGCT 1620  
Qy 541 AlaLeuSerGlyValaProProGlyIyAlaGluSerValHisSerPheTyRHisAlaAsp 560  
Dh 1621 GCCCTCCGGGGCCCCCTCGTGGCGAGAGTGTGTGACAGCTTCTACATGCGCAC 1680  
Qy 561 CybHisIleuGluProValArgCybGlnAlaProProProAspSerProSerGluAlaSer 580  
Dh 1681 TGCACATTAAAGCAGATCGCTGCGACAGGCCCCCTCCAGAGTCCCATTTGAGGATCC 1740  
Qy 581 GlyArgThrValGlySerGlyIyValTyRProThrValHisThrSerProProGlu 600  
Dh 1741 GGCAGACTGTGGGACAGCGGAGAGTGTATCCACCGTCACACAGCCCTCCACCGGAG 1800  
Qy 601 ThrIyAsnGlyIyValaLeuValGluValAlaIleSerSerGlyProProThrLeuThr 620  
Dh 1801 ACCGTGAAGAGAAAGGACATAAGTGTGCTGCCAGCTTGGGCCCCCAACCTCACC 1860  
Qy 621 SerLeuAsnIleProProGlyProTyRserSerMetHisIyIyLeuLeuGlnThrGlnSer 640  
Dh 1861 AGCTTCAACATCCACCGGGCCCTACAGCTCATGACACAAAGTGTGAGAGACAGAGT 1920  
Qy 641 ThrGlyAlaCybGlnSerSerCybIyIleSerSerProCybLeuIyAlaAspSerGly 660  
Dh 1921 ACAGTGTCTGCAAGACTTTTGCAGATTTCCAGCCCTTGTGTAAGACAGACAGTGA 1980  
Qy 661 AlaCybGlyProAspSerCybProTyRcybAlaArgAlaGlyAlaGlyIyValGluLeu 680  
Dh 1981 GCCGTGTGTCAAGACAGTCCCTTACTGTGCCCCGGGCGAGGAGGAGTGTAGCTTC 2040  
Qy 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyRGluphethrGlnAspAla 700  
Dh 2041 GCCGACCGTAAATGCTGTGCTCAGACAGGAGAGATTATAGTTACACACAGGATGCC 2100  
Qy 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
Dh 2101 CAGACAGCACCTTCGGAGACCCCAAGCCGCGGAGGAGGAGCTGGGCCAGATGCA 2160  
Qy 721 GluproSerSerValleuAlaPheTrpArgLeuIleCybAspThrPheArgIyIleVal 740  
Dh 2161 GAGCCAGACTGTGTGTGCTGCTTCTGAGGCTATGTGACACCTTCGAAAGATTGTG 2220  
Qy 741 AspSerIyTyRPhelIyArgGlyIleMetIleAlaIleuValAsnThrLeuSerMet 760  
Dh 2221 GACAGCAATGATCTTGGCCGGGAAATCATGATGCGCATCTGTGTCAACACACTCAGATG 2280  
Qy 761 GlyIleGlyIyTyRHisIleGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
Dh 2281 GGCATTCGAATACACAGAGAGCCCGAGAGCTTACCAACCCCTTGAATACAGCAATC 2340  
Qy 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuIyLeuValTyRgIyProPhe 800  
Dh 2341 GTCTTACACAGCTCTTGTGCTGTGAGATGCTGTGAGCTGTGTGTGTATGTCCTTT 2400  
Qy 801 GlyTyRileuIyAsnProTyRAsnIlePheAspGlyValIleValValIleSerValTTP 820  
Dh 2401 GGTACATCAAGATCCCTTCAACATCTTGAATGTGTATTTGTGTCAACAGGTGTGG 2460  
Qy 821 GluIleValGlyGlnGlnGlyIyGlyLeuSerValIleuArgThrPheArgLeuMetArg 840  
Dh 2461 GAGATCGTGGGACAGAGGGGGGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2520  
Qy 841 ValIleuIyLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValIleuMetIy 860  
Dh 2521 GTGTGAAGCTGT 2580

QY	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer	880
Db	2581	ACCAATGGACAACGCGGCCACCTTCGCAATGCTGTAACTTCATTCATCTTCAGC	2640
QY	881	IleLeuGlyMetHisLeuPheGlyCysIlePheAlaSerGluArgAspGlyAspThrLeu	900
Db	2641	ATCTCGGGCAATGCATCTCTTCGGCTGCAGAGTTTGCTTCAGCGGGATGGGACACCTTG	2700
QY	901	ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	920
Db	2701	CCAGACCGGAAGAATTTGGACTCCTGCTGCGGCATCGACATGCTTTCAATCCTG	2760
QY	921	ThrGlnGluAspTrpAsnLysValLeuTyraGlnIleMetAlaSerThrSerSerTrpAla	940
Db	2761	ACCCAGAGGAGACTGGACAAGATCCTCTACATGTATAGGCTCACGCTCGTGGGCG	2820
QY	941	AlaLeuTyrrPheIleAlaLeuMetThrPheGlyAsnTyrrValIleuPheAsnLeuVal	960
Db	2821	GCCCTTAATTCATATGGCCCTCATGACCTTCGGCACTAGCGCTCTTCAATTTCTGGTC	2880
QY	961	AlaIleLeuValGluGlyPheGlnAlaGluGlnIleSerLysArgGluAspAlaSerGly	980
Db	2881	GCCATTCCTGGTGGAGGCGCTCCAGCGGAG-----	2910
QY	981	GlnLeuSerCysIleGlnLeuProValAspSerGlnIleGlyAspAlaAsnLysSerGlu	1000
Db	2911	-----GGAGATGCGCACMACTCCGAA	2931
QY	1001	SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu	1020
Db	2932	TCAGAGCCCATTTCTTCTCACCCAGCTGTGATGTGATGGGACACAGGAAGATGCTTG	2991
QY	1021	AlaLeuValSerLeuGlyGlnHisProGlnLeuArgLysSerLeuLeuProLeuIle	1040
Db	2992	GCCTTGATGTCCTCGGAGAGACCCGGAGCTGGGAAGACCTGCGCTCATC	3051
QY	1041	IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu	1060
Db	3052	ATCCACACGGCGCGCCACACCCATGCTGCTGCCAAGACACACACCGGCGCTGGGCGAG	3111
QY	1061	AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla	1080
Db	3112	GCGCTGGGACCTCGCGTCGCGCGCACACGACGCGGTGTGGAGAGCTCGGGGCGGCGC	3171
QY	1081	HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla	1100
Db	3172	CACAGAGATGAAGTCAACGCCGCCACGCCCGCAGCTCTCCGCACACGCCCTGGAGCGCTGCA	3231
QY	1101	SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyAlaProSerLeuLys	1120
Db	3232	AGCAGCTGAGCACGACGCGCTCCAGCCGGAACAGCTCGGCGCGTGCACCCAGCCTCAAG	3291
QY	1121	ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlnGlyGlnSerGln	1140
Db	3292	CGGAAGAACCCCAAGTGAAGAGCGCGCGCTCTCTGTGTGGGAAGAGCCAGGAAGCGAG	3351
QY	1141	AspGlnGluGlnSerSerGlyGlnGluArgAlaSerProAlaGlySerAspHisArgHis	1160
Db	3352	GATGAAGAGAGAGACTCAAGAGAGAGCGGCGCACCTGTGCGGCAAGTGAACATCGCCAC	3411
QY	1161	ArgGlySerLeuGluArgGlnAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
Db	3412	AGGGGAGTCCCTCGAGCGGAGGCGCAAGAGTTCTCTTGAACCTGCACAGCACACTCCAGGTG	3471
QY	1181	ProGlyLeuHisArgGThrAlaSerGlyArgGlySerAlaSerGlnHisGlnAspCysAsn	1200
Db	3472	CCAGGGCTGCATCGACTGCACATGCGCGCAAGAGTCTGCTTGTGAGCACACAGACTGCAT	3531
QY	1201	GlyLysSerAlaSerGlyArgGlnAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
Db	3532	GGCAAGTGGCTTCAGGGCGCTGGCGCCGCGCTCGCGCTGATGACCCCCCACTGGAT	3591
QY	1221	GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyIleArgValAlaGlnAlaTrpIle	1240

Db	3592	GGGATACCGCCGATGACGAGGGCACCTTAGCAAAAGGGAAAGGGTCCGGCGGTGATC	3551
Oy	1241	Argh1aArgLeuPProAlaCySTyLeuGluArgAspSerTrpSerAlaTrpIlePhePro	1260
Db	3552	CGAACCCGACCTCCCTGCTGCTGCTCGACGACGACGACTCCGTCAGCTCATCTTCCCT	3711
Oy	1261	ProGlnSerArgPheArgLeuLeuCySHisArgIleIleThrHisSlyMetPheAspHis	1280
Db	3712	CCTCAGTCCAGAGTTTCCGCTCCGTGTGCACCGGATCATCCCAAGAAGTTTCGACAC	3771
Oy	1281	ValValLeuValIleIlePheLeuAsnCySileThrIleAlaMetGluArgProSlyIle	1300
Db	3772	GTCGTCTTCATCATCTTCCTTAAGTCATCAACATCCGCAAGGAGCCCAAAATT	3831
Oy	1301	AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTrpIlePheThrAlaVal	1320
Db	3832	GAACCCCAACGCGCTGAACGCATCTTCTGACCTTCGCAATTACATCTTCACGCGAGTC	3891
Oy	1321	PheLeuAlaGluMetThrValSlySValAlaIleLeuGlyYTrpCySPheGlyGluGlnAla	1340
Db	3892	TTTCTGCTCAAAATGACAGTGAAGGTGTGTGCATCTGGGCTGTTCGGGAGACGGCG	3951
Oy	1341	TyrLeuArgSerSerTrpAsnValIleuAspGlyLeuLeuValIleuIleSerValIleAsp	1360
Db	3952	TACCTGGGAGCAATTGGAACGTGTGGAAGGGGTGTGGTGCTCATCTCCGATCGAC	4011
Oy	1361	IleLeuValSerMetValSerAspSerGlyThrSlySileLeuGlyMetLeuArgValLeu	1380
Db	4012	ATTCTGGTGTCCATGCTCTGTACAGCGGACCAAGATCTCTGGGACATGCTGAGGGTGTG	4071
Oy	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuSlyLeu	1400
Db	4072	CGGCTGCTGGCGAACCCCTGCGCCGCTCAGGGTATGATCGCGGGCGCAAGGGGCTGAAGCTG	4131
Oy	1401	ValValGluThrLeuMetSerSerLeuSlyProIleGlyAsnIleValValIleCySly	1420
Db	4132	GTGGTGAAGACGCTGATGTCTCTCAAGAACCATCGGCAACATGTGATCATCTGTCTGT	4191
Oy	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheSlyGlySlyPhePheVal	1440
Db	4192	GCCTCTTCATCATTTTCGGCATCTTGGGGGTGCAGTCTTCAAGGGAAGTTTTCGTG	4251
Oy	1441	CysGlnGlyGluAspThrArgAsnIleThrAsnSlySerAspCysAlaGluIleAspTyr	1460
Db	4252	TGCACGAGGCGAGATACCAAGAAACATCAACCAATAAATCGAGCTGTGCCAGGCGACGTAC	4311
Oy	1461	ArgTrpValArgHisSlySlyTrpAsnPheAspAsnLeuGlyGlnIleLeuMetSerLeuPhe	1480
Db	4312	CGGGGGTCCGGCAACAAGTCAACTTGGACACTTGGCCAGGCGCTCGATGCTCTGTTC	4371
Oy	1481	ValLeuAlaSerLysAspGlyYTrpValAspIleMetCysAspGlyLeuAspAlaValGly	1500
Db	4372	GTTTTGGCTCCCAAGATGTGGTGGTGAACATCATGACATGCAATGGCGTGAATGCTGGCG	4431
Oy	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
Db	4432	GTGACACGACGACCCATCATGAACACAAACCCCTGGATGCTCGTACTTCATCTCGTTC	4491
Oy	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheAlaGlyValValValGluAsnPhe	1540
Db	4492	CTGTCTCATTTGGGCTTTTGTTCGAAACATGTTGTGGGTGTGGTGGTGGAGAACTTC	4551
Oy	1541	HisLysCySArgGlnHisGlnGlnGluGlnGluAlaArgArgArgGlnGlnSlySArgLeu	1560
Db	4552	CACAAAGTGTGGCAGCACCAAGAGAAAGAGAGGCGCGCGCGAGAGAAAGCGCCTTA	4611
Oy	1561	ArgArgLeuGlnSlySlySArgArg-----LysAlaGlnCySlyS	1573
Db	4612	CGAAGACTGGAGAAAAGAAAGAGATGAAGAGAACAGATGCTGAAGCCCATGTCGAAA	4671
Oy	1574	ProGlyTyrSerAspLysTrpSerArgPheArgLeuLeuValHisHisLeuCyThrSerHis	1593



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GenCore version 5.1.6  
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OW protein - nucleic search, using frame\_plus\_p2n model

Run on: September 18, 2005, 16:26:56 / Search time 2305.32 Seconds  
(without alignments)  
5818.779 Million cell updates/sec

Title: US-09-611-257A-37  
Perfect score: 11904  
Sequence: 1 MDEEBGAGAEBSGQPRSF.....PKKDVLISGLSDPADLDP 2266

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL-frame+ p2n.model -DRV=xlh  
-O=/cg22\_1/USPTO.spool/US09611357/funat.15092005.134300.25163/app.query.fasta.1.4878  
-DB=N-Geneseq.16Dec04 -OPT=faetap -SUFFIX=ring -MINMATCH=0.1 -LOOFCU=0  
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MTN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pclo -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USR=US09611357 @CGN.1.1.3609 @runat.15092005.134300.25163 -NCPU=6 -ICPU=3  
-NO MAP -LARGEOUTRY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC  
-FEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N-Geneseq.16Dec04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11877.5	99.8	7741	4	AAD04756 Human T-t
2	11874	99.7	6892	5	AAE31684 Human alp
3	11815.5	99.3	7648	13	ADQ89063 Human vol
4	11815.5	99.3	7648	13	ADSI6298 Human vol
5	11758.5	98.8	6729	2	AAx83484 Human T-t

6	11741	98.6	6750	2	AAx83481	AAx83481 Human T-t
7	11735.5	98.6	6783	2	AAx83482	AAx83482 Human T-t
8	11727	98.5	6804	2	AAx83483	AAx83483 Human T-t
9	11627.5	97.7	8002	4	AAH98402	AAH98402 Human EST
10	11111	93.3	7286	3	AAZ52309	AAZ52309 Rat pancr
11	10962.5	92.1	6741	2	AAx83488	AAx83488 Rat T-cyp
12	10945	91.9	6762	2	AAx83485	AAx83485 Rat T-cyp
13	10945	91.9	6942	13	ADSI6295	ADSI6295 Rat volta
14	10939.5	91.9	6795	2	AAx83486	AAx83486 Rat T-cyp
15	10925	91.8	6816	2	AAx83487	AAx83487 Rat T-cyp
16	10890.5	91.5	7540	5	AAE31677	AAE31677 Rat alpha
17	6315.5	53.1	3393	4	AAE31678	AAE31678 Rat alpha
18	6222	52.3	7898	2	AAx59081	AAx59081 Human act
19	6216.5	52.2	7898	2	AAx59081	AAx59081 Human act
20	6215.5	52.2	7898	8	ABZ58365	ABZ58365 Human T-t
21	6214.5	52.2	7898	2	AAx59080	AAx59080 Human act
22	5902.5	49.6	6114	2	AAx83490	AAx83490 Human T-t
23	5892.5	49.5	6132	2	AAx83489	AAx83489 Human T-t
24	5713	48.0	6941	2	AAx59082	AAx59082 Human act
25	5496.5	46.2	6990	13	ADSI6296	ADSI6296 Human vol
26	5492.5	46.1	6816	6	AAx59082	AAx59082 Human act
27	5492.5	46.1	6816	8	AAx59082	AAx59082 Human act
28	5492.5	46.1	6816	12	ADH69264	ADH69264 Human T-t
29	5484	46.1	6855	6	AAx59082	AAx59082 Human act
30	5484	46.1	6855	8	ABX93561	ABX93561 Human T-t
31	5484	46.1	6855	12	ADH69266	ADH69266 Human T-t
32	5418.5	45.5	6503	12	ADH69275	ADH69275 Human T-t
33	5366	45.1	5505	2	AAx83492	AAx83492 Human T-t
34	5361.5	45.0	5469	2	AAx83491	AAx83491 Human T-t
35	5209	43.8	5735	5	AAE31679	AAE31679 Rat brain
36	4013.5	33.7	7969	4	ABLO7263	ABLO7263 Drosophil
37	3959.5	33.3	5562	2	AAV57542	AAV57542 Human cal
38	3959.5	33.3	5562	5	AAE31674	AAE31674 Human cal
39	3867	32.5	6073	13	ADSI6299	ADSI6299 C. elegan
40	3461.5	29.1	6933	5	AAE31674	AAE31674 Human cal
41	3427	28.8	2212	5	AAE31681	AAE31681 Human alp
42	2140	18.0	3464	4	AAK94358	AAK94358 Human ful
43	2140	18.0	3464	12	ADJ10400	ADJ10400 Pull leng
44	1971.5	16.6	1669	2	AAx59083	AAx59083 Human act
45	1788.5	15.0	7362	2	AAQ37817	AAQ37817 Sequence

ALIGNMENTS

RESULT 1  
ID AAD04756 standard; cDNA; 7741 BP.  
XX AAD04756;  
DT 17-JUL-2001 (first entry)  
DE Human T-type low voltage activated calcium channel alpha1G-c cDNA.  
XX Human T-type low voltage activated calcium channel alpha1G-c; stress;  
KW epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease;  
KW endocrine disorder; respiratory disorder; peripheral muscle disorder;  
KW muscle excitability; fertilization; contraception; hypertension;  
KW neuronal firing regulation; cardiovascular disorder; gene therapy;  
KW forensic analysis; epidemiological study; neuroleptic; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT 1..522 /\*tag= a  
FT 5'UTR 523..7344  
FT CDS /\*tag= b  
FT /product= "Human T-type low voltage activated calcium  
FT channel alpha1G-c protein"  
FT /transl\_except= (pos:3934..3936, aa:Gln)  
FT /transl\_except= (pos:3946..3948, aa:Gln)  
FT /transl\_except= (pos:5560..5562, aa:Pro)





QY 441 ValTYRILLeuNrglysaIaAlaArgArgLeuNlaGlnValSerArgAlaAlaGlyVal 460  
DB 1843 GTGTAACATCTTGTGTAAGGACGCCGAGGCTGGCTCAGGCTCTCCGGGACGAGGTGTG 1902  
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGlnProGlnProSerSer 480  
DB 1903 CGGGTTGGGTGTGCACAGACCCGACACCTTCGGGGCCGAGGAGCCAGCCAGACG 1962  
QY 481 SerCysSerArgSerSerHisArgArgLeuSerValHisLeuValHisHisHisHis 500  
DB 1963 AGCTGCTTGTGCTCCACCCGCGCTTACCTCCACACCTGTGTGCACACACACAC 2022  
QY 501 HisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 520  
DB 2023 CATCACACACACACACACCTGGGCAATGGGACGCTCAGGGGCCCCCGGAGCCGAG 2082  
QY 521 TLeGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540  
DB 2083 ATCCAGACAGGGAGTGCATAGGGGTCCCGCAGCTCAGCTGACACACACCTGACGCT 2142  
QY 541 AlaLeuSerGlyAlaProProGlyValAlaGlySerValHisSerPheTYRHisAlaAsp 560  
DB 2143 GCCCTTCCGGGGCCCCCTGTGTGGCGAGAGTCTGTGCACAGCTTCTACCATGCCGAC 2202  
QY 561 CysHisLeuGlnProValArgCysGlnAlaProProProArgSerProSerGlyAlaSer 580  
DB 2203 TGCCACTTAAGACGATCCGCTGCAGGCGCCCTCCAGGTCCCATCTGAGAGCATCC 2262  
QY 581 GlyArgThrValGlySerGlyValValTYRProThrValHisThrSerProProProGln 600  
DB 2263 GGCAGGACTGTGGCAGCGGAGAGTGTATCCACCGTGACACACAGCCCTCCACCGAG 2322  
QY 601 ThrLeuLeuValGlyValAlaLeuValGlyValAlaLeuSerSerGlyProProThrLeuThr 620  
DB 2323 AGCTGAAGGAGGAGGACTGTAGAGGTGGCTGCCAGCTTGGGCCCCCACCCTCAC 2382  
QY 621 SerLeuAsnLLeuProProGlyProTYRSerSerMetHisLeuLeuGlnThrGlnSer 640  
DB 2383 AGCTCAACATCCACCCGGGCCCCCTACAGCTCCATGACCAAGCTGTGAGACACAGAGT 2442  
QY 641 ThrGlyAlaCysGlnSerSerCysValAlaLeuSerProCysLeuValAlaAspSerGly 660  
DB 2443 ACAGGTGCTGCCAAAGCTCTTGGCAAGATCTCCAGCCCTTCTTGAAAGCAGACAGTGA 2502  
QY 661 AlaCysGlyProAspSerCysProTYRCysAlaArgAlaGlyAlaGlyGlyValGlyLeu 680  
DB 2503 GCTGTGTGTCCAGACAGCTGCCCTTACTGTGTCCGGGCGGGGAGGGAGGTGAAGCTC 2562  
QY 681 AlaAspArgGlnMetProAspSerAspSerGlnAlaValTYRGluphetThrGlnAspAla 700  
DB 2563 GCCACCTGTAATTCCTGACTCAGACAGCAGAGGAGTTTATGATTACACAGAGATGCC 2622  
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
DB 2623 CAGCAGCAGGACCTCCGGGACCCCAACGCGCGGCAACGAGCCTGTGGCCACAGATGA 2682  
QY 721 GluproSerSerValLeuAlaPheThrArgLeuHisCysAspThrPheArgLysIleVal 740  
DB 2683 GAGCCCAAGCTGTGTGTGCTTCTGTGAGGCTTAATCTGTGACCTTCCGAAAGTTGTG 2742  
QY 741 AspSerLysTYRPhenGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
DB 2743 GACAGCAAGTACTTTGGCCGGGGAATCATGATCCGATCTGTGTCAACACACTCAGCATG 2802  
QY 761 GlyIleGlyTYRHisGlnGlnProGlnGlnLeuThrAsnAlaLeuGlnIleSerAsnIle 780  
DB 2803 GGCATTCGAATACACAGACAGCCGAGAGGCTTACCAAGCCCTTAAGAAATCAGCAACATC 2862  
QY 781 ValPheThrSerLeuPheAlaLeuGlnMetLeuLeuValLeuLeuValTYRGIYProPhe 800  
DB 2863 GTCTTACCAAGCTCTTGTGCTGTGAGATGCTGTGAAAGCTGCTTGTGTATGTCTCTTT 2922

QY 801 GlyTYRILLeuAsnProTYRAsnLLeuPheAspGlyValIleValValIleSerValTYR 820  
DB 2923 GGTCAACATCAAGATCTCTTACACATCTTCGATGTGTATCTGTGCTACACCGGTGTG 2982  
QY 821 GluIleValGlyGlnGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
DB 2983 GAGATGTGGGCCAGACAGGGGGGGCGGCTGTGGTGTCTCGGACCTTCGCGCTGATGGCT 3042  
QY 841 ValLeuLeuLeuValLArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860  
DB 3043 GTGCTAAGCTGTGTGTCTTCCGCGGCTGCACAGCCAGCTGTGTGTGTGTGTGTGAAG 3102  
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuMetLeuPheIlePheIlePheSer 880  
DB 3103 ACCATGACAACTGTGCACCTTCTGACATGTCTTATGCTTCTTCACTTCACTTCACTGAC 3162  
QY 881 TLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGlyLysArgAspGlyAspThrLeu 900  
DB 3163 ATCTGGGACATGATCTCTTGGCTGCAGATTGGCTGTGAGCGGATGGGACACCTTG 3222  
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTPAlaIleValTYRValPheGlnIleLeu 920  
DB 3223 CCAGACCGGAAGATTGTAATCTTGTCTGTGGCCATGTCACTGTCTTTCAGATCTG 3282  
QY 921 ThrGlnGlnAspThrAsnLeuValLeuTYRAsnGlyMetAlaSerThrSerSerTPAla 940  
DB 3283 ACCCAGAGGACTGGAACAAAGTCTCTACAAAGTATGAGCTTCCACGTGCTCTGGGCG 3342  
QY 941 AlaLeuTYRPhelIleAlaLeuMetThrPheGlyAsnTYRValLeuPheAsnLeuLeuVal 960  
DB 3343 GCCCTTATTTCACTTCCCTCAGCTCAGCTTGGCACTAGCTGTCTTTCAATTTGGTGTG 3402  
QY 961 AlaIleLeuValGlnGlyPheGlnAlaGlnGlnIleSerLysArgGlyAspAlaSerGly 980  
DB 3403 GCCATCTGTGTGAGGCTTCCAGCGGAGAAATCAGCAACAGGAGATGCGAGTGA 3462  
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyValAspAlaAsnLysSerGln 1000  
DB 3463 CAGTTAAGCTGTATTCAGCTGTGTGACTCCAGGGGGGAATGCAACAGTCCGA 3522  
QY 1001 SerGlnProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu 1020  
DB 3523 TCAGAGCCCAATTTCTTCTCACCAAGCTGTGATGTGGGACAGGAAGTGTGTG 3582  
QY 1021 AlaLeuValSerLeuGlyGlnHisProGlnLeuArgLysSerLeuProProLeuIle 1040  
DB 3583 GCTGTGTGTCTCGGAGAGACCCGAGACTCGGAAAGCTGTGCGCGCTTCATC 3642  
QY 1041 TLeHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGln 1060  
DB 3643 ATCCACACGGCCGACACCAATGTGTGTCCCAAGAGCACACAGACGGGCTGTGGCGAG 3702  
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGlnProGlyAlaAla 1080  
DB 3703 GCGTGTGGCCCTGTGTGTGCGCCGACACAGACAGCGGTGTGGCAGGCTGTGGGCGGCG 3762  
QY 1081 HisGlnMetLysSerProProSerAlaArgSerSerProHisSerProTPSerAlaAla 1100  
DB 3763 CACGAGATGAAGTCAACGCCCAAGCGCCGACGCTTCCGACAGCCCTGAGAGGCTGCA 3822  
QY 1101 SerSerThrPheThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
DB 3823 AGCAGCTGACACAGCAGGCTCCAGCGGAAACAGCTCGGCGGTGACCCAGCCTGAG 3882  
QY 1121 ArgArgSerProSerGlyLysArgArgSerSerLeuLeuSerGlyGlnGlnGlnSerGln 1140  
DB 3883 CGGAGAGCCCAATGTGAAGCGCGCTCCCTGTGTGTGGGAGAGGCAAGGAGGAGCAG 3942  
QY 1141 AspGlnGlnGlnSerSerGlnGlnGlnArgAlaSerProAlaGlySerAspHisArgHis 1160  
DB 3943 GATGAAGAGGAGAGCTCAGAAAGAGAGCGGCGCACCTCGGGCAGTGTACATTCGCGAC 4002  
QY 1161 ArgGlySerLeuGlnAlaGlnAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180

4003 AGGGGCTCCCTGAGAGGGAGGCCAAGATTCTTTGACTGCGCAACACATCGACGGTG 4062  
1181 ProGlyLeuNhiSaRgThraLaSerGlyAArglySerAlaSerGluNhiSgLnAspCysAsn 1200  
4063 CCAGGGCTGCATGCATGCGCACTGGCCGAGGGGTGCTTCTTGAGCACCAGGACTGCAT 4122  
1201 GlyLysSerAlaSerGlyAArgLeuAlaArgAlaLeuNhiProAspAspProProLeuAsp 1220  
4123 GGCAAATCGGCTTCAGAGGCGCTGGCCCGGCGCTGCTGATATACCCCACTGAT 4182  
1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerGlyGlyValArgAlaTrpIle 1240  
4183 GGGGATGACCCCGATACAGAGGCCAACCTGAGCAAAAGGGAAAGGGTCCGCGGTGATC 4242  
1241 ArgAlaArgLeuProAlaCysTrpLeuGluAArgAspSerTrpSerAlaTrpIlePhePro 1260  
4243 CGAGCCCGAAGCTCCCTGCTGCTGCTGAGCGAGACTCCGTGTCAGCTTACCTTCCCT 4302  
1261 ProGlnSerAArgPheAArgLeuLeuCysHisAArgIleIleThrHisLysMetPheAspHis 1280  
4303 CCTCAATCCAGGTTCGCGCTCTGTGTACCCGATCATCACCAAGAAGTTTCGACAC 4362  
1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluAArgProLysIle 1300  
4363 GTGGTCTTGTCTCATCTTCTCTTAATCGATACCATCGCCATGAGCGCCCAAAATT 4422  
1301 AspProHisSerAlaGluAArgIlePheLeuThrLeuSerAsnTrpIlePheThrAlaVal 1320  
4423 GACCCCAACAGCGCTGAACGCACTTCTCGACCTCCCAATTACCTTCCACCGCAGTC 4482  
1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340  
4483 TTTCCTGCTGAATATGACATGAAAGTGTGTGCACTGAGCTGTGGAGGAGCGGCG 4542  
1341 TyrLeuAArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360  
4543 TACCTCGAGAGCATGTGGAAAGTGTGACGGGCTGTGGTCTCATCTCCGTCATCGAC 4602  
1361 IleLeuValSerMetValSerAspSerGlyTrpLysIleLeuGlyMetLeuAArgValLeu 1380  
4603 ATTCTGTGTCCATGTGCTCTGACAGCGGCAACCAATCTCGGGCATGTGAGGGTGTG 4662  
1381 ArgLeuLeuAArgThrLeuAArgProLeuAArgValIleSerAArgIleGlnGlyLeuLysLeu 1400  
4663 CGGCTCTGTGGACCCCTGCGCCGCTCAGGATATCAGCGGCGCAAGGGCTGAAGCTG 4722  
1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420  
4723 GTGGTGAAGACGCTGATGTCTCATCTGAACCAATCGGCAACATTGTATCATCTGCTGT 4782  
1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440  
4783 GCCTTCTTCTCATCTTTCCGCACTTGGGGGTGCACTCTTCAAGAGGAATTTTTCGTG 4842  
1441 CysGluGlyGluAspThrAArgAsnIleThrAsnLysSerAspCysValGlnAlaSerTrp 1460  
4843 TGCAGAGGCAAGATATCCAGAAATCATCAACCAATTAATTCGACTGTGCCAGAGCAATTC 4902  
1461 ArgTrpValAArgHisLysTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480  
4903 CGGTGGGTCCGGCAACAATCACTTGAACAACCTTGGCCAAGCCTGATGTCCCTGTTCC 4962  
1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTrpAArgGlyLeuAspAlaValGly 1500  
4963 GTTTTGGCTCCCAAGATGCTTGGGTGACATCATATGATGGCTGGATGTCTGTGGGC 5022  
1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuLysTrpPheIleSerPhe 1520  
5023 GTGGACCAAGAGCCCATCATGAACCAACCCCTGGATGTGCTGATCATCTGTGTTCC 5082  
1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPhe 1540

5083 CTGCTCATTTGCGCTTCTTGTCTTGAACATGTTTGTGGGNTGTGTGTGAGAACTTC 5142  
1541 HisLysCysAArgGlnHisGlnGluGluGlnValaAArgAArgGluGluLysAArgLeu 1560  
5143 CAAAGTGTGGCAGACACAGAGAGAGAGAGAGGCGCGCGCGAGAGAGAGGCGCTTA 5202  
1561 ArgAArgLeuGluLysLysAArgArg-----LysAlaGlnCysLys 1573  
5203 CGAAGACTGAGAAAAGAAAGAGAGTAAAGAGAACAGATGCTGMAAGCCAGAGCAAA 5262  
1574 ProTrpTrpSerAspTrpSerAArgPheAArgLeuValHisHisLeuCysThrSerHis 1593  
5263 CTTACTACTCCGACTACTCCCGCTTCCGGCTCTCGTCCACACTTGTGACACAGCCAC 5322  
1594 TyrLeuAspLeuPheIleThrGlyValIleGlyLysAsnValValThrMetAlaMetGlu 1613  
5323 TACCTGGACCTTTCATACAGAGTGTCAATGGGCTGAAAGTGTGCACATGAGCCATGAG 5382  
1614 HisTrpGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTrpIlePheThr 1633  
5383 CACTACAGACAGCCCAAGTTCTGATAGAGCTCGAAGATCTGCACTACATCTTCACT 5442  
1634 ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheAArgPhePhe 1653  
5443 GTCATCTTGTCTTGGAGTCAGTTTCAAACTTGTGGCTTGTTCCTGCGTTCCTTC 5502  
1654 GlnAspAArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr 1673  
5503 CAGGACAGGTGAAACACACTGACCTGGCCATTTGTGTGCTCATATAGGGCATACG 5562  
1674 LeuGluGluIleGlyValAsnAlaSerLeuProIleAsnProThrIleIleAArgIleMet 1693  
5563 CTGAGAAATGAGGTCAAGCTTCGCTGCGCCATCAACCCACATCATCCGATCATG 5622  
1694 ArgValLeuAArgIleAlaAArgValLeuLysLeuLeuLysMetAlaValGlyMetAArgAla 1713  
5623 AGGGTGTGGCATGCTCCGAGTGTGAAAGCTGTAAGATGTGCTGTGGGATGTGGGGCG 5682  
1714 LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet 1733  
5683 CTGTGGACACGGTATGAGGCGCTGCGCCAGGTGGGAACTGTGAACTTCTTCATG 5742  
1734 LeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp 1753  
5743 TTGCTGTTTTCATCTTTGACGCTGTGGCGTGAAGCTCTTTGAGAACCTGAGGTGAC 5802  
1754 GluThrHisProCysGluGlyLeuGlyAArgHisAlaThrPheAArgAsnPheGlyMetAla 1773  
5803 GAGACACACCCCTGTGAGGGGCTGTGGCGGTCAATGCCACTTTCGAACTTTGGCATGTGCC 5862  
1774 PheLeuThrLeuPheAArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr 1793  
5863 TTCTTAACCTTTCAGGTCTTCCAGGTGTCCAAGGTGCAATTGGAATGGAATTAAGAAACACC 5922  
1794 LeuAArgAspCysAspGlnGluSerThrCysTrpAsnThrValIleSerProIleTrpPhe 1813  
5923 CTCGGGACTGTGACCAAGAGTCCACCTGTCAACAACGATCATCTCGCTATCTACTTT 5982  
1814 ValSerPheValLeuThrAlaGlnPheValLeuValaAsnValIleAlaValLeuMet 1833  
5983 GTGCTCTTGTGCTGACGGCCAGTTTCGTGTAGTCAACAGTGTATGCGCCCTGTGATG 6042  
1834 LysHisLeuGluGluSerAsnLysGlnAlaLysGluGlnAlaGluLeuGlnAlaGluLeu 1853  
6043 AAGCACTTGAAGAAAGCAACAAGAGGCAAGAGGAGGCGGAGCTGAAGCTAGAGCTG 6102  
1854 GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu 1873  
6103 GAGCTGAGATAAACCTCATGAGCCCAAGCCCACTGCGCACTGGGAGGCCCTTCTCCTC 6162  
1874 TrpProGlyValGluGlyProAspSerProAspSerProLysProGlyValaLeuHisPro 1893  
6163 TGGCTGTGGGTGAGAGGCGCCGACAGCCCGACAGCCCAAGCTGTGGGCTCTGTGACCCA 6222

QY	1894	ALAAlaHisAlaArgSerAlaSerHisPheSerLeuGlnHisProThrMetGlnProHis	1913
Db	6223	GGGGCCACAGCGAGATCAGCTCCACCTTTTCCCTGGAGCAACCCACGATGACACCCAC	6282
QY	1914	ProThrGlnLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThr	1933
Db	6283	CCACGAGAGCTCCAGAGACCAAGATTACTAGCTGTGGGAAGTCTGGGGTCAAGCCGAAG	6342
QY	1934	HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeu	1953
Db	6343	CACCTCTGGCCCAATGACAGCTAATGTGTGGCATGGAGACCTGGCCGAGGGGCCCTGG	6402
QY	1954	GlnHisArgGlyTTPGlyLeuProLysAlaGlnSerGlySerValIleSerValHisSer	1973
Db	6403	GGACACAGGGGCTGGGGGCTCCCAAAAGCTACAGGCTCCGTCTTGTCCGTTCACTCC	6462
QY	1974	GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisIleLeuGln	1993
Db	6463	CAGCCACAGATACAGGCTACCTGACGCTTCCCAAAAGATGACCTCATCTCTCCAG	6522
QY	1994	ProHisSerAlaProThrTTPGlyThrIleProLysLeuProProGlyArgSerPro	2013
Db	6523	CCCCACAGCGCCCCAACCTGGGGGACCATCCCAAACTGCCCCACAGAGAGCTCCCT	6582
QY	2014	LeuAlaGlnArgProLeuArgArgGlnAlaIleArgThrAspSerLeuAspValGln	2033
Db	6583	TTGGCTCAGAGGCCACTCAGCGCGCAGGACACATTAAGACTGACTCTTGTGAGGTTAG	6642
QY	2034	GlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAla	2053
Db	6643	GGTGTGGGCAAGCCGGGAAGACTCTGTGCAGAGGTGAGTGGGCGCTCCCGCCCTGGCC	6702
QY	2054	ArgAlaTyrSerPheTTPGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis	2073
Db	6703	CGGGCCCTAATCTTTCTGGGGCCAGTCAAGTACCCAGGCAAGCACTCCCGCAGCCAC	6762
QY	2074	SerLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTTP	2093
Db	6763	AGCAAGATCTCCAGACCATGACCCCGCACCCCTTCCAGGCGCCAGAAACCAACTGG	6822
QY	2094	GlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGlnLeuSerTTPIle	2113
Db	6823	GGCAAGGGCCCTCCAGAGACCAAGACGCTTGAAGTGGACACAGACCTGAGCTGAGTT	6882
QY	2114	SerLysAspLeuLeuProProGlyGlyGlnGlnGluProProSerProArgAspLeuLys	2133
Db	6883	TCAAGAGACCTCTCGCCCCCTGGGGCCAGAGAGAGCCCATCCCAAGGGAAGCTGAAG	6942
QY	2134	LysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTTPLeuAspGlu	2153
Db	6943	AAGGTCTACAGCGTGAAGGCCAGAGCTGCCAGCGCCGAGCTTACCTCTGGCTGATAG	7002
QY	2154	GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisIleGlyLys	2173
Db	7003	CAGAGAGACCTCTATGCGCCGTCAAGCTGCTGGACACGGGCTCCCAACCCCACTGGGG	7062
QY	2174	ThrAspProSerAsnLeuGlyGlyGlnProLeuGlnGlyProGlySerArgProLysLys	2193
Db	7063	ACAGACCCCTTAACCTTGGGGGCGAGGCTCTTGGGGGGCCCGGAGCGGCCCAAGAA	7122
QY	2194	LysLeuSerProProSerIleThrIleAspProProGlnSerGlnGlyProArgThrPro	2213
Db	7123	AAACTCAGCCCCGCTAATATCAACATAACCCCCCGAGAGCAAGATGCTCTGGAGCCCCG	7182
QY	2214	ProSerProGlyIleCysLeuArgArgArgAlaProSerSerAspSerLysAspProLeu	2233
Db	7183	CCCAAGCCTGGATCTGCTCCGAGGAGAGGGGCTCGTCCAGAGACTTCAAGGATCCTTGG	7242
QY	2234	AlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSer	2253
Db	7243	GCCTCTGGCCCCCTCGACAGATGGCTGCTCGCTCCCAAAAGATATGTCTGTAGT	7302

QY	2254	LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro	2266
DB	7303	CTCTCGGTTTAACTCTGACCCAGACAGCTGSAACCC	7341
RESULT 2			
ID	AAAF31684		
XX	AAAF31684	standard; cDNA; 6892 BP.	
AC	AAAF31684;		
XX			
DT	09-APR-2001	(first entry)	
XX			
DE	Human alpha-IG T-type calcium channel cDNA.		
XX			
KW	Human; antiarrhythmic; anticonvulsant; hypotensive; cardiac; noctropic;		
KW	T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;		
KW	hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel;		
KW	ss.		
OS	Homo sapiens.		
XX			
XX	W0200102561-A2.		
PN			
PD	11-JAN-2001.		
XX			
XX	04-JUL-2000; 2000MO-CA000794.		
PF			
XX			
PR	02-JUL-1999; 99US-00346794.		
XX			
PA	(NEUR-) NEUROMED TECHNOLOGIES INC.		
XX			
P1	Snutch TP, Balllie DL;		
DR	WPI; 2001-123111/13.		
XX			
DR	P-PSDB; AAB66481.		
XX			
XX	Novel T-type calcium channel alpha-1 subunit gene useful for treating		
PT	cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and		
P7	epilepsy.		
XX			
PS	Example 3; Fig 6; 103pp; English.		
XX			
CC	The present sequence is given in a specification providing sequences and		
CC	partial sequences for three types of mammalian (human and rat) T-type		
CC	calcium channel subunits. An expression cassette has been generated which		
CC	comprises a nucleotide sequence encoding a T-type calcium channel alpha_1		
CC	subunit operably linked to control sequences to effect its expression.		
CC	The novel calcium channel nucleic acids and proteins are useful for		
CC	treating conditions characterised by undesirable levels of T-type calcium		
CC	channel activity such as cardiac hypertrophy, cardiac arrhythmia,		
CC	hypertension, sleep disorder and epilepsy		
XX			
SO	Sequence 6892 BP; 1315 A; 2223 C; 2017 G; 1337 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	0	Length:	6892
Score:	11874.00	Matches:	2261
Percent Similarity:	99.82%	Conservative:	1
Best Local Similarity:	99.78%	Mismatches:	4
Query Match:	99.75%	Indels:	0
DB:	5	Gaps:	0
US-09-611-257A-37 (1-2266) x AAFA31684 (1-6892)			
QY	1	MeAspGluGluGluAspGlyAlaGlyIleuSerGlyInProArgSerPheMet	20
DB	51	ATGAGCAGAGAGAGATGAGACGGGCGCCAGAGAGTGGGACAGCCCGAGGCTTCATG	110
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyIleuArgProGlyProGlySerAlaGlyIleuAsp	40
DB	111	CGGCTCAAGCACTGTCTGGGGGGCCGGGGCCGGGCGGGGCTCAGCAGAAAAGAC	170
QY	41	ProGlySerAlaAspSerGluAlaGluGlyIleuProTyrProAlaIleuAlaProVal	60

Db	171	CCGGGACCGGAGCTCCGAGCGGAGGGCGTCCGTA	CCCGGGCTGGGCGCCCGGAGT	230
Qy	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80	
Db	231	TTCTTCTACTTGACCAAGACAGCCGCCCGGAGCGTGTCTCCGCAAGCTCTGTAAC	290	
Qy	81	ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100	
Db	291	CCCTGGTTTGAGCCCATCAGCATGTGTGATCTCTTCAACTGCGGTGACCCCTGGGCAATG	350	
Qy	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120	
Db	351	TTCCGGCCATGCGAGCAATGCTGTGACTCCGAGCGCTGCGGATCTCGCAGGCGCTTT	410	
Qy	121	AspAspPheIlePheAlaPhePheAlaValAluMetValValIlyMetValAlaLeuGly	140	
Db	411	GATGACTTTCATCTTGGCTTCTTTGGCGGTGAGATGGTGGTGAAGATGGTGGCGCTTGGGC	470	
Qy	141	IlePheGlyIlySerCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal	160	
Db	471	ATCTTTGGGAAAAAGTGTACTACCTGGAGACACTTGGAAACCGGCTTGACTTTTCAATGCT	530	
Qy	161	IleAlaGlyMetLeuGlnTyrSerSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180	
Db	531	ATCCAGAGGAATGCTGGAGTACTCGCTGACCTGCAGAACTGCACTTCTCAGCTGTGAG	590	
Qy	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200	
Db	591	ACAAGTCCGTGCTGCGACCCGCTCAGGGCCATTACCGGGTGCACAGACGCCCACTCTT	650	
Qy	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220	
Db	651	GTCAGTGTGCTGGATACGCTCCCATGCTGGGGCAACGCTCGCTGCTCTCTTCTTCT	710	
Qy	221	ValPhePheIlePheGlyIleValGlyValGlnLeuThrAlaGlyLeuLeuArgAsnArg	240	
Db	711	GTCCTCTTCATCTTCGGATGCTGGGCGCTCAGCTGGGGCAGGGCGCTTGGAAACCGA	770	
Qy	241	CysPheLeuProGlnAsnPheSerLeuProLeuSerValAspLeuGlnArgTyrTyrGln	260	
Db	771	TGCTTCTTACTTGAAATTTTCAAGCTTCCCTTGAGCTGTGACCTGTGAGCCCTATTACAG	830	
Qy	261	ThrGlnAsnGlnAspGlnSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280	
Db	831	ACAGAGAACGAGATGAGAGAGCCCTTCATCTGCTCCAGCAAGCGGAGAACGGCATGCGG	890	
Qy	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300	
Db	891	TCCGCGAGAACGCGCCACGCTGCGCGGGACGGGGCGGTGGCCCACTTCGGGTCTG	950	
Qy	301	AspTyrGlnAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrPasnGlnTyrTyr	320	
Db	951	GACTATGAGGCTTCAACACAGCTCCAGCAACACCACTGTGTCACTGTGAACCGATCTAC	1010	
Qy	321	ThrAsnCysSerAlaGlyGlnHisAsnProPheGlyGlyAlaIleAsnPheAspAsnIle	340	
Db	1011	ACCAACTGCTCAGCGGGGAGACACACCCCTTCAAGGGCGCATCACTTTGACAACATT	1070	
Qy	341	GlyTyrAlaTyrPheAlaIlePheGlnValIleThrLeuGlnGlyTyrPheValAspIleMet	360	
Db	1071	GGCTATGCTGTGATCGCATCTTCCAGGTATCAAGCTGAGGGCTGGGTGCAATCATG	1130	
Qy	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380	
Db	1131	TACTTTGTGATGAGATGCTATCTTCTTCAACATTTCATCTTCACTTCTTCATCATC	1190	
Qy	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGln	400	
Db	1191	GTCGGGCTCTTCTTCAATCAATCACTGCTGCTGGTGTGATGTGACGAGGTTCTCAGAG	1250	
Qy	401	ThrIyGlnArgGlnSerGlnLeuMetArgGlnGlnArgValArgPheLeuSerAsnAla	420	
Db	1251	ACCAAGCAGCGGAAAGCCACTGATGCGGAGACAGGTGTGGGCTTCTGTCCAAAGCC	1310	
Qy	421	SerThrLeuAlaSerPheSerGlnProGlySerCysTyrGlnGlnLeuLeuTyrLeu	440	
Db	1311	AGCACTTGCTGACTTCTTGACCCCGGAGCTGCTATGAGAGAGCTGTCCAAAGTACTTG	1370	
Qy	441	ValTyrIleLeuArgGlyAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460	
Db	1371	GTGTACATCTTCTGTGAAGCAGCCGAGGTGTGCTGAGCTTCTGGAGCAGAGGTGTG	1430	
Qy	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlnGlnThrGlnProSerSer	480	
Db	1431	CGGCTGGCGCTCAGACGCCACAGCACTCCGCGGGGCGAGAGACCCAGCCCAAGCAGC	1490	
Qy	481	SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisIleHisHis	500	
Db	1491	AGCTGCTCTCCCTCCACCGCGGCTATCCGTCCACCACTGTGACCACTCAACAC	1550	
Qy	501	HisHisHisIleTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520	
Db	1551	CATCAACCACTACACCTTGGGAAATGGAGCGTCAAGGGCGCCCGAGCCAGCCGAG	1610	
Qy	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro	540	
Db	1611	ATCCAGACAGGAGATGCCAATGGTCCCGAGCTCATGCTGCCACCACTCGACCCCT	1670	
Qy	541	AlaLeuSerGlyAlaProProGlyGlyValAlaGlnSerValHisSerPheTyrHisAlaAsp	560	
Db	1671	GCCCTCCCGGGGCCCCCTGTGTGGCAGAGCTGTGACAGCTTCTACATGCGCGAC	1730	
Qy	561	CysHisIleGlnProValArgCysGlnAlaProProProArgSerProSerGlnAlaSer	580	
Db	1731	TGCCATTAGACCAAGTCCGTGCGACGGCGCCCTCCAGGTCCCATCTGAGGCAATCC	1790	
Qy	581	GlyArgThrValGlySerGlyIleValTyrProThrValHisThrSerProProProGlu	600	
Db	1791	GCGAGACTGTGGGACGGAGAGGTGTATCCACCTGTGACACACCACTCTCCACCGGAG	1850	
Qy	601	ThrLeuGlyGlnValAlaLeuValGlnValAlaIleSerSerGlyProProThrLeuThr	620	
Db	1851	ACGCTGAAGAGAGAGCACTGTATGAGGTGTGCTGACGTCTGGGCCCCCAACCTCACC	1910	
Qy	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisIlyIleLeuGlnThrGlnSer	640	
Db	1911	AGCCTCAACATCCACCCGGGCGCTCAGCTTCATGCAAGCAAGCTGTGAGAACACAAGT	1970	
Qy	641	ThrGlyAlaCysGlnSerSerCysIlyIleSerSerProCysLeuValAlaAspSerGly	660	
Db	1971	ACAGGTGCTCGCAAGCTCTTGGAAATCTCCAGCCCTTCTGAAAGCAGACAGTGA	2030	
Qy	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyValGlnLeu	680	
Db	2031	GCTGTGTGCCAAGACGTGCCCTTCACTGTGCTCCGGGCGGAGGAGGTGAGACTC	2090	
Qy	681	AlaAspArgGlnMetProAspSerAspSerGlnAlaValTyrGlnUpheThrGlnAspAla	700	
Db	2091	GCCGACCGGTAAATGCTCACTCAGACAGCAGGACAGTTATGAGTTACACACAGAGTGC	2150	
Qy	701	GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla	720	
Db	2151	CAGCAGAGGACTCCGGGACCCCGACAGCGGGCGGACAGGACCTGGGCCCGCATGCA	2210	
Qy	721	GluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgIlyIleVal	740	
Db	2211	GAGCCCACTCTGTGCTGGCTTCTGAGAGGTTATTCGTGTGACACTTCCGAAATGTTGTG	2270	
Qy	741	AspSerIlyTyrPheGlyArgGlyTylMetIleAlaIleLeuValAsnThrLeuSerMet	760	
Db	2271	GACACCAAGTACTTTGGCGGGGAATCATGATCCCATCTCGTCAACACACTCAGCATG	2330	
Qy	761	GlyIleGlnTyrHisGlnGlnProGlnGlnLeuThrAsnAlaLeuGlnIlySerAsnIle	780	
Db	2331	GGCATCGAATACCAAGACCAAGCCGAGAGGCTTACCAAGCGCTTGAAGAAATACGAACTC	2390	

Qy	781	ValPheThiSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPhe	800
Db	2391	GTCTTCACCAAGCCCTTTCGCCCTGGAAATCTCTGTGAAGCTGCTGTGTAATGGCTCTT	2450
Qy	801	GlyTyrLysAspProTyrAsnLysPheAspGlyValLysValLysSerValTyr	820
Db	2451	GGCTACATCAAGATCCCTTACACATCTTGATGTGTCAATTGGTGATCAACGGTGTGG	2510
Qy	821	GluLysLeuGlyGlnGlnGlyGlyLysSerValLeuArgThrPheArgLeuMetArg	840
Db	2511	GAGATCGTGGGCCGACGAGGGGGGGCGCTGTGGGTGTGGGACCTTCGCCCTGATCGCT	2570
Qy	841	ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys	860
Db	2571	GTGCTGAAGCTGGGCGCCTTCTTCCGCGCGGTGAGGGAGCTGGGTGGTCCATGAAG	2630
Qy	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheLysPheSer	880
Db	2631	ACCATGACACACGTGGCCACCTTTCGATGTGCTTATGCTCTTCAATCTTCAATTCAGC	2690
Qy	881	LysLeuGlyMetCHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu	900
Db	2691	ATCTGGGCAATGCATCTTCTTGCGCTGCAAGTTTCTCTGAGCGGATGGGACACCTGT	2750
Qy	901	ProAspArgLysAsnPheAspSerLeuLeuThrAlaLysValThrValPheGlnLysLeu	920
Db	2751	CCAAACCGGAAGAATTTTGACTCCTTCTCGGGCCATCGTCACTGTCTTCAATCTTCAAT	2810
Qy	921	ThrGlnGluAspTyrAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTyrAla	940
Db	2811	ACCCAGAGAGACTGGACAAAGTCTCTTCAATGTATGGCTCCAGCTGTCTCTGGGGCG	2870
Qy	941	AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal	960
Db	2871	GCCCTTATTTCATTTGCCCTCATACCTTCGGCAACTACGGTCTTCAATTGGCTGTCTC	2930
Qy	961	AlaLysLeuValGluGlyPheGlnAlaGluGlnLysSerLysArgGluAsnAlaSerGly	980
Db	2931	GCCATTCTGTGGAGGGCTTCCAGCGGAGAAATCAGCAACCGGAAGATGCCAGTGGGA	2990
Qy	981	GlnLeuSerCysLysGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu	1000
Db	2991	CAGTTAAGCTATATTCAGTCTGCTGTGACTCCAGGGGGGGAAGATGCCAACAGTCCGAA	3050
Qy	1001	SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu	1020
Db	3051	TCAAGAGCCGATTTCTTCTCAACCCAGCTGGATGTATGGGGACAGAAAGATGCTTGTG	3110
Qy	1021	AlaLeuValSerLeuGlyLysHisProGluLeuArgLysSerLeuLeuProProLeuIle	1040
Db	3111	GCCTTGGTGTCCTCGGAGAGCACCCGGAGCTGGGAAGACCTGTGGCGCTCTCATTC	3170
Qy	1041	IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLysGlyLys	1060
Db	3171	ATCCACACGCGCGCCACACCATGTGCTGCCCAAGACACCAACGCGGCTGTGGCGAG	3230
Qy	1061	AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyValAla	1080
Db	3231	GCGCTGGGCCCTCGTGGTGGCGCCGACCAAGACGGGTGGGACAGAGCTGGGGCGGCC	3290
Qy	1081	HisGluMetLysSerProProSerThrAlaArgSerProHisLysSerProTyrMetSerAla	1100
Db	3291	CACAGAGTAAGTACCGCCACGCGCCGCAAGCTTCCGACAGCCCTCGAGGCGCTGCA	3350
Qy	1101	SerSerTyrThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys	1120
Db	3351	AGCAGCTGACACGAGGCGCTCCAGCCGGAACAGCTCGGCCCGGACCCAGCCTGAAG	3410
Qy	1121	ArgArgSerProSerGlyLysArgArgSerLeuLeuSerGlyLysGlyGlnLysSerGln	1140
Db	3411	CGGAGAACCCCAAGTGAAGACGGCGGTCTCTGTGTTCGGAGAAAGCCAGAAAGCCAG	3470

[illegible]

Db	4551	GTGACACGAGAGCCCATCATGAAACCAACACCCCTGGATGCTCTGACTTCACTTCGTGC	Db	5631	AGCCCCAGCCCACTCGGCACATGGGAGAGCCCTTCTCTGGCTGGGCTGGAAGGCCCC	5630
Qy	1521	LeuLeuLlValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnDhe	Qy	1881	AspSerProAspSerProIysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla	1900
Db	4611	CTGCTCATTTGTGGCTCTTCTTGTCTCGAACAATGTTGTGTGGTGGTGGAGAACAATTC	Db	5691	GACAGCCCCGACAGCCCCCAAGCCTGGGGCTCTGCACCCAGCGGGCCACGCAAGATCAAGCC	5750
Qy	1541	HisIysCysArgGlnHisGlnGlnGlnGlnGlnAlaArgArgArgGlnGlnIlysArgLeu	Qy	1901	SerHisPheSerLeuGlnHisProThrMetGlnProHisProThrGlnLeuProGlyPro	1920
Db	4671	CACAAAGTGTAGGACGACACGAGAGAAAGAGAGCCCGCGCGGAGGAGAGAAAGCCCTA	Db	5751	TCCCACTTTTCCCTGGAGACACCCACAGATGAGGCCACCCACGAGACTCCACAGACA	5810
Qy	1561	ArgArgLeuGlnIlysIysArgArgIysAlaGlnCysIysProDlyThrSerAspIysSer	Qy	1921	AspLeuLeuThrValArgIysSerGlyValSerArgThrHisSerLeuProAsnAspSer	1940
Db	4731	CGAAGACTGAGAAAAAGAGAAAGAAAGCCCACTGTGAAACCTTACTACTCCCACTACTCC	Db	5811	GACTTACTGACTGTGGGAGAGAGCTGGGGGTCAAGCCGACGCACTCTCTGCCAATGACAGC	5870
Qy	1581	ArgPheArgLeuLeuValHisHisIleuCysThrSerHisSerTyrlleuAspLeuPheIleThr	Qy	1941	TyrMetCysArgHisGlySerThrAlaGlnGlyProLeuGlnGlyHisArgGlyTyrGlyLeu	1960
Db	4791	CGCTTCGGGCTCTCTGCTCCACCACTGTGTGACACGACCACTACTGGACCTCTTCACTACA	Db	5871	TACATGTGTGGCATGTGAGAGCACTGGCGAGGGCCCTTGGGACACAGGGGCTGGGGGCTC	5930
Qy	1601	GlyValIleGlyIleuAsnValIleThrMetAlaMetGlnHisSerTyrlnglnProGlnIle	Qy	1961	ProIysAlaGlnSerGlySerValIleuSerValHisSerGlnProAlaAspThrSerTyr	1980
Db	4851	GGTGTCAATCGGGCTGAAACGTAATCACCAATGGCCATGAGACACTACACAGAGCCCAATT	Db	5931	CCCAAAAGCTCAGACAGGCTCGCTTGTCCGTTCCTCACTCCAGCCAGCAAGATCAAGCTTAC	5990
Qy	1621	LeuAspGlnAlaLeuIysIleCysAsnTyrIlePheThrValIlePheValIleuGlnSer	Qy	1981	IleLeuGlnLeuProIysAspAlaProHisIleuGlnProHisSerAlaProThrTyr	2000
Db	4911	CTGATATAGGCTCTGAAAGATCTGCAACTCATCTTCACTGTATCTTGTCTGTGAGTCA	Db	5991	ATCTTGACGCTTCCCAAAATGACACTATCTGTCTTCAGGCCCAAGGCCCAACTCGG	6050
Qy	1641	ValPheIysLeuValAlaPheGlyPheArgArgPheGlnAspArgTyrAsnGlnIleu	Qy	2001	GlyThrIleProIysLeuProProGlyArgSerProLeuAlaGlnIysProLeuArg	2020
Db	4971	GTTTTCAAACTTGTGGCTTGTGGTTTCCGTGGTCTTCTTCACGAGCAGGTGGAAACAGCTG	Db	6051	GGCACCATCCCCAAATGCGCCCCCAACAGGACGCTCCCTTGTGGCTCAGAGGCACTCAGG	6110
Qy	1661	AspLeuAlaIleValLeuIleuSerIleMetGlyIleThrIleuGlnGlnIleGlyValAsn	Qy	2021	ArgGlnAlaAlaIleArgThrAspSerIleuAspValGlnGlyIleuGlySerArgGlnAsp	2040
Db	5031	GACCTGGCCATGTGCTGTGCATCATATGAGGCATCAGCCGTGAGGAAATTCAGAGTCAAC	Db	6111	CGCCAGCAGCAATTAAGACTACTCTTGGACGTTACAGGGCTGTGGAGCGCGGAGAAAC	6170
Qy	1681	AlaSerIleuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	Qy	2041	LeuLeuAlaGlyValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTyrGly	2060
Db	5091	GCCCTGGCTGCCATCAACCCACCATCATCTCCGATCATAGAGGGTGTGGCATTTCCCGCA	Db	6171	CTGTGGCAGAGGTGAGTGGGCTCTCCCGCCCTCGCCGCGGCTTACTCTTTCTGGGGC	6230
Qy	1701	ValLeuIysIleuIysMetAlaValGlyMetArgAlaIleuIleuAspThrValMetGln	Qy	2061	GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerIysIleSerIysHisMet	2080
Db	5151	GTGCTGAAGCTGCTGAGAGATGGCTGTGGGCATCGGGCGCTGTGGACACGGTGAATGCG	Db	6231	CAGTCAAGTACCCAGGACAGGAGCACTCCGACACCAAGCAAGATCTCCAAAGCACATG	6290
Qy	1721	AlaLeuProGlnIvalGlyAsnLeuGlyIleuIleuPheMetLeuIleuPhePheIlePheAla	Qy	2081	ThrProProAlaProCysProGlyProGlnProAlantTyrGlyIysGlyProProGlnIthr	2100
Db	5211	GCCTTGCCCCAGGAGGGGAAACCTGGGACCTTCTCATGTGTGTGTTTTCATCTTTGCA	Db	6291	ACCCCGCAGCCCTTGGCCCAAGCCCAAGAACCACTGGGGAGAGGGCCCTCCAGAGACC	6350
Qy	1741	AlaLeuGlyValGlnLeuPheGlyIysAspLeuGlnCysAspGlnIthrHisProCysGlnGly	Qy	2101	ArgSerSerLeuGlnIleuAspThrGlnIleuSerTyrIleSerGlyAspLeuLeuProPro	2120
Db	5271	GCTCTGGGCGGTGGAGCTCTTTGGAGACCTGGAGTGTGAGCAGACACACCCCTGTAGGGCC	Db	6351	AGAAAGCAGCTTAAGTTGAGACAGAGACTGAGACTGATTTTCAGAGACCTCTGCCCTCT	6410
Qy	1761	LeuGlyIyrHisAlaThrPheArgAsnPheGlyMetAlaPheIleuThrIleuPheArgVal	Qy	2121	GlyGlyGlnGlnGlnIupProProSerProArgAspLeuIysIysCysTyrSerValGlnAla	2140
Db	5331	CTGGGCGGTCAATGCACTTTCGAACTTGGCAATGAGCTTCTTCAACCTCTTCGAGATC	Db	6411	GGCGGCAAGAGAGGCCCATCTCCAGCGGACCTGAAGAAGTCTTACAGCGTGGAGCC	6470
Qy	1781	SerThrGlyAspAsnTyrPasnGlyIleMetIysAspThrIleuArgAspCysAspGlnGln	Qy	2141	GlnSerCysGlnArgArgProThrSerTyrPheAspGlnGlnIysArgHisSerIleAla	2160
Db	5391	TCCCAAGGTGACATATGGATGGCATTTAAGAAGACACCCCTCGGGACGTGACCAAGAG	Db	6471	CAGAGCTGCAGAGCGCGGCTACGCTCTGGCTGGATGTGACAGAGAGACACTATATCCCC	6530
Qy	1801	SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValIleuThrAla	Qy	2161	ValSerCysIleuAspSerGlySerGlnProHisIleuGlyIthrAspProSerAsnLeuGly	2180
Db	5451	TTCACCTGTACAACAACGATCATCTCGCTCATCTACTTGTGTCTTCCGTGTGACGGCC	Db	6531	GTCAGCTGCTGGACAGCGGCTCCCAACCCACCTGGGACAGACACCCCTTACACTTGGG	6590
Qy	1821	GlnPheValIleuValAsnValValIleAlaValIleuMetIysHisIleuGlnIuserAsn	Qy	2181	GlyGlnProLeuGlnGlyIProGlySerArgProIysIysIysIysIysLeuSerProProSerIle	2200
Db	5511	CAGTTTCGTGCTAGTCAACGTTGTGATGCGCTGTCTATGAAGACCTGTGAGAGAGCAAC	Db	6591	GGCCAGCTCTTGGGGGGCTGGAGCGCGGCCCAAGAAAAAACTCAGCCCGCTAGTATC	6650
Qy	1841	LysGlnAlaIysGlnGlnIvalGlnLeuGlnAlaGlnIleuGlnIleuMetIysThrIleu	Qy	2201	ThrIleAspProProGlnIserGlnGlyProArgTyrProProSerProGlyIleCysLeu	2220
Db	5571	AAGAGAGCCAAAGAGAGAGCGCGAGCTAGAGGCTGAGCTGGAGCTGGAAGATGAAGCCCTC	Db	6651	ACCATAGACCCCCGAGAGCAAGGCTCTCGAGACCCGCGCCAGCCCTGTGATCTGCTCTC	6710
Qy	1861	SerProGlnProHisSerProLeuGlySerProPheLeuTyrProGlyValGlnGlyPro	Qy	2221	ArgArgArgAlaProSerSerAspSerIysAspProLeuAlaSerGlyProProAspSer	2240
Db	1880		Db	6711	CGAGAGAGGGCTCTCGTTCAGCACTCCAAAGATATCCCTTGCGCTCTGGCGCCCTTCAGACG	6770



QY 2241 MetAlaIaSerProSerProLyAlaValLeuSerLeuSerGlyLeuSerSerAsp 2260  
CC |||||  
XX ATGGCTGCTCTGCGCCCTCCCAAGAAAGATGCTGAGTCTCTCCGGTTATCTCTGAC 6830  
DB 6771

QY 2261 ProAlaIaSerProSerPro 2266  
CC |||||  
XX 6831 CCAGCAGACCTGAGACCC 6848  
DB

RESULT 3  
ADQ89063  
ID ADQ89063 standard; cDNA; 7648 BP.  
AC  
XX ADQ89063;  
XX  
XX 21-OCT-2004 (first entry)  
XX  
XX Human urological disorder related protein 4421 encoding cDNA SEQ.15.  
DE  
XX urological disorder; uropathic; cytostatic; urinary incontinence;  
KW benign prostatic hyperplasia; human; gene; ss.  
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XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH 1. 7134  
FT CDS /tag= a  
FT /product= "urological disorder related protein 4421"  
PN  
XX W02004065576-A2.  
XX  
XX 05-AUG-2004.  
XX  
XX 14-JAN-2004; 2004WO-US000750.  
XX  
XX 15-JAN-2003; 2003US-0440318P.  
PR 04-FEB-2003; 2003US-044783P.  
PR 27-MAR-2003; 2003US-0457901P.  
PR 08-MAY-2003; 2003US-0468775P.  
PR 19-MAY-2003; 2003US-0471614P.  
PR 16-JUN-2003; 2003US-0478742P.  
PR 18-JUL-2003; 2003US-0488529P.  
PR 30-JUL-2003; 2003US-0491156P.  
PR 02-SEP-2003; 2003US-0495949P.  
PR 26-SEP-2003; 2003US-0506332P.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
PA  
XX Karicheti V, Siles-Santiago I, Eliasof SD;  
PI MPI; 2004-562167/54.  
DR P-PDB; ADQ89064.  
XX  
XX  
XX Use of polypeptides related to urological disorders, e.g. 44390, 54181,  
PT 211 or for identifying a compound capable of treating a urological  
PT disorder or identifying and treating a subject having a urological  
PT disorder.  
XX  
XX Claim 1; SEQ ID NO 15; 542pp; English.  
PS  
XX  
XX The present invention describes the use of polypeptides related to  
CC urological disorders for identifying a compound capable of treating a  
CC urological disorder, identifying a subject having a urological disorder,  
CC or treating a subject having a urological disorder. Also described: (1) a  
CC method for identifying a compound capable of treating a urological  
CC disorder; (2) a method for identifying a subject having a urological  
CC disorder; and (3) a method for treating a subject having a urological  
CC disorder. The compound has uropathic and cytostatic activities. The  
CC polypeptides related to urological disorders are useful for identifying a  
CC compound capable of treating a urological disorder, identifying a subject  
CC having a urological disorder, or treating a subject having a urological  
CC disorder. Disorders include urinary incontinence and benign prostatic  
CC hyperplasia. The present sequence encodes a human urological disorder

CC related protein, which is used in the exemplification of the present  
CC invention.  
XX  
XX Sequence 7648 BP; 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;  
SQ

Alignment Scores:  
Pred. No.: 0 Length: 7648  
Score: 11815.50 Matches: 2264  
Percent Similarity: 95.29% Conservative: 1  
Best Local Similarity: 95.25% Mismatches: 111  
Query Match: 99.26% Indels: 2  
DB: Gaps: 13

US-09-611-257a-37 (1-2266) x ADQ89063 (1-7648)

QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20  
CC |||||  
XX 1 ATGGACGAGGAGGAGGATGAGCGGGGCGCGAGGAGCGGAGACGCCCGGAGCTTCATG 60  
DB

QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyAlaArgProGlyPProGlySerAlaGlyValAsp 40  
CC |||||  
XX 61 CGGCTCAACGACCTGTCGGGGGCGGGGGCGGGCGGGCGGGGCTCAAGAAAGAGAC 120  
DB

QY 41 ProGlySerAlaAspSerGlyAlaGlyAlaGlyLeuProTyrProAlaLeuAlaProValVal 60  
CC |||||  
XX 121 CCGGACGCCCGGAGCTCCAGCGCGAGGGGCTGCTCCGACCGGCGCTGGCCCGCTGCTT 180  
DB

QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80  
CC |||||  
XX 181 TTCTTCTACTTGAGCCAGGACAGCCGCCCGGAGGCTGAGTCTCCGACGAGCTGTAAAC 240  
DB

QY 81 ProTyrPheGluArgGlnSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
CC |||||  
XX 241 CCTGTGTTTGAAGCCATCAGCATGTGTGTCATCTTCACTGACGCGACCTGGGCGATG 300  
DB

QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
CC |||||  
XX 301 TTCGGCCATGCGAGCATCGCTGTGATCTCCAGGGCTCCGGANCTCGAGGCTTT 360  
DB

QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValIlyMetValAlaLeuGly 140  
CC |||||  
XX 361 GATGACTTCATCTTGTGCTTCTTGGCCGTGAGATGTGTGAAGATGTGGCTTGGCG 420  
DB

QY 141 IlePheGlyIlyblyCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal 160  
CC |||||  
XX 421 ATCTTTGGAAAAAGTGTACCTGGGAGACATYTGAAACCGGCTGTGCTTTTCATGTC 480  
DB

QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
CC |||||  
XX 481 ATGCGAGGAGATGCGAGTACTGCTGACCTGCAGAACGTCACTTCTCAGCTGTCAAG 540  
DB

QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
CC |||||  
XX 541 ACAATCGGTGGTGGACCGCTCAGGCGCATTAACCGGGTGCCACAGATGCCGATCTT 600  
DB

QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
CC |||||  
XX 601 GTCACTTGTGCTGCGATGACGCTGCCATGCTGGGCAACGCTCGCTGCTTCTTTC 660  
DB

QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuThrAlaGlyLeuLeuArgAsnArg 240  
CC |||||  
XX 661 GTCTTCTTCATCTTCGCGATGCTGGGCTGACGCTGGGCGAGGCTGCTTGGAAACGA 720  
DB

QY 241 CysPheLeuProGluAsnAspSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
CC |||||  
XX 721 TGCTTCTTACTGAGTAATTCAGCTCCCTTGAGCTGAGCCTGATTAACAG 780  
DB

QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
CC |||||  
XX 781 ACAAGAGACGAGGATGAGAGCCCTTCACTGTGCTCCAGACGCGGAAACGGATCGG 840  
DB

QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
CC |||||

Db 841 TCCTGCAGAAAGCGTGCACAGCTGCAGGGGAGCGGGGCGGTGCCACCTTGCGGTCTG 900  
QY 301 AAPTYYGIUAlaIYrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnIYrTYR 320  
Db 901 GACTATGAGGCTTCAACAACAGCTCCACACACACCACTGTGTCAACAGTCAAGTCTCAG 960  
QY 322 ThrAsnCySerAlaGlyGlnIuHIsaAnProPheIYsGlyAlaIleAsnPheAspAnile 340  
Db 961 ACCAACTGCTCAGCGGGGAGCACAAACCTTTCAAGGGGCGCCATCACTTTGACAAACATT 1020  
QY 341 GLYTYrAlaTrpIleAlaIlePheGlnValIleThrLeuGlnGlyTrpValAspIleMet 360  
Db 1021 GGCTATGAGCTGCATGCCATCTTCCAGGTATCATCACTGGAGGGGTGCGGTCCGACATCATG 1080  
QY 361 TYrPheValMetAspAlaHisSerPheTYrAsnPheIleTYrPheIleLeuIleIle 380  
Db 1081 TACTTGTGATGGATCTCATCTCTTCACAATTTCATCTACTTCACTCTCCATCATCTC 1140  
QY 381 ValGIYSerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
Db 1141 GTGGGCTCTCTTCTTCATGATCAACCTGTGCTGTGGTGAATTGCCACGCACTTCTCAGAG 1200  
QY 401 ThrIYsGlnArgIuSerGlnLeuMetArgIuGlnArgValArgPheLeuSerAsnAla 420  
Db 1201 ACCAAGCAGCGGGAAGCCAGCTGATGCGGGAGCAGGCTGCGGTTCCTGTCACAGCC 1260  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTYrGlnIuLeuLeuIYrIleu 440  
Db 1261 AGCACCCTGGCTAGCTTCTCTGAGCCCGGACGCTGATGAGAGCTGCTCAAGTCACTG 1320  
QY 441 ValTYrIleuArgIYsAlaIaArgArgLeuAlaGlnValSerArgAlaIaGlyVal 460  
Db 1321 GTGTACATCTCTTGTAAAGGAGAGCCCGAGGCTGGCTCAGGTCCTCTCGGGAGAGAGGTG 1380  
QY 461 ArgValGIYLeuLeuSerSerProAlaProLeuGIYGIYGIYGIYGIYGIYGIYGIYGIY 480  
Db 1381 CGGGTGGGCTGCTCAGAGCCAGACCCCTCGGGGGCCAGAGACCCAGCCACAGC 1440  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisIleuValHisIleuHisIleuHis 500  
Db 1441 AGCTGCTCTGCTCCACCGCGCTATCCGTCCACCACTGGTGAACCAACCAACCAAC 1500  
QY 501 HisIleuHisIleuIYrHisIleuGIYAsnGIYThrLeuArgAlaProArgAlaSerProGlu 520  
Db 1501 CACACACACACCTACCACTCGGGCAATGGAGCGCTCAGGGGCCCGCGGGCACCGCGAG 1560  
QY 521 IleGlnAspArgAspAlaAsnGIYSerArgArgLeuMetLeuProProSerThrPro 540  
Db 1561 ATCCAGGACAGGGATGCCAATGGGTCCCGCAGGCTCATGCTGCACACACCTCGAGCGCT 1620  
QY 541 AlaLeuSerGIYAlaProProGIYGIYAlaGluSerValHisSerPheTYrHisAlaAsp 560  
Db 1621 GCCCTCTCGGGGCCCCCTGGTGGGAGAGTCTGTGCACAGCTTCTTACATGCGCAG 1680  
QY 561 CysHisIleuGlnIuProValArgCysGlnAlaProProArgSerProSerGIYAlaSer 580  
Db 1681 TGCACATTAGAGCAAGTCCGCTCCAGGCGCCCCCTCCAGGTCCCATATGAGGATCC 1740  
QY 581 GLYArgThrValGIYSerGIYIYsValTYrProThrValHisThrSerProProGlu 600  
Db 1741 GGCAGAGACTGTGGGAGCGGGAAGTGTATCCACAGTGACACACAGCCCTCCACCGGAG 1800  
QY 601 ThrLeuIYsGlnIYsAlaLeuValGIYValAlaIaSerSerGIYProProThrIleuThr 620  
Db 1801 ACCCTGAAGAGAAAGCACTAGTAGAGTGTGCCAGCTGTGGCCCCCAACCTCCACC 1860  
QY 621 SerLeuAsnIleProProGIYProTYrSerSerMetHisIYsLeuLeuGlnIuThrGlnSer 640  
Db 1861 AGCTCAACATCCACCCCGGCGCTTACAGCTCCATGACACAGTCTCGAGACACAGAGT 1920  
QY 641 ThrGIYAlaCysGlnSerSerCysIYsIleSerSerProCysLeuIYsAlaAspSerGIY 660  
Db 1921 ACAGGTGCTGCGCAAGCTCTTGCAGAATCTCCAGCCCTTGTTGAAAGCAGACAGTGGAG 1980

QY 661 AlaCysGIYProAspSerCysProTYrCysAlaArgAlaGlyAlaGlyIYGIYValGIYLeu 680  
Db 1981 GCTTGAGTCCAGACAGCTGCCCTTACTGTGTCCCGGGCCGGGAGAGGTGAAGCTC 2040  
QY 681 AlaAspArgGluMetProAspSerAspSerGIYAlaValTYrGIYIuPheThrGlnAspAla 700  
Db 2041 GCGGACCGTGAATGCTGTGACTCAGACAGCGAGCGAGTTTATGATTTCACACAGATGCC 2100  
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgIuArgSerLeuGIYProAspAla 720  
Db 2101 CAGCACAGGAGCTCCGGAGCCCGACAGCGCGGCAACGAGGCTGAGCCCAATGCA 2160  
QY 721 GIYProSerSerValIleuAlaPheTrpArgLeuIleCysAspThrPheArgIYsIleVal 740  
Db 2161 GAGCCAGCTCTGTGTGCTGCTTCTGAGGCTTAATCTGTGACACTTCGAAAGATTGTG 2220  
QY 741 AspSerIYsTYrPheGIYArgGIYIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
Db 2221 GACAGAGATCTTTGGCGGGGAATCATGATCGCATCTGTGCACACACTCAGCATG 2280  
QY 761 GIYIleGIYrHisGlnIuProGIYGIYIuLeuThrAsnAlaLeuGlnIleSerAsnIle 780  
Db 2281 GGCAATCGAATATCACAGAGAGCCGAGAGCTTACCAAGCCCTGGAATCAGAAACATC 2340  
QY 781 ValPheThrSerLeuPheAlaLeuGlnMetLeuLeuIYsLeuValTYrGIYProPhe 800  
Db 2341 GTCTTCACAGCTCTTGTGCTTGAGATGCTGTGAAAGCTCTGTGTATGTCTCTTT 2400  
QY 801 GIYTYrIleIYsAsnProTYrAsnIlePheAspGIYValIleValIleSerValTrp 820  
Db 2401 GGCTACATCAAGATCCCTCAACAACATCTTCATGTGTGATGATGATGATCAGCGTGG 2460  
QY 821 GIYIleValGIYGIYGIYGIYGIYGIYLeuSerValIleuArgThrPheArgLeuMetArg 840  
Db 2461 GAGATCGTGGGACACAGGGGGGGCGGCTGTGCTGAGCTGGGACCTTCGCTGATGCT 2520  
QY 841 ValIleuIYsLeuValArgPheLeuProAlaLeuGlnArgIuLeuValValLeuMetIYs 860  
Db 2521 GTGCTGAAGCTGTGCTGCTCTGCGCGGCTGCAGCGGCACTGTGTGCTCATGAAAG 2580  
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880  
Db 2581 ACCATGAGCAACGTGAGCAACTTCTTGATGATGCTGTTATGCTTTCATCTTCACTCAGC 2640  
QY 881 IleLeuGIYMetHisIleuPheGIYCysIYsPheAlaSerGIYArgAspGIYAspThrLeu 900  
Db 2641 ATCTGGGCAATCATCTTTCGGCTGCAAGTGTGCTCTGAGCGGGATGGGAGCACCTTG 2700  
QY 901 ProAspArgIYsAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920  
Db 2701 CAGAGCCGGAAGATTTTGAATCCTTGTGCTGTGGCAATGTCATCTGTCTTCAGATCCG 2760  
QY 921 ThrGlnIuAspTrpAsnIYsValIleuTYrAsnGIYMetAlaSerThrSerSerTrpAla 940  
Db 2761 ACCCAGAGAGACTGGAACAAAGTCCCTTCAATGTATGAGCTCCACAGTCCGCTCGGGG 2820  
QY 941 AlaIleuTYrPheIleAlaLeuMetThrPheGIYAsnTYrValIleuPheAsnLeuVal 960  
Db 2821 GCCCTTATTTCAATGCTCTCATGACCTTGGCAACTAGTGTCTTTCATATTGTGTGTC 2880  
QY 961 AlaIleLeuValGIYGIYPheGlnAlaGlnIuIleSerIYsArgGIYAspAlaSerGIY 980  
Db 2881 GCATTTGTGTGAGGGCTTCCAGGCGAGAGAAATCAGCAACGGGAAATCGAGTGGAG 2940  
QY 981 GlnLeuSerCysIleGlnIuProValAspSerGlnGIYGIYAspAlaAsnIYsSerGIY 1000  
Db 2941 CAGTTAAGGTGATTCAGGTGCTGTGCATCCAGGGGGGAGATGCCAACAAATGCCGA 3000  
QY 1001 SerGIYIuProAspPhePheSerProSerIleuAspGIYAspGIYAspArgIYsIYsIYs 1020  
Db 3001 TCAGAGCCCGAATTTCTTTCACACCGCTGATGTGTATGGGGAGACAGGAAGAGTGTGG 3060

Qy	1021	AlaleuValSerleuGlyGluHisProGluLeuArgLysSerLeuLeuProProleuIle	1040	
Db	3061	GCCTTGCTGTCCTCGGAGAGACCCGAGCTGGAGAACCTCGCCCTCATC	3120	
Qy	1041	ILHiePhrAlaIaIaThrProMetSerLeuProLysSerThrSerThrglyLeuGly	1060	
Db	3121	ATCCACAGCGCGCCACACCATTCCTGCTCCCAAGACACACAGCGGCTGGGAG	3180	
Qy	1061	AlaleuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla	1080	
Db	3181	GGCTGGGCGCTGCTGCGCGCCGACACGAGCGGGTGGCAGAGCTCGGGCGGC	3240	
Qy	1081	HisGlyMetLysSerProProSerAlaArgSerSerProHisSerProTTPSerAla	1100	
Db	3241	CACAGATGAAGTACCGCCACGCGCCGCGAGCTCTCCGACACCCCTGGAGGCTGCA	3300	
Qy	1101	SerSerTrpThrSerArgArgSerSerArgHisSerLeuGlyArgAlaProSerLeu	1120	
Db	3301	AGCAGCTGACACAGCGCTCCAGCGGAAAGCTCGGCGCTGACCCAGCTGAG	3360	
Qy	1121	ArgArgSerProSerGlyGluArgArgSerLeuSerGlyGluGlyGluSerGln	1140	
Db	3361	CGGAGAACCCAAATGGAGAGCGCGGCTCTGTTGCGGAGAAAGCGAGAGCGAG	3420	
Qy	1141	AspGluGluGluSerSerGlyGluGluArgAlaSerProAlaGlySerAspHisArgHis	1160	
Db	3421	GATGAAGAAGAGACTCAGAAAGAGAGCGGCGACCTCGCGGAGTGCATCGCCAC	3480	
Qy	1161	ArgGlySerLeuGluArgGlyAlaLysSerSerPheAspLeuProAspThrLeuGly	1180	
Db	3481	AGGGGGTCCCTGGAGCGGAGCCAAAGATCTTTGACTGCGACACACTCGAGTG	3540	
Qy	1181	ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn	1200	
Db	3541	CCAGGCGCTGATCCCATCTGCAAGTGGCGGAGGTCTGTTCTGAGCACCAAGATCGCAT	3600	
Qy	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProleuAsp	1220	
Db	3601	GGCAAGTCGCGCTTCAGGGCGCTGCGCCGCGGCTCGCGCTGATGACCCCGCATGAT	3660	
Qy	1221	GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle	1240	
Db	3661	GGGAGTAGCGCGATGACGAGGGCACTGAGCAAGGAGAAAGGGTCCGCGCTGATC	3720	
Qy	1241	ArgAlaArgLeuProAlaCysTrpLeuGluArgAspSerTrpSerAlaTrpIlePhePro	1260	
Db	3721	CGAGCCGACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3780	
Qy	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280	
Db	3781	CCTCAGTCCAGAGTTCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3840	
Qy	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300	
Db	3841	GTGGTCTTGTATCATCTCTTAACTGCATCACTGACCATGCGCAGAGCGCCCAAAAT	3900	
Qy	1301	AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTrpIlePheThrAlaVal	1320	
Db	3901	GACCCCAACAGCGCTGAAACGATCTTCTGACCTCTCCATTTACATTTACCGCAGTC	3960	
Qy	1321	PheLeuAlaGluMetThrValLysValAlaAlaLeuGlyTrpCysPheGlyGluGlnAla	1340	
Db	3961	TTTCTGGCTGAAATGACAGTGAAGGTGGTGCACCTGGGCTGTGGGGAGCAGCG	4020	
Qy	1341	TrpLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValIleSerValIleAsp	1360	
Db	4021	TACCTGCGAGACAGTGGAGCGTCTGAGCGGCTGTTGCTCATCTCGCTCATTCAC	4080	
Qy	1361	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380	
Db	4081	ATTCTGCTGTCATGCTCTCTGACAGCGGACCAAGATCTGGGAGATCTGAGGGTGTG	4140	
Qy	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400	
Db	4141	CGGCTGCTGGACCTCTGGCGCCGCTCAGGGTATACCGCGCGAGGGGCGAGAGCTG	4200	
Qy	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys	1420	
Db	4201	GTGTGGAGACCGCTGATGTCCTCATCTGAAACCATCGGCAACATTTGTATCATCTCTGT	4260	
Qy	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheVal	1440	
Db	4261	GGCTTCTTCACTATTTTGGCATCTTGGGGGTGACCTTCAAGAGGAAGTTTTCGTG	4320	
Qy	1441	CysGlnGlyLysAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTrp	1460	
Db	4321	TGCCAGGCGAGATACAGGAAATCAACCAAAATTCGACCTGCGCAGGCGCAGTTAC	4380	
Qy	1461	ArgTrpValArgHisLysTrpAsnPheAspLeuGlyGlnAlaLeuMetSerLeuPhe	1480	
Db	4381	CGGTGGGTCGGCACAAGTACATTGTGACAACTTGGCCAGGCGCTGATGTCCTGTTTC	4440	
Qy	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTrpAspGlyLeuAspAlaValGly	1500	
Db	4441	GTTTTGCCCTCCAAAGATGTTGGTGGTGCATCATGATGATGAGTGGCTGTGAGGC	4500	
Qy	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTrpPheIleSerPhe	1520	
Db	4501	GTGACCAAGACGCCCATCATGAAACACACACCTGATGCTGCTGATCTCATCTGCTTC	4560	
Qy	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPhe	1540	
Db	4561	CTGTCTATTTGGCTCTTCTTGTCTGAAATCATGTTTGGGTGTGGTGGAGAACTTC	4620	
Qy	1541	HisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysAspGlu	1560	
Db	4621	CACAAAGTGGGAGACACCGAGAGAAAGAGAGCGCGGCGGAGAGAAAGCGCTA	4680	
Qy	1561	ArgArgLeuGluLysLysLysArgArg	1568	
Db	4681	CGAAGACTGAGAAAGAAAGAAAGAAATCTAATGCTGACATGAAATTCCTCCGACAG	4740	
Qy	1569	-----LysAlaGlnCysLysProTrpTrpSerAspTrpSerArgPhe	1582	
Db	4741	TGAGCAGCGCTGGTGCAGAACCCAGTGCAAACTTACTTACCTCCGCTTC	4800	
Qy	1583	ArgLeuLeuValHisHisLysLeuCysThrSerHisTrpLeuAspLeuPheIleThrGlyVal	1602	
Db	4801	CGGCTCTCTGTCACCACTTGTGCACAGCACGACATCACTGACCTTTCATCACAGGCTC	4860	
Qy	1603	IleGlyLeuAsnValValIleThrMetAlaMetGluHisTrpGlnGlnProGlnIleLeuAsp	1622	
Db	4861	ATCGGGCTGAACGTGTGCACATGCGCATGAGACATCACAGACGCCCGATTTCTGAT	4920	
Qy	1623	GluAlaLeuLysIleCysAsnTrpIlePheThrValIlePheValLeuGluSerValPhe	1642	
Db	4921	GAGGCTTGAAGATCTGCACTCATCTTCACTGTATCTTTGTCTTGAGTCAAGTTTC	4980	
Qy	1643	LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu	1662	
Db	4981	AAACTTGTGCTTTGTTTCCGTGCGTCTTCCAGGACAGGTGGAACAGCTGAGACTG	5040	
Qy	1663	AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer	1682	
Db	5041	GCCATTTGCTGCTCATATGAGGATACAGCTGAGGAATCGAGGTCAACGCTTC	5100	
Qy	1683	LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu	1702	
Db	5101	CTGCCCATTAACCCACATCATCTCGCATATGAGGGTGTGCGCATTTGCCGAGTCTGT	5160	
Qy	1703	LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValIleMetGlnAlaLeu	1722	
Db	5161	AAGCTGCTGAAGATGCTGTGGGATGCGGCGCTGTGACACCGGTGATGACGGCCCTG	5220	
Qy	1723	ProGlnValGlyLeuLeuGlyLeuLeuPheMetLeuLeuPhePheAlaIleLeu	1742	

Db 5221 CCCAGGTGGGAACTTCTTCATGTTGTTTTCATCTTTGAGCTCTG 5280  
Qy 1743 G1YValG1uLeuPheG1YAspLeuG1uCyAspG1uThiHisProCyseG1uG1YLeuG1Y 1762  
Db 5281 GGGGTGAGACTTTTGGAGCCTGGAGTGTGACGAGACACACCCCTGTAGAGGCTGGAGC 5340  
Qy 1763 ArgHisAlaThrPheArgAsnPheG1YMetAlaPheLeuThiLeuPheArgValSerThr 1782  
Db 5341 GGTCAATGCCACTTTTGGAACTTTGGCAATGGCTTCTTAACCTCTTCCGAGCTTCCACA 5400  
Qy 1783 G1YAspAsnTrpAsnG1YLeuMetLYAspThrLeuArgAspCyAspG1uG1uSerThr 1802  
Db 5401 GGTGAACAATTGGAACTTATGAAAGACACCTCCGGAACTGTGACAGAGTCCACC 5460  
Qy 1803 CyETyrAsnThyValIleSerProIleYrPheValSerPheValLeuThrAlaGlnPhe 1822  
Db 5461 TGTTCACAAACAGGTGTCACTTCGCTTATCTTCTGTCTCTCTGTGACGGCCGAGTTC 5520  
Qy 1823 ValLeuValAsnValValIleAlaValLeuMetLYseHisLeuG1uG1uSerAsnLYseG1u 1842  
Db 5521 GTCTAGTCAACGTGTGATCGCCGTGCTGATGAAACACTGGAGAGAGACAAAGAG 5580  
Qy 1843 AlaLYseG1uG1uAlaG1uLeuG1uAlaG1uLeuG1uLeuG1uMetLYseThrLeuSerPro 1862  
Db 5581 GCCAAGAGAGAGCCGAGCTAGAGCTGAGCTGAGCTGAGATGAAGACCTCAAGCCCC 5640  
Qy 1863 GlnProHisSerProLeuG1YSerProPheLeuTrpProG1YValG1uG1YProAspSer 1882  
Db 5641 CAGCCCACTCGGCACTGGGCAAGCCCTTCTCTGCTGGGGTCAAGAGCCCGCAAGC 5700  
Qy 1883 ProAspSerProLYseProG1YAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis 1902  
Db 5701 CCGGACAGCCCAAGCTGGGGCTTGTGACCCAGCCGCGAGATCAGCTCCAC 5760  
Qy 1903 PheSerLeuG1uHisProThr----- 1909  
Db 5761 TTTTCCCTGGAGCAGCCCAAGAGACAGAGCTGTTGACACCATATCCCTGATATCCAG 5820  
Qy 1909 ----- 1909  
Db 5821 GGCTCCCTGGAGTGGAGCTGAAGCTGATGAGACAGAGCTGGAGAGCCAGGGGGCAGCCC 5880  
Qy 1909 ----- 1909  
Db 5881 TCTGCTTCCCTTCTGCCCCCAGACCTGGAGAGCTCCGACCCACAGATCCCTTACGCTGAG 5940  
Qy 1909 ----- 1909  
Db 5941 ATGAGAGCTCTGTCTGAGCTGAGAGATTGTGTGAACCGTCTGTCTTACGCTTG 6000  
Qy 1909 ----- 1909  
Db 6001 ACGGATGACTTTTGGCTGATGACATGACACACTTCTTACTAGTCCCTGGAGAGCAAT 6060  
Qy 1910 MetGlnProHisProThrG1uLeuProG1YProAspLeuLeuThyValArgLYseSerG1Y 1929  
Db 6061 ATGCAAGCCCAACCCCAAGAGCTGCAAGACAGACCAAGATTAATGACTGTGCGAAGTCTGG 6120  
Qy 1930 ValSerArgThrHisSerLeuProAsnAspSerLYMetCyAsnArgHisG1YSerThrAla 1949  
Db 6121 GTCAAGCCGAACGCACTCTGCGCCCAATGACAGCTAATGTGTGGCATGGAGCACTGCC 6180  
Qy 1950 G1uG1YProLeuG1YHisArgG1YTrpG1YLeuProLYseAlaGlnSerG1YSerValLeu 1969  
Db 6181 GAGGGGACCTTGAGACAGAGGCTGGGGCTCCCAAGAGCTAGTCAGGCTCCGCTTG 6240  
Qy 1970 SerValHisSerGlnProAlaAspThrSerLYrIleLeuG1uLeuProLYseAspAlaPro 1989  
Db 6241 TCGCTTCACTCCCAAGCAGAGATACCAAGTATCACTCTGAGCTTCCCAAAGATGACACT 6300  
Qy 1990 HisLeuLeuGlnProHisSerAlaProThrTrpG1YThrIleProLYseLeuProProPro 2009  
Db 6301 CATCTGCTCAGGCCCAAGAGCCCAAGCTGGGGGACCATTCGCCAAATGCGCCCAACA 6360

Qy 2010 G1YArgSerProLeuAlaG1uArgProLeuArgArgG1uAlaAlaIleArgThrAspSer 2029  
Db 6361 GAGAGCTCCCTTGTGCTCAGAGGCACTCAGGCCCAAGCAGACATTAAGATCACTTCC 6420  
Qy 2030 LeuAspValGlnG1YLeuG1YSerArgG1uAspLeuAlaG1uValSerG1YProSer 2049  
Db 6421 TTGAGAGTTCAAGGCTGTGGGAGCCGGGAAGACCTGTGGCAGAGGTGATGGGCTTCC 6480  
Qy 2050 ProProLeuAlaArgAlaTyrSerPheTrpG1YGlnSerSerThiGlnAlaGlnGlnHis 2069  
Db 6481 CCGCCCTGGCCCGGCTTACTCTTCTGGGGCCAGTCAAGTACCAGACAGAGAC 6540  
Qy 2070 SerArgSerHisSerLYseIleSerLYseHisMetThrProProAlaProCyAspProG1YPro 2089  
Db 6541 TCCCGAGCCACAGAAAGTCTTCAAGACATGACATCCCGCCAGAGCCCTTGTGCCAGGCCA 6600  
Qy 2090 G1uProAsnTrpG1YLYseG1YProProG1uThyArgSerSerLeuG1uLeuAspThrG1u 2109  
Db 6601 GAACCAACTGGGGGAGAGGCCCTCCAGAGACCAAGACAGCTTAGATTGGACACGGAG 6660  
Qy 2110 LeuSerTrpIleSerG1YAspLeuLeuProProG1YG1YGlnG1uG1uProProSerPro 2129  
Db 6661 CTGAGCTGATTTCAGAGACCTCTGCCCCCTGGCGGCAAGAGAGACCCCAATCCCA 6720  
Qy 2130 ArgAspLeuLYseLYseCysTyrSerValG1uAlaGlnSerCysG1uArgArgProThrSer 2149  
Db 6721 CCGGACCTGAGAAAGTCTACGCTGAGAGGCCCAAGAGCTGCCAGCCCGGCTTACGCTCC 6780  
Qy 2150 TrpLeuAspG1uG1uArgArgHisSerIleAlaValSerCysLeuAspSerG1YSerGln 2169  
Db 6781 TGGCTGATGAGACAGAGAGACATCTTATCGCCGTGAGCTGCTGAGACAGCGGCTCCCA 6840  
Qy 2170 ProHisLeuG1YThyAspProSerAsnLeuG1YG1YGlnProLeuG1YG1YProG1YSer 2189  
Db 6841 CCCCACCTGGGACAGACCCCTTAACTTGGGGGCGCAGCCCTTGGGGGGCTTGGAGC 6900  
Qy 2190 ArgProLYseLYseLeuSerProProSerIleThrIleAspProProG1uSerGlnG1Y 2209  
Db 6901 CGGCCCAAGAAAACCTCAGCCCGCTGATACATACATAGACCCCCCGAGAGCCAAAGT 6960  
Qy 2210 ProArgThrProProSerProG1YIleCysLeuArgArgAlaProSerSerAspSer 2229  
Db 6961 CCTCGGAGCCCGCCAGCCCTGTATGTGCTCCGAGAGAGGGCTCCGTCAGCACTCC 7020  
Qy 2230 LYseAspProLeuAlaSerG1YProProAspSerMetAlaAlaSerProSerProLYseLYs 2249  
Db 7021 AAGGATCCCTTGGCTGTGGCCCCCTGACAGCATGCTGCTGCTGCCCTCCCAAGAAA 7080  
Qy 2250 AspValLeuSerLeuSerG1YLeuSerSerAspProAlaAspLeuAspPro 2266  
Db 7081 GATGTGCTGAGTCTCTCGGTTTATCTTGAACCAAGACAGACTGGACCCC 7131

RESULT 4  
ADSL16298  
ID ADSL16298 strand; DNA; 7648 BP.  
XX  
AC ADSL16298;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human voltage-dependent alpha 1g subunit calcium channel (CACNA1G) DNA.  
XX  
KW Voltage-dependent ion channel; drug candidate;  
KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;  
KW anticonvulsant; antiarrhythmic; human; alpha 1g subunit; ds.  
OS Homo sapiens.  
XX  
PN US2004175761-A1.  
XX  
PD 09-SEP-2004.  
XX

PF 01-MAR-2003; 2003US-00377139.  
XX  
PR 01-MAR-2003; 2003US-00377139.  
XX  
PA (MACK/) MACKINNON R.  
PA (MACK/) MACKINNON A L.  
PA (JIAN/) JIANG Y.  
PA (RUTA/) RUTA V.  
XX  
XX  
PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;  
XX  
XX WPI; 2004-642122/62.  
DR  
DR REFSEQ; NM\_018996.  
XX  
PT Screening drug candidates that target voltage dependent ion channel  
PT protein, involves contacting screening protein with chemical compound,  
PT which is drug candidate and determining whether chemical compound binds  
PT to screening protein.  
XX  
PS Disclosure; SEQ ID NO 10; 61pp; English.  
XX  
CC The invention relates to the composition of matter suitable for use in  
CC identifying chemical compounds that bind to voltage-dependent ion channel  
CC proteins. The composition comprises a screening protein that consists of  
CC an ion channel voltage sensor domain of the ion channel protein  
CC immobilised on a solid support. The invention is useful for identifying  
CC chemical compounds (drug candidate) that bind to voltage-dependent ion  
CC channel proteins. The drug candidate of the invention is utilised for  
CC treating a condition mediated by aberrant electrical activity that  
CC initiates uptake or release of neurotransmitters and contraction of  
CC muscles. The drug candidate of the invention is also utilised for  
CC treating epilepsy and arrhythmia. The present sequence is a voltage-  
CC dependent calcium channel DNA.  
XX  
SQ Sequence 7648 BP; 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 0 Length: 7648  
Score: 11815.50 Matches: 2264  
Percent Similarity: 95.29% Conservative: 1  
Best Local Similarity: 95.25% Mismatches: 1  
Query Match: 99.26% Indels: 111  
DB: 13 Gaps: 2  
US-09-611-257A-37 (1-2266) x ADS16298 (1-7648)  
QY 1 MetAspGluGluGluAspGlyValAGluGluSerGlyGluProArgSerPheMet 20  
DB 1 ATGAGCGAGGAGGAGATGAGCGGCGCGAGAGATCGGAGACCCCGAGCTTCATG 60  
QY 21 ArgLeuAsnAspLeuSerGlyValAGlyValArgProGlyProGlySerAlaGluValAsp 40  
DB 61 CGGCTCAACGACTCTCGGGGCGCGGGCGCGGGCGGGGCTACGAGAAAAGAC 120  
QY 41 ProGlySerAlaAspSerGlyValAGluGlyLeuProGlyProAlaLeuValProVal 60  
DB 121 CCGGCGAGCGCGGACTCGGAGCGGAGGCGCTGCGTACCCGCGGCTGGCCCGCTGTT 180  
QY 61 PhePheTyrLeuSerGlyAsnSerArgProArgSerTyrGlyLeuValGlyValCysAsn 80  
DB 181 TTCTTCTTCACTTGACCGAGACCGCGCGCGAGCTGCTCTCCGACCGCTCTGAC 240  
QY 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnGlyValThrLeuGlyMet 100  
DB 241 CCCGCTTTTGAGCCGATACGATGTGTGTCATCTTCCTCACTGCGTACCCCTGGGATG 300  
QY 101 PheArgProGlyGluAspIleAlaCysAspSerGlyValGlyValIleGluAlaPhe 120  
DB 301 TTCCGGCGCATCGAGGACATCGCTGTGATCCAGCGCTCCGAGATCTTCAGAGCTTT 360  
QY 121 AspAspPheIlePheAlaPhePheAlaValAGluMetValValGlyMetValAlaGluGly 140  
DB 361 GATGACTTCATCTTGTCTTCTTGTGCGTGAAGATGTGTGAAGATGTGTGCTTGGGC 420

QY 141 IlePheGlyValGlyCysTyrLeuGlyValAspThrTyrAsnArgLeuAspPhePheIleVal 160  
DB 421 ATCTTTGGGAAAAAGTTACCTGGGAGACACTTGAGACCGGCTTGACTTTTCACTGTC 480  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGluAsnValSerPheSerAlaValArg 180  
DB 481 ATCGCAGGATGCTGAGATCTGCTGAGACTGCGACAGATGATGCTTCTCAGCTGCAGG 540  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
DB 541 ACAGTCGCTGTGTGGACCGCTCAGGCGCATTAACCGGCTGCGCAGATGCGCATCTT 600  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyValAsnValLeuLeuLeuCysPhePhe 220  
DB 601 GTACACTGTGCTGTGATACGCTGCGCATGTGGGCAAGCTCTGCTGCTCTCTCTTC 660  
QY 221 ValPhePheIlePheGlyIleValAGlyValAGluMetTyrAlaGlyLeuLeuArgAsnArg 240  
DB 661 GTCTTCTTCATCTTCGCGCATCTCGCGCTCCAGCTGTGGGAGGCGCTGCTCGGAACCGA 720  
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
DB 721 TGCTTCCTACTGAGATTCACGCTCCCTGAGCGGTGACCTGGAGCGCTATTACAG 780  
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
DB 781 ACAGAAACAGAGATGAGAGCCCTTCATCTGCTCCAGCACGAGCAAGACGCAATGCGG 840  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyValGlyValProProCysGlyLeu 300  
DB 841 TCTTCAGAAAGCTGCTGCCAGCTGCGCGGGAGCGGGGCGGTGCCACCTTCGGCTG 900  
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrPheGlnTyr 320  
DB 901 GACTATGAGGCTTACAAACAGCTCCAGCAACACCACTGTGTCAACCTGAGAACCTACTAC 960  
QY 321 ThrAsnCysSerAlaGlyValIleAsnProPheValAGlyValIleAsnPheAspAsnIle 340  
DB 961 ACCAAGCTCTCAGCGGGGAGCAACCCCTTAAGGGCGCCATCAACTTGTGACAACTT 1020  
QY 341 GlyTyrAlaThrIleAlaIlePheGluValIleThrLeuGluGlyTyrValAspIleMet 360  
DB 1021 GGCTATGCTGTGATTCGCGATCTTCAGGTATACGCTGAGAGGCTGGGTGCATCATG 1080  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
DB 1081 TACTTGTGATGATGTCTATCTCTCTACAACTTCACTTCACTCTCCATCATC 1140  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
DB 1141 GTGGGCTCTCTTCTTCATGATCAACCTGTGCTGTGTGTGATTCACGACGCTTCTCAG 1200  
QY 401 ThrIleGluArgIleSerGluLeuMetArgGluGluArgValArgPheLeuSerAsnAla 420  
DB 1201 ACCAAGCAGGAGAAACCACTGATGCGGAGAGAGCTGTGGCTTCTCTCAAGCC 1260  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuValTyrLeu 440  
DB 1261 AGCACCTGTGCTTCTCTGAGCCCGGACGCTGATAGAGAGCTCAAGTACTCTG 1320  
QY 441 ValTyrIleLeuArgGlyValAlaArgArgLeuAlaGluValSerArgAlaAlaGlyVal 460  
DB 1321 GTGTACATCTTGTGTAGGAGCGCGGAGCTGCTCAGGTCTCTCGGAGAGAGGTGTG 1380  
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyValGlnGluThrGlnProSerSer 480  
DB 1381 CGGCTTGGGCTGCTCAGCAGCCAGACCCCTCGGGGCGCAGAGAACCCAGCCAGAGAGC 1440  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisIleHisIleHis 500  
DB 1441 AGTGTCTCTGCTCCACCGCGCTATCCGTACCACTGCTGTGACCACTGCTGCTGCTG 1500

QY	501	HisHshisshisTyrHisLeuGlyValAsnGlyThrLeuArgAlaProAlaGlaSerProGlu	520
Db	1501	CATCAACCACCACTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGCGACGGAG	1560
QY	521	ILlegnaapaagaaPaAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
Db	1561	ATCCAGGACAGAGGATGCCAATGGGTCCCGAGGCTCATGTCGACCAACCTCGACGCTT	1620
QY	541	AlaLeuSerGlyAlaProProGlyGlyValaGluSerValHisSerPheTyrHisAlaAsp	560
Db	1621	GCCCTCTCCGGGGCCCCCCCCGGTGGGGCAAGTCTGTGCACACACTTCTACATGCCGAC	1680
QY	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
Db	1681	TGCCACTTAGAGCCAGTCCGCTGGCAGGCGCCCCCTCCAGGTCCCATCTGAAGCATCC	1740
QY	581	GlyArgThrValGlySerGlyIleValTyrProThrValHisThrSerProProProGlu	600
Db	1741	GGCAGGACTGTGGGAGCGGGAGGTGTATCCACCGTGACACACAGCCTTCACCGGAG	1800
QY	601	ThrLeuIysGluIysAlaLeuValGluValAlaIleSerSerGlyProProThrLeuThr	620
Db	1801	ACCGTGAAGGAGAAGGACACTAGTAGAGGTGGCTGCAGCTTGGGGCCCCCAACCTCAC	1860
QY	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisIleLeuGluThrGlnSer	640
Db	1861	AGCCTCAACATCCCAACCCGGGCCCTACAGCTCCATGCAACAAGCTGTGGAGACACAGT	1920
QY	641	ThrGlyAlaCysGlnSerSerCysIleHisSerProCysLeuIysAlaAspSerGly	660
Db	1921	ACAGGTGCTGCAAGGCTCTTGCAAGATCTCCAGCCTCTTGAAAGCAAGACAGTGA	1980
QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680
Db	1981	GCTCTGTGTCAGACAGCTGCCCTCACTGTGCTCCGGGCGGAGGAGGAGTGAAGTCT	2040
QY	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla	700
Db	2041	GCCGACCGTGAATAGCTGACTGACAGACGACGACGACGACGACGACGACGACGACGAC	2100
QY	701	GlnHisSerAspLeuArgAspProHisSerArgArgGlnAspSerLeuGlyProAspAla	720
Db	2101	CAGCACACACGACCTCCGGGACCCCCACAGCGGGGACACGAGCTGTGGGCCAGATGA	2160
QY	721	GluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgIleVal	740
Db	2161	GAGCCCACTGTGTCTGTGGCTTCTGAGGCTAATCTGTGACACTTCCGAAAGATTGTG	2220
QY	741	AspSerIysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet	760
Db	2221	GACAGCAAGTACTTGGCCGGGGAAATCATGATCCGCATCTGTGTCAACACACTCAGATG	2280
QY	761	GlyIleGlyTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle	780
Db	2281	GGCATCGAATACCAAGACAGCCGACGAGGCTTACCAAGCCGCTTAGAATACAGAACATC	2340
QY	781	ValPheThrSerLeuPheAlaLeuGluMetLeuLeuIysLeuLeuValTyrGlyProPhe	800
Db	2341	GTCCTTACCAGGCTTTTGCCCTGGAGATGCTGTAAGCTGTGTGTATAGTCCCTT	2400
QY	801	GlyTyrIleIysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyr	820
Db	2401	GGCATCATCAAGAAATCCCTACAACTTCTTGATGGTGTCAATTGTGTATCAGCGTGGG	2460
QY	821	GluIleValGlyGlnGlnGlyGlyIleLeuSerValLeuAspGlnPheArgLeuMetArg	840
Db	2461	GAGATCGTGGGCGACAGAGGGGGCGGCTGTGCGGTGCGGACCTTCCGCTATGGGT	2520
QY	841	ValLeuIysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValIleMetCys	860
Db	2521	GTGCTGAAGCTGTGTGCTTCTGTCCGGCGCTGACGCGGACGCTGTGTCTCATGAG	2580
QY	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer	880

Db	2581	ACCATGGACAAGTGGCCACCTTCTGCATGCTCTTAATGCTTCAATCTTCACG	2640
QY	881	ILeleuGlYweChIsleupheGlYCySlVsPheAlAserGlUarGAspGlYAsPThrLeu	900
Db	2641	ATCTGTGGGCAATGCATCTCTTCCGCTGCAGATTTTGCCCTGAGCGGGATGGGACACCTG	2700
QY	901	ProAspAryGlyAsnPhAsnPhAsPserLeuLeuTPAlAlIeValThrValPheGlnIlleu	920
Db	2701	CCAGACCGGAAGAAATTTTGACTGCTGCTCGGGCCATCATCTGCTTTCCAGATCTCTG	2760
QY	921	ThrGlnGlUasPThrPAsnLysValIleuYrAsnGlYWeArLAserThrsSerTPAlA	940
Db	2761	ACCCAGAGAGATCGGAACAAAGTCTCTTAACAAGTGAATGGCTTCCACGTCGCTCTGGGG	2820
QY	941	AlAleuTYrPheIlleAlAleuMetThrPheGlYAsnTYrValIleuPheAsnLeuLeuVal	960
Db	2821	GCCTTTATTTCAATTTGCCCTCAAGACCTTGGGCACTGAGTGTCTTCAATTTGCTGATG	2880
QY	961	AlAlIleuValGlUglYpHeGlnAlglUglIlIleSerLysArgGlUasPAlAserGlY	980
Db	2881	GCCATTTCTGTGGAGGGGCTTCCAGGCGGAGAAATCGCAAAAGGGAGATGCGAGTGA	2940
QY	981	GlUleuSerCySlIleGlUleuPProValAspSerGlNGlYGlYAspAlAsenLysSerGlU	1000
Db	2941	CAGTTAAGCTGTATTCAGCTGCTGCTGACTCCACAGGGGGGAATGCCACAAGTCCGA	3000
QY	1001	SerGlUProAsPphePheSerProSerLeuAspGlYAspGlYAspAryGlySlVsCySleu	1020
Db	3001	TCAGAGCCCGAATTTCTTCAACCAAGCTGGATGGTGAATGGGACAGGAAGAATGCTTG	3060
QY	1021	AlAleuValSerLeuGlYGlUHIAsProGlUleuAryGlySerLeuLeuProPoleuIlIe	1040
Db	3061	GCCTTGTGTGCCCTGGAGAGACACCGGAGCTCGGAGAGCCTGTGCGCGCTTCATC	3120
QY	1041	IlIeIleThrAlAlaIlePProMetSerLeuProLysSerThrsSerThrGlyIleuGlYGlU	1060
Db	3121	ATTCACACGCGCGCACACCAATGCTGCTCCCAAGACACACGACGGGCTGGGGGAG	3180
QY	1061	AlAleuGlYProAlAserAryGThrsSerSerSerGlYSerAlglUProGlYAlAlA	1080
Db	3181	GCCTGTGGCCCTGCTGCCGCCGACACAGACAGCGGTGGGCAAGCCTGGGGGGGCC	3240
QY	1081	HIAsGlUleYrLysSerProProSerAlAAsrSerSerProHisSerProTPSerAlAlA	1100
Db	3241	CACAGAGATGAAGTCAACGGCCACAGGCGCGGACGCTTCCGACAGCCCTCGAGCGCTGA	3300
QY	1101	SerSerTPThrSsrAryArGsrSerSerAryAsnSerLeuGlYArgAlAProSerLeuLys	1120
Db	3301	AGCAGCTGGACCAACAGAGCGCTCCAGCGGAAACGCTCGGCGGTGACCCAGCTGAAG	3360
QY	1121	ArgArGsrProSerGlYGlUArGArGsrSerLeuLeuSerGlYGlUglYGlNGlUserGlN	1140
Db	3361	CGAGAAAGCCCAAGTGAAGAGCGCGGCTCTCTGTTCGGGAAGAAAGCCAGAGAGCCAG	3420
QY	1141	AspGlUglUglUserSerGlUglUglUArgAlAserProAlAgLysrAspHIAsrGHIs	1160
Db	3421	GATGAAGAGGAGACTCAGAAAGAGAGACGGGCGACCTCGGGCAGTGAACATCGCCAC	3480
QY	1161	ArgGlYserLeuGlUArgGlUAlAlYsSerSerPheAspLeuProAsPThrLeuGlnVal	1180
Db	3481	AGGGGGTCCCTCGAGCGGGAGGCCCAAGTTCCTTTAAGCTGCCAGACACATCGCAGGTG	3540
QY	1181	ProGlYleuHIAsrGThrAlAserGlYArgGlYSerAlAserGlUHIsglNAspCyAsn	1200
Db	3541	CCAGGCGCTGCATCGCATCTGCCATGGCGCCAGAGGTCTCTCTAGACACACGAGACTGAA	3600
QY	1201	GlYrYsSerAlAserGlYArgLeuAlAArgAlAleuAryProAsPProProLeuAsP	1220
Db	3601	GGCAAGTCCGGTTCAAGGCGGCGTGGCCCGGAGCCCTGAGGCTGATGAACCCCACTGAT	3660
QY	1221	GlYAspAspAlAspAspGlUglYAsnLeuSerLysGlYglUArgValAArgAlATPPIle	1240

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Db 3661 GGGGATGACCCCGATGACGAGGGACCTTACGAAAGGGAAACGGCTCCGCGGTGATC 3720
Qy 1241 ArgAlaArgLeuProAlaCyStryLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
    |||||
Db 3721 CGAGCCCGGACTCCCTGCTGCTGCTGCTGAGCGAGACTCCGTGTAGCTTACCTTCCCT 3780
Qy 1261 ProGlnSerArgPheArgLeuLeuCyStryIleIleThrHisIleValMetPheAspHis 1280
    |||||
Db 3781 CCTCAGTCCAGAGTTCCTCCCTGCTGTGCACCGGATCATCAACCAAGAGTTTCAGCAC 3840
Qy 1281 ValValLeuValIleIlePheLeuAsnCyStryIleIleThrIleAlaMetGluArgProIle 1300
    |||||
Db 3841 GTGGTCTTGTTCATCATCTTCTTACTGATCAACATCCGATGAGAGCCGCCAAATTT 3900
Qy 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
    |||||
Db 3901 GACCCCAACAGCGGTGAACGATCTTCTGACCTTCCAAATTACATTTCAACGGAGTCTC 3960
Qy 1321 PheLeuAlaGluMetThrValIleValValAlaLeuGluTyrCysPheGluGluAla 1340
    |||||
Db 3961 TTTCTGCTGATAAATGACAGTGAAGGTGTGTGCACTGGGCTGTGCTTCCGGGAGCAGCG 4020
Qy 1341 TyrLeuArgSerSerTrpAsnValLeuAspGluLeuValLeuIleSerValIleAsp 1360
    |||||
Db 4021 TACCTGCGAGACGATTGAAAGTGTCTGACGCGCTGTGTGTGCTCATCTCCGTATGAC 4080
Qy 1361 IleValSerMetValSerAspSerGluTyrHisIleLeuGluMetLeuArgValLeu 1380
    |||||
Db 4081 ATTCTGCTGTCATGCTCTGACAGCGGACCAAGATCTCTGGGCAAGCTGAGGAGTCTG 4140
Qy 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGluIleValLeu 1400
    |||||
Db 4141 CGGCTGCTGCGGACCCCTGCGCCCTGAGGTGATCAGCGGCGCAGCGGCTGAAAGCTG 4200
Qy 1401 ValValGluThrLeuMetSerSerLeuValProIleGluValIleValIleCysCys 1420
    |||||
Db 4201 GTGGTGAAGACGTGATGCTCTCACTGAACCCATCGCAACATTTGATGATCTGCTGT 4260
Qy 1421 AlaPhePheIleIlePheGluIleLeuGluValAlaGluLeuPheGluVal 1440
    |||||
Db 4261 GCCTTCTTCATCATTTTCCGCATCTTGGGGGTGAGCTTTCAAGGAGAGTTTTCGTG 4320
Qy 1441 CysGluGluGluArgThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
    |||||
Db 4321 TGCACAGGCGCAGGATACCAAGGACATCAACCAATGAATGGACTGTGCGGAGCTTAC 4380
Qy 1461 ArgTrpValArgHisIleValSerTrpAsnPheAsnLeuGluValAlaLeuMetSerLeuPhe 1480
    |||||
Db 4381 CGGTGGGTCCGGCCAAAGTACAACTTTGACAACTTGACCAAGCTGATGTCTCTGTTC 4440
Qy 1481 ValLeuAlaSerLysArgGluTyrValAlaAspIleMetTyrAspGluLeuAspAlaValGlu 1500
    |||||
Db 4441 GTTTTGGCTTCCAAAGATGTTGGTGTGACATCATGATGCAATGGCTGAGATGCTGTGGC 4500
Qy 1501 ValAspGluGluProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520
    |||||
Db 4501 GTGGACCAAGAGCCCATCATGAACCAACAACCCCTGATGCTGTGATCTTCACTCTGCTTC 4560
Qy 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGluValValValGluAsnPhe 1540
    |||||
Db 4561 CTGTCTCATTTGGGCTTCTTGTCTTGAACATGTTTGTGGGTGTGGTGTGGAACATTC 4620
Qy 1541 HisLysCysArgGluHisGluGluGluGluValAlaArgArgArgGluGluValArgLeu 1560
    |||||
Db 4621 CACAAAGTGTGGCGACACACAGAGAGAGAGAGGCGCGCGGAGAGAGAACGCGCTA 4680
Qy 1561 ArgArgLeuGluValLysValArgArg----- 1568
    |||||
Db 4681 CGAAGACTGGAGAAAGAGAGAAATCTAATGCTGACGATGAATTCCTCCGAGC 4740
Qy 1569 -----LysAlaGluCysLysProTyrTyrSerAspTyrSerArgPhe 1582
    |||||
Db 4741 TCAGCCAGCGCTGCGTCAAGAGCCCAAGTGCAAACCTTACTACCGACTACTCCGCTTC 4800
    |||||

Qy 1583 ArgLeuLeuValHisHisIleCysThrSerHisIleTyrLeuAspLeuPheIleThrGluVal 1602
    |||||
Db 4801 CGGCTCTCTGTCACCACTTGTGACACAGCCACTTCTGACTTCTTCACTCAAGGTGTC 4860
Qy 1603 IleGluLeuAsnValValThrMetAlaMetGluHisIleTyrGluGlnProGlnIleLeuAsp 1622
    |||||
Db 4861 ATCGGCTGAACGTGTATCCATGAGCATGAGACCTTACAGCAGGCCCAAGATTCTGAGT 4920
Qy 1623 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642
    |||||
Db 4921 GAGCTCTGAAGATCTGCAACTACATCATCTGATCATCTTTGTCTGAGTCAAGTTTC 4980
Qy 1643 LysLeuValAlaPheGluPheArgArgPhePheGlnAspArgTrpAsnGluLeuAspLeu 1662
    |||||
Db 4981 AAACCTGTGGCTTTTGTCCGTCCGTCTTCCAGAGACAGGTGAACAGCTGAGCACCTG 5040
Qy 1663 AlaIleValLeuLeuSerIleMetGluIleThrLeuGluGluIleGluValAsnAlaSer 1682
    |||||
Db 5041 GCCATTGTGCTGTTCATCATGAGGCATACGCTGAGAGAAATCGAGGTCAACGCTTCG 5100
Qy 1683 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgValLeu 1702
    |||||
Db 5101 CTGCCATCAACCCCAACATCATCCGCATCATGAGGCTCTGGCATTCGCCGAGTGTGCTG 5160
Qy 1703 LysLeuLeuLysMetAlaValGluMetArgAlaLeuLeuAspThrValMetGluAlaLeu 1722
    |||||
Db 5161 AAGCTCTGAAGATGAGTGTGGCATGCGGCGCTCTGAGACAGGTGTGCGAGGCTTCG 5220
Qy 1723 ProGlnValGluValLeuGluIleLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu 1742
    |||||
Db 5221 CCCAGGTGGGAAACCTGGAGCTTCTTCACTGTGTGTGTTTCACTTTTGACAGCTCTG 5280
Qy 1743 GluValGluLeuPheGluLysPheGluCysAspGluThrHisAspCysGluGluLeuGlu 1762
    |||||
Db 5281 GGGTGAAGCTCTTTGGAAGACCTGAGTGTGACGAGACACACCCCTGTGAGGCGCTGGG 5340
Qy 1763 ArgHisAlaThrPheArgAsnPheGluMetValAlaPheLeuThrLeuPheArgValSerThr 1782
    |||||
Db 5341 CGTCAATGCCACTTTTGGAACTTTGGCATGCGCTTCTTAACCTCTTCCGAGTCTCCAC 5400
Qy 1783 GlyAspAsnThrAsnGluIleMetLysAspThrLeuArgAspCysAspGluGluSerThr 1802
    |||||
Db 5401 GTGACAAATTGAAATGACATTAAGAAGAACCTTCGGAGCTGTACACAGAGTCCACC 5460
Qy 1803 CysTrpAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822
    |||||
Db 5461 TGCCTAACACGCTCATCTCGCTATCTTGTGTCTTGTGCTGACGCGCCAGTTC 5520
Qy 1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1842
    |||||
Db 5521 GTGCTAGTCAACGTGTGATCGCGCTGATGATGAACACTTGAGAGAGCAACAAGAGAG 5580
Qy 1843 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerPro 1862
    |||||
Db 5581 GCCAAGAGAGGCGCAGCTGAGGCTGAGCTGAGACTGAGAGTGAAGAACCTTCACGCC 5640
Qy 1863 GlnProHisSerProLeuGluLysSerProPheLeuTrpProGluValGluGluProAspSer 1882
    |||||
Db 5641 CAGCCCACTCGGCATCTGGGAGGCCCTTCTCTTGGCTGTGGCTGAGGGCCCCGACAGC 5700
Qy 1883 ProAspSerProLysProGluAlaLeuHisAspProAlaHisIleAlaArgSerAlaSerHis 1902
    |||||
Db 5701 CCCGACAGCCCCAAGCTGGGGCTGTGACCCAGCGGCCCAACGAGATCAGCTCCAC 5760
Qy 1903 PheSerLeuGluHisProThr----- 1909
    |||||
Db 5761 TTTTCCCTGAGACCCCAACGAGACAGGACGCTGTTGAACCAATATCCTGCTGATCCAG 5820
Qy 1909 ----- 1909
    |||||
Db 5821 GGCTCCCTGAGTGGAGCTGAAGCTGATGACGAGCTGGACAGGCCCAAGGGGCGCAGCCC 5880
    |||||
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QY 1909 ----- 1909  
Db 5881 TCTGCTTCCCTTTCGCCCCAGCCTGGAGAGGCTCCGACCACAGATCCCTTACTGTAG 5940  
QY 1909 ----- 1909  
Db 5941 ATGAGAGCTCTGTCTGTGACGTGACAGATGTGTGTGAACCGGTCTGTCTGTAGCTTG 6000  
QY 1909 ----- 1909  
Db 6001 ACGGATGACTCTTTCGCTGATGACATGACACACTCTTAATTAGTCCCTGGAGAGCAAT 6060  
QY 1910 MetGlnProHisProThrGlnLeuProGlyProAspLeuLeuThrValArgIlySerGly 1929  
Db 6061 ATGCAGCCCCACCCCAACGAGCTGCAAGACAGACTTACTGACTGTGCGGAGGTCTGG 6120  
QY 1930 ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla 1949  
Db 6121 GTGAGCGGAACGCACTCTGTGCCCATTGACAGCTACATGTCGTGCGATGGAGCACTGCC 6180  
QY 1950 GlnGlyIProLeuGlyIHisArgGlyIYTPGlyLeuProIlyAlaGlnSerGlySerValLeu 1969  
Db 6181 GAGGGGCCCCCTGGGACACAGGGGCTGGGGCTCCCAAGCTCAGTCAGGCTCCGCTTG 6240  
QY 1970 SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProIlyAspAlaPro 1989  
Db 6241 TCCGTTTCACTCCCAACGACAGATACAGCTACATCTGAGCTTCCCAAGATGACCT 6300  
QY 1990 HisLeuLeuGlnProHisSerAlaProThrTyrGlyIThrIleProIlyLeuProPro 2009  
Db 6301 CATCTGCTCAGACCCCAACAGCGGCCCAACCTGGGGACCATCCCAACTGCCCCACCA 6360  
QY 2010 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2029  
Db 6361 GAGCGCTCCCTTGGCTCAGAGGCCACTCAGCGGCAGACCAATTAAGACTGACTCC 6420  
QY 2030 LeuAspValGlnGlyLeuGlySerArgGlyAspLeuLeuAlaGlyValSerGlyProSer 2049  
Db 6421 TTGGACGTTCAAGGCTCTGGGAGCCGGGAAGACTCTGCGAGAGTGAAGTGGCCCTCC 6480  
QY 2050 ProProLeuAlaArgIleTyrSerPheTyrGlyIleSerSerThrGlnAlaGlnGlnHis 2069  
Db 6481 CCGCCCTGGCCCGGGGCTACTCTTCTGGGGCCAGTCAAGTACCAGACAGCAGCAC 6540  
QY 2070 SerArgSerHisSerIlySeriIleSerIlyHisMetThrProProAlaProCysProGlyPro 2089  
Db 6541 TCCCGAGACCAAGAGATCTCAAGCAATACCCCGCAGCCCTTGGCCCAAGGCCCA 6600  
QY 2090 GlnProAsnTyrGlyIlySerGlyProProGlyIThrArgSerSerLeuGlnLeuAspThrGln 2109  
Db 6601 GAACCCAACTGGGGCAAGGGCCCTCCAGAGACCAAGACAGCTTAAGTTGACACGGAG 6660  
QY 2110 LeuSerTyrIleSerGlyAspLeuLeuProProGlyIlyGlnGlnGlnIlyProProSerPro 2129  
Db 6661 CTGAGCTGATTTCAAGAGACTCTGAGCCCTCGGGGCGCAGAGAGAGCCCATCCCA 6720  
QY 2130 ArgAspLeuIlySeriCysTyrSerValGlnAlaGlnSerCysGlnArgArgProThrSer 2149  
Db 6721 CGGAGACCTGAAGAGTGTACACGCTGGAGGCCCAAGAGCTGCGAGCGCCCTTACGTC 6780  
QY 2150 TyrLeuAspGlnGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGln 2169  
Db 6781 TGGCTGATAGAGAGAGACACTTATGCGGTACGCTGACGCTGGAACAGCGGCTCCAA 6840  
QY 2170 ProHisLeuGlyIThrAspProSerAsnLeuGlyIlyGlnProLeuGlyIlyProGlyIlySer 2189  
Db 6841 CCCACCTGGGCAACAAGCCCTCTAACCTTGGGGGCGAGGCTCTTGGGGGCGCTGGAGAG 6900  
QY 2190 ArgProIlySeriIlySeriProProSerIleThrIleAspProProGlyIlyGlnGly 2209  
Db 6901 CGGCCCAAGAAAAAATCAGACCCGCTTAATATACCATATACACCCCGGAGAACAGGT 6960  
QY 2210 ProArgThrProProSerProGlyIlyCysLeuArgArgArgAlaProSerSerAspSer 2229

Db 6961 CCTGGACCCCGCCAGCCCTGTATCTGCTCCGAGAGAGGGCTCCGTCCAGGACATCC 7020  
QY 2220 LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProIlySyls 2249  
Db 7021 AAGGATCCCTTGGCTCTGGGCCCCCTTCAAGCAAGCTGCTGCTCCCTCCCAAGAAA 7080  
QY 2250 AspValLeuSerLeuSerGlyIlyLeuSerSerAspProAlaAspLeuAspPro 2266  
Db 7081 GATGTGAGTCTCTCCGATTATCTTGACCCAGACAGACTGGACCCC 7131  
RESULT 5  
AA83484  
ID AA83484 strand; cDNA; 6729 BP.  
AC AA83484;  
AT 07-DEC-1999 (first entry)  
DE Human T-type voltage-gated Ca channel alpha-1-G (hcaVT1d) cDNA.  
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.  
XX Homo sapiens.  
OS  
PN WO9929847-A1.  
PD 17-JUN-1999.  
PF 30-OCT-1998; 98WO-US023161.  
PR 05-DEC-1997; 97US-00985809.  
PA (LOYO ) UNIV LOYOLA CHICAGO.  
PI Perez-Reyes E, Cribbs LL;  
XX WPI: 1999-394972/33.  
XX DR P-PSDB; AA114589.  
XX PS New T-type voltage-gated calcium channels.  
XX Disclosure: Page 58-67; 138bp; English.  
XX This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hcaVT1d. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The CC sequences AA83481-83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AA114598. Cells CC expressing the T-type voltage-gated calcium channel proteins can be used CC to screen for drugs which affect calcium channels. Methods are also CC disclosed for treating a disease or disorder associated with a deficiency CC in a native T-type calcium channel nucleic acid, e.g. to treat CC cardiomyopathy, epilepsy, etc  
XX  
SQ Sequence 6729 BP; 1283 A; 2168 C; 1975 G; 1303 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 0 Length: 6729  
Score: 11758.50 Matches: 2242  
Percent Similarity: 98.94% Conservative: 0  
Best Local Similarity: 98.94% Mismatches: 1  
Query Match: 98.78% Indels: 23  
DB: 2 Gaps: 1

US-09-611-257a-37 (1-2266) x AAX83484 (1-6729)

QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20  
Db 1 ATGGACGAGGAGGAGATGAGAGCGGGCGCGGAGAGTCCGGGACAGCCCGGAGCTTCATG 60  
QY 21 ArgLeuAnaAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGlyLeuAsp 40  
Db 61 CGGCTCAACACGCTGTGGGGGGCGGGGGGGCGGGGGCGGGGGCTCAGCAGAAAGAGAC 120  
QY 41 ProGlySerAlaAspSerGlyAlaGlyGlyLeuProGlyProAlaLeuAlaProVal 60  
Db 121 CCGGGCGCGCGGACTCCGAGGCGGAGGGGGCTGCCGACCCGGGGCTGGCCCGGGTGT 180  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgTyrValCysAsn 80  
Db 181 TTCTTCTTACTTGACCGAGACAGCCGCCCGGAGCTGGTGTCTCCGACGGTCTGTAC 240  
QY 81 ProTyrPheGluArgLysSerMetLeuValIleLeuLeuAnaCysValIleLeuGlyMet 100  
Db 241 CCGGTGGTTGAGCGCATCAGCATGTGTGTATCTTCTCAACTGCTGACCCCTGGGCATG 300  
QY 101 PheArgProCysGluAspGlyLeaIleCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
Db 301 TTCGGGCGATGCGAGCATCGCTGTGACTCCGAGCGCTGCCGATCTGCGAGGCTTT 360  
QY 121 AspAspPheIlePheAlaPhePheAlaValIleuMetValValIleuMetValIleuGly 140  
Db 361 GATGACTTCATCTTGGCTTCTTGGGTGGAGATGGTGGAGATGGTGGCTTTGGGC 420  
QY 141 IlePheGlyLeuAlaCysTyrLeuGlyAspTyrTrpAsnArgLeuAspPheIleVal 160  
Db 421 ATCTTTGGGAAAAAGTGTATCTGGAGACACTTGGAAACCGGCTTGACTTTTCATGCTC 480  
QY 161 IleAlaGlyMetLeuGlyTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
Db 481 ATCCAGAGGATGCTGAGTACTCTGCTGACTGACAGAACGTCACACTTCTCAGCTGTAGG 540  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 541 ACAAGTCGGTGTGCTGCAACCGCTCAAGGCGCATTTAACCGGGTGGCCAGACATCGATCCT 600  
QY 201 ValIleLeuLeuLeuAspTyrTrpLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
Db 601 GTCAAGTTGGCTGGGANTAGCTGCCATGCTGGGCAACGTCGTCGCTGTGCTTCTTC 660  
QY 221 ValPhePheIlePheGlyIleValIleGlyValIleGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
Db 661 GTCTTCTTCATCTTCGGCATGCTGGCGCTCCAGCTGTGGGCGAGGCGTGTTCGGAACCGA 720  
QY 241 CysPheLeuProGlyuAsnPheSerLeuProLeuSerValAspLeuGlyuArgTyrTyrGln 260  
Db 721 TGCTTCTCACTGAGAAATTCAGCTCCCTCGAGCGTGGACCTGGAGCGCTATTACAG 780  
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
Db 781 ACAGAGAAAGAGATGAGAGCCCTTCATCTGCTCCAGCCAGCGAGAAAGGATGGCG 840  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
Db 841 TCTCGAGAAACGTGGCCACGCTGGCGGGGAGCGGGGCGGGTGGCCACTTGGCGTCTG 900  
QY 301 AspTyrGlyuAlaTyrAsnSerSerSerAsnThrCysValAsnTrpAsnGlnTyrTyr 320  
Db 901 GACTATGAGGCTTACAAAGCTCCAGCAACCACTGTGTCACTGGAACCAATACAC 960  
QY 321 ThrAsnCysSerAlaGlyIleuIleAsnProPheLeuGlyAlaIleAsnPheAspAsnIle 340  
Db 961 ACCAAGCTGCTACGGGGGAGCAACCCCTTCAAGGGCGGCATCACTTTGACAAACATT 1020  
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlyGlyTyrValAspIleMet 360

Db 1021 GGCTATGCTGGATGCGCATCTTCCAGTCACTACGCTGAGGGCTGGTGCATCATG 1080  
QY 361 TyrPheValMetAspAlaIleSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
Db 1081 TACTTGTATGATGATCTCATCTTCTTCAATTCATCTACTCATCTCTCCATCATCTC 1140  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
Db 1141 GTGGGCTCTCTTCTTCAAGATCAACTGTGCTGGTGTATTCGCCAGCATCTTCAGAG 1200  
QY 401 ThrLeuGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
Db 1201 ACCAAGCAGCGGGAAGCCAGCTGATGGCGGAGCAGCGTGGCGTTCCTGTCAACGCC 1260  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGlyGluLeuLeuLeuTyrLeu 440  
Db 1261 AGCACCCTGGCTGACTTCTCTGAGCCCGGACGCTGTATGAGGAGCTGTCAAGTACTG 1320  
QY 441 ValTyrIleLeuArgGlyAlaIleArgArgLeuAlaGlnValSerArgAlaIleGlyVal 460  
Db 1321 GTGTACATCTTCTGTAAAGGACGCCGAGGCTGGCTCAGGCTCTTGGGACGAGGTGTG 1380  
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
Db 1381 CGGCTTGGGCTGCTCAGCAGCCAGCACCCTCGGGGGCGCAGGAGACCCAGCCACAGC 1440  
QY 481 SerCysSerArgSerIleArgArgLeuSerValIleIleIleValIleIleIleIleIle 500  
Db 1441 AGCTGCTGCTGCCACCGCCGCTATCCGTCCACACCTGCTGACCAACCAACCAAC 1500  
QY 501 HisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 520  
Db 1501 CATCACCAACACATCAACCTGGGCAATGGGACCTGAGGCGCCCGGGGACCGGAG 1560  
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540  
Db 1561 ATCCAGAGCAGGATGCAATGGTCCCGCGGCTCATGTGCAACACCTCGAGCGCT 1620  
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValIleSerPheTyrHisAlaAsp 560  
Db 1621 GCCCTCCGGGGCCCCCTCGTGGCGGAGTCTGTGACAGCTTCACTACATGCGCAG 1680  
QY 561 CysHisHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGlyAlaSer 580  
Db 1681 TGCACATTAAGCAGTCCCTGCTCCAGGCGCCCTCCAGGTCCTCATGTAGGACATCC 1740  
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600  
Db 1741 GGCAGACTGTGGGACGGGAAAGTGTATCCACCGTGACACAGCCCTCCACCGGAG 1800  
QY 601 ThrLeuLysGlyLysAlaLeuValIleValAlaIleSerSerGlyProProThrLeuThr 620  
Db 1801 ACGCTGAAGAGAAAGGACATAGTAGTGTGCGCAGCTGTGGGCCCCCAACCTCACC 1860  
QY 621 SerLeuAsnIleProProGlyProTyrTyrSerSerMetHisIleTyrLeuLeuGlnSer 640  
Db 1861 AGCTCAACATCCACCCGGGCTTCAAGCTCAATGACAAAGCTGTGGAGACAAAGT 1920  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
Db 1921 ACAAGTCCCTGCCAAGCTTTCAGAGATCTCCAGCCCTTGTGAAAGCAGACAGTGA 1980  
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyLeuGluLeu 680  
Db 1981 GCGTGTGTCAGACAGCTCCCTACTGTGCCGGGCGGGGCGAGGAGGTGAGACTC 2040  
QY 681 AlaAspArgIleuMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
Db 2041 GCCAAGCGTGAATGTGTACTGACAGAGGAGGAGCTTATAGTTTCAACAGAGATGCC 2100  
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
Db 2101 CAGCAGAGCACTCCGGGACCCCAAGCCGCGGAGAGGAGGCTGGGCCCAAGATGCA 2160

QY 721 GluProSerSerValIleuAlaIleuAlaPheTTPArgIleuIleCysAspThrPheArgIleVal 740  
Db 2161 GAGCCAGAGCTGTGTGGCTTGTGGAGCTATCTGTGACACCTTCCGAAAGATTGG 2220  
QY 741 AspSerIleTyrPheGlyArgGlyIleMetIleAlaIleuValAsnThrLeuSerMet 760  
Db 2221 GACAGCAAGTACTTGGCCGGGGAATCATGATCGCATCTGGTGTCAACACTCAGCATG 2280  
QY 761 GlyTlIleGluTyrHiIseGluGlnProGluGluLeuThrAsnAlaIleuGluIleSerAsnIle 780  
Db 2281 GGCATGGAATACCAACAGACGCCGAGAGCTTACCAACGCCCTAGCAAAATCAGCAATC 2340  
QY 781 ValPheThrSerIleuPheAlaIleuGluIleuMetIleuLeuLeuValTyrGlyProPhe 800  
Db 2341 GTCTTACCAAGCTCTTGTGCTGTGAGATGTCTGAAAGCTGTGTGTGTGTGTCTCTT 2400  
QY 801 GlyTyrIleuAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyr 820  
Db 2401 GGCTACATCAAGATCCCTACACATCTTGATGTGTATGTGTGTATGTGTGTGTGTGTG 2460  
QY 821 GluIleValGlyGlnGlnGlyGlyIleuSerValIleuArgThrPheArgIleuMetArg 840  
Db 2461 GAGATGTGGCCAGCAGGAGGGGGCGGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTG 2520  
QY 841 ValIleuLeuValArgPheLeuProAlaIleuGlnArgGluIleuValValIleuMetLys 860  
Db 2521 GTCTGAAAGTG 2580  
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880  
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QY 921 ThrGlnGluAspTyrAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTyrAla 940  
Db 2761 ACCAAGAGAGCTGGAACAAGTCTCTCAATGATGATGCTTCCAGTGTGTGTGTGTGTGTG 2820  
QY 941 AlaLeuTyrPheIleAlaIleuMetThrPheGlyAsnTyrValIleuPheAsnIleuVal 960  
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QY 961 AlaIleuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980  
Db 2881 GCCATTCTGTGTGAGGCTTCCAGGCGAG----- 2910  
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyValAspAlaAsnLysSerGln 1000  
Db 2911 -----GAGATGCCAAAGTCCGAA 2931  
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020  
Db 2932 TCAGACCGCGATTTCTTCAACCAACCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2991  
QY 1021 AlaLeuValSerIleuGlyGluHiIseProGluLeuArgLysSerLeuLeuProLeuIle 1040  
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QY 1041 IleHiIseThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGln 1060  
Db 3052 ATCCACACGGCGCGCACACCATG 3111  
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080  
Db 3112 GCCTGTGGCGCTG 3171

QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTyrPheAlaAla 1100  
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QY 1101 SerSerTyrPheThrSerArgArgSerSerArgAsnSerLeuGlyValArgAlaProSerIleuLys 1120  
Db 3231 AGCAGCTGAGCAGCAGCGCTGCCAGCCGGAACACCTCGCGCGTGCACCCAGCTGTAG 3291  
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QY 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160  
Db 3352 GATGAAGAGGAGCTCAGAAAGAGAGGGGCAACCTCGCGGAGTACATGCGCAC 3411  
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrIleuGlnVal 1180  
Db 3412 AGGGGCTCCCTGAGCGGAGGCGCAAGATTCTTGTACCTGTCCAGACACTGTGAGGTG 3471  
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200  
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QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeuAsp 1220  
Db 3532 GCGAAGTGGCTTCAAGGGGCGCTGGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3591  
QY 1221 GlyAspAspAlaAspAspGluGluLysLeuSerLysGlyGluArgValArgAlaTyrIle 1240  
Db 3592 GGGGATGACCGCGAAGAGAGGGCAACCTGAGCAAAAGGGGAACGGGTCCGCGGTGATC 3651  
QY 1241 ArgAlaArgLeuProAlaCysTyrIleuGluArgAspSerTyrPheAlaTyrIlePhePro 1260  
Db 3652 CGAGCCGAGCTCCCTGCTGTGCTG 3711  
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280  
Db 3712 CCTGATCGAGTTCCGCTCCTG 3771  
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300  
Db 3772 GTGTGTCTTGTATCATCTTCTTAACTGATCAATCAATCGCATCGATGAGCGCCCAAAAT 3831  
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLysSerAsnTyrIlePheThrAlaVal 1320  
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QY 1321 PheLeuAlaGluMetThrValLysValAlaAlaIleuGlyTyrCysPheGlyGluGlnAla 1340  
Db 3892 TTTCTGTGGTAATGACAGTGAAGGTGGTGGCATCGGGCTGTGTGTGTGTGTGTGTGTGTGTG 3951  
QY 1341 TyrLeuArgSerSerTyrAsnValIleuAspGlyLeuLeuValIleuIleSerValIleAsp 1360  
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Db 4012 ATCTG 4071  
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysIleu 1400  
Db 4072 CGGCTG 4131  
QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420  
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QY 1421 AlaPhePheIleIlePheGlyTyrIleuGlyValGlnLeuPheLysGlyLysPhePheVal 1440  
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QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460

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Qy 1461 ArgTrpValArgHisIleTyraAsnPhaAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
Db 4312 CGGAGGATCCGGCAGCAAGTACAACTTTGACAACTTGGCCAGGCCCTGAGATGCTCCTTTC 4371
Qy 1481 ValLeuAlaSerIleAspGlyTTPValAspIleMetTyraAspGlyLeuAspAlaValGly 1500
Db 4372 GTTTGGCTCTCAAGATGTGTTGGGTGAGCATGATGAGTGGGTGATGCTGTGTGGCC 4431
Qy 1501 ValAspGlnGlnProIleMetAsnHisAsnProThrMetLeuLeuTyrrPheIleSerPhe 1520
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Qy 1541 HisIleCysAspArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLeu 1560
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Qy 1561 ArgArgLeuGluIleValIleValIleValIleValIleValIleValIleValIleVal 1600
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Qy 1581 ArgPheArgLeuLeuValHisHisIleLeuCysThrSerHisIleTyrrLeuAspLeuPheIleThr 1600
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Db 4792 CTGATGAGGCTCTGAAAGATGTGCAACATTCATCTTCACTGTCATCTTGTGTGTGAGTCA 4851
Qy 1641 ValPheIleValAlaPheGlyPheArgArgPhePheGlnAspArgTTPAsnGlnLeu 1660
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Qy 1761 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780
Db 5212 CTGGGCGCTCATGCCACTTTTGGAACTTTGGCATGGCTTCTTCACTTCCGATTC 5271
Qy 1781 SerThrGlyAspAsnTTPAsnGlyIleMetIleAspThrIleLeuArgAspCysAspGlnGlu 1800
Db 5272 TCACAGAGTGAACAAATTGGAATGCAATATGAAGGACACCTTCGGGAGCTGTGACACAGAG 5331
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Qy 1861 SerProGlnProHisSerProLeuGlySerProPheLeuTTProGlyValGluGlyPro 1880
Db 5512 AGCCCCAGGCCCACTGCGACATGGGAGAGCCCTTCTGCTGCTGGGTGGAGGGCCCC 5571
Qy 1881 AspSerProAspSerProIleValIleLeuHisProAlaHisAlaIleArgSerAla 1900
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Db 5692 GACTTACTGACTGTGGGAAAGTCTGGGGTCAAGCCGAACGACTCTGCGCCAAATGACAGC 5751
Qy 1941 TyrrMetCysArgHisGlySerThrAlaGluGlyProLeuGluIleHisArgGlyTTPGlyLeu 1960
Db 5752 TACATGTGTGGCATGGAGACATGCGCGAGGGGCCCTGGGAGACAGGGGCTGGGGCTC 5811
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Db 5812 CCAAAGCTAGTGAAGCTCTGCTTGTGCTTCACTCCAGACAGACAGTACAGCTAC 5871
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Db 5872 ATCCTGAGCTTCCCAAGATGACACTCATCTGCTCAGCCCAAGCGCCCAACTGG 5931
Qy 2001 GlyThrIleProIleValLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArg 2020
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Qy 2041 LeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrrSerPheTTPGly 2060
Db 6052 CTGCTGGCAGAGTGAAGTGGGCTCTCCCGCTGGCCGGGGCTTACTTCTTGGGGC 6111
Qy 2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerIleValIleMet 2080
Db 6112 CAGTCAAGTACCAAGCAGCAGCACTCCCGAGCCAGACAGCAAGATCTCCAGACATG 6171
Qy 2081 ThrProProAlaProCysProGlyProGluProAsnTTPGlyIleGlySerProGluThr 2100
Db 6172 ACCCGGCAAGCCCTTGTCCAGAGCCCAAGAACCAACTGGGAGAGGCCCTTCCAGAAC 6231
Qy 2101 ArgSerSerLeuGluLeuAspThrGluLeuSerTTPIleSerGlyAspLeuLeuProPro 2120
Db 6232 AGAAGCAGCTTAAAGTTGACACAGAGCTGAGTTCAGAGAGACTCTTGGCCCCCT 6291
Qy 2121 GlyIleGlnGluGluProProProSerProArgAspLeuIleValCysTyrrIleSerValGluAla 2140
Db 6292 GCGCGCAGAGAGAGGCCCATCCCAAGGAGCTTGAAGAGTGTTCACAGCTGGAGGCC 6351
Qy 2141 GlnSerCysGlnArgAspProThrSerTTPLeuAspGluGlnArgArgHisSerIleAla 2160
Db 6352 CAGAGCTGCAAGCCCGGCTTACGTCTGCTGATGAGAGAGAGACACTCTATGACC 6411
Qy 2161 ValSerCysLeuAspSerGlySerGlnProHisIleLeuGlyThrAspProSerAsnLeuGly 2180
Db 6412 GTACGCTGCTGAGCAAGCGGTCCCAACCTCGGAGCAGAGCCCTCTAACCTTGGG 6471
```



QY AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyr 320  
 |||  
 Db GACTATAGAGGCTTCAACAGCTCCAGCAACACCACTGTGTCACTGAACCACTACTAC 960  
 QY ThrAsnCysSerAlaGlyGluHisAsnProPheIysGlyAlaIleAsnPheAspAsnIle 340  
 |||  
 Db ACCAAGCTCTCAGCGGGAGACACACCCCTTCAGAGGGCCGCTCAACTTGTGACAACATT 1020  
 QY G1YrYrAlaTyrIleAlaIlePheGlnValIleThrLeuGlnGlyTyrValAspIleMet 360  
 |||  
 Db GGCTATGCTCGGATGGCATCTTCAGGTATCAAGCTGAGGGCTGGGTTCGATCATG 1080  
 QY TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuIleIle 380  
 |||  
 Db TACTTGTGATGATGTCTCATCTCTTCACAAATTTCATCTCACTTCCTCATATC 1140  
 QY ValG1YSerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
 |||  
 Db GTGGGCTCTCTTCATGATCAACCTGTGCTGTGTGTGATTCGACGCACTTCAGAG 1200  
 QY ThrIysGlnArgGlnSerGlnLeuMetArgGlnGlnArgValArgPheLeuSerAsnAla 420  
 |||  
 Db ACCAAGCAGCGGAAAGCACTGATGGGAGCAGGGTGTGGGTTCTGTCCAAAGCC 1260  
 QY SerThrLeuAlaSerPheSerGlnProGlySerCysTyrGlnGlnLeuLeuTyrLeu 440  
 |||  
 Db AGCACCTGGGCTACTCTCTGAGCCCGGACGTGCTATGAGGAGCTGCTCACTACACTG 1320  
 QY ValTyrTrIleLeuArgValAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
 |||  
 Db GTGTACATCTCTTCTTAAGGCAAGCCGCGAGCTGTCAAGTCTCGGGCAGCAGGTGTG 1380  
 QY ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlnGlnTyrGlnProSerSer 480  
 |||  
 Db CGGGTGGGCTGCTCAGCAGCCAGCAACCTCGGGGGCCAGGAGCCCAAGCCCAAGAGC 1440  
 QY SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisIleHis 500  
 |||  
 Db AGCTGCTCTCGCTCCACCGCGCTATCCGTCCACCACTGGTGACCAACACACACACAC 1500  
 QY HisHisHisIleTyrHisIleGlnValAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
 |||  
 Db CATCAACCACTACCTAGCTGGCAATGGAGAGCTCAGAGGCCCGCGGCAAGCCCGAG 1560  
 QY IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540  
 |||  
 Db ATCCAGAGCAGGATGCCAATGGGTCCCGCGCTCATGCTGCCACCACTTCAGCGCT 1620  
 QY AlaLeuSerGlyAlaProProGlyGlyValaGlnSerValHisSerPheTyrHisIleAsp 560  
 |||  
 Db GCCCTCTCGGGGGCCCCCTGGTGGCGCAAGTGTGCAAGCTTCTCAATGCCAGC 1680  
 QY CysHisIleLeuGlnProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
 |||  
 Db TGCCACTTAGAGCCAGTCCGTGCGCAGGGCGCCCTCCAGGTCCCAATCGAGCATCC 1740  
 QY G1YrArgThrValGlySerGlyValValTyrProThrValHisThrSerProProProGlu 600  
 |||  
 Db GGCGAGACTGTGGGCGAGCGGAGGTGTATCCCACTGGACACCAAGCCCTCCACCGGAG 1800  
 QY ThrLeuIysGlnValValaLeuValGlnValAlaAlaSerSerGlyProProThrLeuThr 620  
 |||  
 Db ACGCTGAAGAGAGGACACTAGTAGAGGTGGCTGCAAGCTCGGGCCCCCAACCTTCACC 1860  
 QY SerLeuAsnIleProProGlyProTyrSerSerMetHisIysLeuLeuGlnThrGlnSer 640  
 |||  
 Db AGCCTCAACATCTCCACCGGGCCCTTACAGCTTCATGCAAGCTGTGAGACACAGAGT 1920  
 QY ThrGlyAlaCysGlnSerSerCysIysIleSerSerProCysLeuValaAspSerGly 660  
 |||  
 Db ACGAGTGGCTGCGCAAGCTCTTGCAGAGATCTCAAGCCCTGTGTTGAAAGCAGACAGTGG 1980  
 QY AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGlnValaGlnLeu 680

Db GCCTGTGCTCAGACAGCTGCCCTTACTGTGCCCGGGCCGAGGGAGGTGGAGCTC 2040  
 QY AlaAspArgGlnMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
 |||  
 Db GCCGACCGTGAATGTGCTGACTCAGACAGCGAGCGAGTTATGATTCAACACAGGATGCC 2100  
 QY GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720  
 |||  
 Db CAGCAGCAGCAGCTCCGGAGCCCCACAGCGCGGAGCAGAGCCTGGGCCAGATGCA 2160  
 QY GluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgIleVal 740  
 |||  
 Db GAGCCAGCTCTGTGCTGTGCTTCTGAGAGCTTATGTGACACCTTCGAAAGATTGTG 2220  
 QY AspSerIysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
 |||  
 Db GACAGCAAGTATTGGCCGGGGAATCATGATGCCATCTGTGTCAACACACTCAGCATG 2280  
 QY GlyTrIleGlnTyrHisGlnGlnProGlnGlnLeuThrAsnAlaLeuGlnIleSerAsnIle 780  
 |||  
 Db GGCAATGCAATACCAAGCAGCAGCCCGAGAGCTTACCAAGCCCTAGAAATCAGCAATC 2340  
 QY ValPheThrSerLeuPheAlaLeuGlnMetLeuLeuIysLeuLeuValTyrGlyProPhe 800  
 |||  
 Db GTCTTACAGCCTCTTGTGCTTGGAGATGCTGTGAGCTGTGTGTATGATCCTTT 2400  
 QY GlyTyrTrIleIysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTyr 820  
 |||  
 Db GGCTACATCAAGAAATCCCTTCAACATCTTCATGATGTGTATGTGATCAGCGTGTG 2460  
 QY GlnIleValaGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840  
 |||  
 Db GAGATCGTGGCCAGCAGCGGGGGCGGCTGTGCTGTGGAGCTTCCCTCGATGCGT 2520  
 QY ValLeuIysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetIys 860  
 |||  
 Db GTGCTGAAGCTGTGCGCTTCTCTGCGCGCTGACGCGGAGCTGTGTGTCTCATAG 2580  
 QY ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880  
 |||  
 Db ACCATGAGACAGGAGGCACTTCTGTGATGCTGTATGCTTTCATCTTCATCTTCAGC 2640  
 QY IleLeuGlyMetHisIleLeuPheGlyCysIysPheAlaSerGlnArgAspGlyAspThrLeu 900  
 |||  
 Db ATCTGGGCAATGATCTCTTCCGTGCAAGTTGCCCTGAGCGGAGTGGAGACCTTG 2700  
 QY ProAspArgIysAsnPheAspSerLeuTyrAlaIleValThrValPheGlnIleLeu 920  
 |||  
 Db CCAGACCGGAAGAAATTTTGACTCTGTGCTGTGGCCATGTCTACTGTCTTCAGATCTTG 2760  
 QY ThrGlnGlnAspTyrAsnIysValLeuTyrAsnGlyMetAlaSerThrSerSerTyrAla 940  
 |||  
 Db ACCAGAGAGAGACTGGAACAAAGTCTCTTACAAATGTATGGCTTCACAGTGTGCGGCG 2820  
 QY AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960  
 |||  
 Db GCCCTTATTTCAATGGCTTCATGACCTTCGCAACTACAGTGTGCTTCAATTTGCTGCTC 2880  
 QY AlaIleLeuValaGlnGlyPheGlnAlaGlnGlnIleSerIysArgGlnAspAlaSerGly 980  
 |||  
 Db GCCATTTGTGGAGGGGCTTCAGGGAG----- 2910  
 QY GlnLeuSerCysIleGlnLeuProValaAspSerGlnGlyIysAspAlaAsnIysSerGln 1000  
 |||  
 Db -----GGAAGTGCACCAAGTCCGAA 2911  
 QY SerGlnProAspPhePheSerProSerLeuAspGlyIysAspGlyIysCysLeu 1020  
 |||  
 Db TCAGAGCCGCAATTTCTTCTCAACCAAGCTGAGTGTATGGGAGCAGAGAAAGTGTGTG 2991  
 QY AlaLeuValSerLeuGlyGlnHisArgProGlnLeuArgIysSerLeuLeuProProLeuIle 1040

Db 2992 GCCTTGATGTCCTGGAGAGACCCGAGCTGGAGAAGCCTGCTGCCTCATC 3051  
QY 1041 TLeh1ThrAlaIaIaPhroMetSerLeuProIySerTherThrAlaIyLeuGlyIu 1060  
Db 3052 ATCCACACGCGCCGACACCATGTGCTGCCAAGACACGACGCGGCTGGCGAG 3111  
QY 1061 AlaLeuGlyProIaSerArGaTgThrSerSerSeGlySerAlaIuProGlyAlaIa 1080  
Db 3112 GCGCTGGCCCTTCGCTCGCCGCCACACAGACAGCGGGTCGCAAGCCTGGGGCGCC 3171  
QY 1081 HisGluMetIySerProProSerAlaArGSerSerProHisSerProTTPSerAlaIa 1100  
Db 3172 CACGAGATGAAGTCACCGCCACGCGCCGACCTTCGCCACAGCCCTGGAGCGCTGCA 3231  
QY 1101 SerSerTTPThrSerArGaTgSerSerArGaSerLeuGlyArGaIaProSerLeuIyS 1120  
Db 3232 AGCAGCTGACCCAGCGAGCGCTCACCGGACAGCCTCGCGTGCACCCAGCTGAAG 3291  
QY 1121 ArgArSerProSerGlyGlyArGaTgSerLeuLeuSerGlyGlyIuGlyIuSerGlyIu 1140  
Db 3292 CGGAGAACCCCAAGTCGAGAGCGCGCTCCCTTGTCCGAGAAAGCCAGAGACCAAG 3351  
QY 1141 AspGluGluIuSerSerGluGluIuArGaIaSerProAlaGlySerAphIaArGHis 1160  
Db 3352 GATGAAGAGGAGACTCAGAAAGAGAGCGGCGCAGCCTGCGGCAGTGACCATCCGCCAC 3411  
QY 1161 ArgGlySerLeuIuArGlyIuAlaIySerSerPheApuLeuProApuThrLeuGlyIuAl 1180  
Db 3412 AGGAGGGCTCTGAGCGGAGGCGCAAGAGTTCCTTGACTCGCAACACATCGCAGGTG 3471  
QY 1181 ProGlyLeuHisArGThrAlaSerGlyArGlySerAlaSerGlyIuHisGluIuAspCySaAn 1200  
Db 3472 CCAAGGGTGATGCACTGCGCACTGGCCAGAGGTCTGTTCTGAGCACCAAGCATCGCAAT 3531  
QY 1201 GlyIySerAlaSerGlyArGaIeAlaIeArGaIeArGaIeArGaIeArGaIeArGaIe 1220  
Db 3532 GGCAGAGTCGGCTTCAGAGGCGCTCGCGCCGCGCTCGCTGATACCCGCCCATCGGAT 3591  
QY 1221 GlyAspAspAlaAspAspGluIyAsnLeuSerLeuGlyGlyIuArGaIeArGaIeArGaIe 1240  
Db 3592 GGGAGATGACCCGATACAGAGGCAACCTGAGCAAAAGGAGAGGGATCCGCGGTGATC 3651  
QY 1241 ArgAlaArgLeuProAlaCySArIyLeuGluArGAspSerTTPSerAlaTyrIlePhePro 1260  
Db 3652 CAGGCCGACTCCCTGCTGCTGCTGCTGAGCAGACTCCGTGTCACCTCAATCTTCCT 3711  
QY 1261 ProGluSerArGpheaArgLeuLeuCySHisArGlyIeIleThrHisIySmetPheApuHis 1280  
Db 3712 CCTCAGTCCAGGTTCGCGCTCTGTGTCAACCGATCATCACCAAGATGTTGACACAC 3771  
QY 1281 ValValLeuValIleIlePheLeuAsnCySleThrIleAlaMetGlyIuArGProIySle 1300  
Db 3772 GTGATCTTGTATCATCTTCTTAATGATCATCAATCCAGAGAGGCCCAAAAT 3831  
QY 1301 AspProHisSerAlaIuArGlyIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320  
Db 3832 GACCCCAACGCGCTGAAGCATCTTCGACCCCTCCAAATTAACATCTTCAACGCAAGTC 3891  
QY 1321 PheLeuAlaGluMetThrValIyValValAlaLeuGlyTTPCySPhelGlyIuGlyIuAla 1340  
Db 3892 TTTCTGCTGAAATGACAGTGAAGTGTGGCACTGGGCTGTGCTTCGGGGAGCGGG 3951  
QY 1341 TyrLeuArGSerSerTTPAsnValIleuAspGlyLeuLeuValLeuIleSerValIleAsp 1360  
Db 3952 TACCTGGGAGCAATTGAGAACTGTGAGAGGCTGTGTGCTCATCTTCGTCATCGAC 4011  
QY 1361 IleLeuValSerMetValSerAspSerGlyTThrIySleLeuGlyMetLeuArGaIeVal 1380  
Db 4012 ATTCTGTGTCCATGTGTCTGACAGCGGCAACCAAGATCTCGGCAATGCTGAGGGTGTG 4071  
QY 1381 ArgLeuLeuArGThrLeuArGProLeuArGaValIleSerArGaIaGluGlyIuLeuSleu 1400  
Db 4072 CCGCTCTGGAGACCTGCGCGCTCAGAGGTGATGACCGGCGCAGGGGCTGAAGCTG 4131  
QY 1401 ValValGluThrLeuMetSerSerLeuIyAspProIleGlyAsnIleValIleCyS 1420  
Db 4132 GTGTGAGAGCCCTATGTCTTCACTGAACCCATCGGACCATTTGTATCTGTCTGT 4191  
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGluLeuPheGlyIyAspPheVal 1440  
Db 4192 GCGTTCCTCATCTTGGGCACTTGGGGGTGAGCTTCCAAAGGAAAGTTTTCGTG 4251  
QY 1441 CySginglyIuAspThrArGaSnIleThrAsnIySerAspCySaIaGluIuAspTyr 1460  
Db 4252 TCCAGGGGAGAGATACAGAAACATCACCAATTAATGGACTGTGCCAGGCGCATAC 4311  
QY 1461 ArgTTPValArGHisIySerTyrAsnPheAspAsnLeuGlyIuAlaLeuMetSerLeuPhe 1480  
Db 4312 CCGTGGTCCGCAACATGAACATTTGACAACTTGGCCAGGCCCTGATGCTCTGTTCC 4371  
QY 1481 ValLeuAlaSerIyAspGlyTTPValAspIleMetTyrAspGlyLeuAspAlaValGly 1500  
Db 4372 GTTTTGCCCTCAAGATGTGTGGTGACATGTACGATGGGCTGGATGCTGTGGGC 4431  
QY 1501 ValAspGluGluProIleMetAsnHisAsnProTTPMetLeuLeuTyrPheIleSerPhe 1520  
Db 4432 GTGACACAGACCCCATATGAACCAACCCCTGATGTGCTGTACTTCATCTTCGTTCC 4491  
QY 1521 LeuLeuAlaValAlaPhePheValLeuAsnMetPheValGlyValIValIuAsnPhe 1540  
Db 4492 CTGCTCATTTGTGGCTCTTCTTGTCTTGAACATGTTGTGGGTGTGTGTGAGAACTTC 4551  
QY 1541 HisIySArGaGluHisGluGluIuGlyIuAlaArGaTgArGluGlyIyAspArGaLeu 1560  
Db 4552 CAAAGTGTCCGACACACAGAGAGAGAGAGCGCGCGCGGAGAGAGAGCGCTTA 4611  
QY 1561 ArgArGluGluIyIyAspArg-----LysAlaGluCySlys 1573  
Db 4612 CCAAGATGAGAAAGAGAGAGTGAAGAGAAACAGATGCTGAAGCCAGTGCAGAA 4671  
QY 1574 ProTyrTyrSerAspTyrSerArGpheaArgLeuLeuValHisIleLeuCySTherHis 1593  
Db 4672 CTTTACTACTCCGACTACTCCCGCTTCGGGCTCCGTGTCCACACTTGTGACCAAGCCAC 4731  
QY 1594 TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValIleMetAlaMetGlu 1613  
Db 4732 TACTGAGACCTTTCATCAAGGTGTCACTGGGCTGAAGCTGTGACCATGCGCTGAGG 4791  
QY 1614 HisTyrGluGluProGluIleLeuAspGluAlaLeuIySleCySAsnTyrIlePheThr 1633  
Db 4792 CACTACAGACACCCCAAGTTCTGATGAGGCTGGAAGATCTGCACTCAATCTTCACT 4851  
QY 1634 ValIlePheValLeuGlySerValPheIySLeuValAlaPheGlyPheArGpPhePhe 1653  
Db 4852 GTTCATCTTGTCTTGGAGTCAAGTTTCAAACTTGTGGCTTGTGTTCCGTGCTTCTTC 4911  
QY 1654 GluAspArGtTTPAsnGluLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr 1673  
Db 4912 CAGGACAGGTGAACAAGCTGGAACCTGGCCATTTGTGCTGTCCATCATAGGAGTCAAG 4971  
QY 1674 LeuGluGluIleGlyValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet 1693  
Db 4972 CTGGAGAAATGAGGTCAACCTGCGCTGCCATCAACCCACATCATCTCCGACATCAG 5031  
QY 1694 ArgValIleuArGlyAlaArGValIleuIySLeuLeuIySmetAlaValaGlyMetArGaIa 1713  
Db 5032 AGGTGCTCCGCAATTGCCGAGTGTGAAGCTGTGAAGATGTGCTGTGGGAGTGGGGGG 5091  
QY 1714 LeuLeuAspThrValMetGluAlaLeuProGluValGlyAsnLeuGlyLeuLeuPheMet 1733  
Db 5092 CTGCTGAGACAGGTATGACGCGCTGCGCCAGGTGGGAAACCTGAGACTTCTTCTTCAATG 5151  
QY 1734 LeuLeuPhePheIlePheAlaIleuGlyValGluLeuPheGlyAspLeuGluIuCySasp 1753  
Db 5152 TTGTGTTTTCATCTTTCACCTCTGGAGCTGTGAGCTCTTGTGAGACCTGAGGTGAC 5211



QY	1254	GLuThRhiApRoCyBgLuGIyLeuDiYArghiSaIatnRheArGaSpHeGIyMeLa	1773
Db	5212	GAGACACACCCCTGGAGGCGCTGGCGCATGCCACTTTCGGAACTTGGCATGGCC	52711
QY	1774	PhelEuThRLeuPheArGValSerThriGlyAspAntTPaNgInGIyIleMeLyAspThr	17933
Db	5272	TTCTCAACCCCTCTCCGAGTCTCCACAGGTGACAAATTGGAATGGCATTTATTAAGACACC	53311
QY	1794	LeuYrGaSPCyAspRGInGluSerThrCyStrYrAntnRValIleSerProIIeYrPhe	18133
Db	5332	CTCGGAGCTGTGACAGAGATCCACTCTGCTACACACGGTCATCTCCCTCATCTACTT	53911
QY	1814	ValSerPheValLeuThRAlaGInPheValIleuValAaenValIleAlaValLeuMet	18333
Db	5392	GTGTCTCTTGAGTGTGAAGGCCCGACAGTGTGTAGTCAACGTGTGTATGGCCGTGTAGT	54511
QY	1834	LyshiBLeuGIuGluSerAsnLySGuAlaLySGluGluIaGIuLeuGIuAlaGIuLeu	18533
Db	5452	AAGCACCTGGAGGAGAGACAAACAGAGGCCCAAGGAGGGCCGAGCTGAGAGCTGAGT	55111
QY	1854	GIuLeuGIuMeLyThRLeuSerProGInProHisSerProLeuGIySerProPheLeu	18733
Db	5512	GAGCTGGAGATGAAACCTTCAGCCCCCAGCCCCCACTGGCACTGGAGGCCCTTCTTC	55711
QY	1874	TrpProGIyValGIuGIyProAspSerProAspSerProLySProGIyAlaLeuHiAPRo	18933
Db	5572	TGGCTGGGGTGTGAAGGCCCGGACAGCCCGACAGCCCCCAAGCGTGGGGCTGTGACCCA	56311
QY	1894	AlaAlaHiSaIaArGSeRAlaSerHiAPheSerLeuGIuHiAProThMeGIuProHis	19133
Db	5632	GCGGCCACCGGAGATCAAGCTCCCACTTTCTCCCGAGACACCCACATGACAGCCAC	56911
QY	1914	ProThRGIuLeuAProGIyProAspLeuThRValAArgLySSeGIyValSerArGThr	19333
Db	5692	CCCAAGGAGCTGCAGAGCACAGACTTACTGTGATGGAGAGTCTGGGGTGAACCCGAAC	57511
QY	1934	HisSerLeuProAsnAspSerTyMetCyArGHiSGIySerThRAlaGIuGIyProLeu	19533
Db	5752	CACCTCTGCCCAAGACAGCTACATGTGTGGCATGGGAGACCTCGAGGGGCCCTGTG	58111
QY	1954	GIyHiSaRGIyTrPGIyLeuProLySaIaGInSerGIySerValLeuSerValHiSer	19733
Db	5812	GGACACAGGGGCTGGGGGCTCCCAAACTCAGTCAAGGCTCCGTGTCCGTTCACATCC	58711
QY	1974	GIuProAlaAspThSerTyTrIleuGIuLeuProLySaAPAlaProHiBLeuLeuGIu	19933
Db	5872	CAGCCAGAGAAACAGCTACATCTGTGAGCTTCCCAAGATGACCTCATCTGTCTCAG	59311
QY	1994	ProHisSerAlaProThRTrPGIyThRIleProLySLeuProProGIyArGSeRPro	20133
Db	5932	CCCCACAGGCCCCCAACTGGGGGACACATCCCAAACTGTCCCCACAGAGAGCTCCCT	59911
QY	2014	LeuAlaGInArGProLeuArGArGIuAlaAlaAlaIleArGThrAspSerLeuAspValGIn	20333
Db	5992	TTGGCTCAGAGGCCACTCAGCGCGCAGGACAGCAATTAAGACTGACTCTTGGACCTTCA	60511
QY	2034	GIyLeuGIySerArGGIuAspLeuLeuIaGIuValSerGIyProSeRProProleuAla	20533
Db	6052	GCTCTGGGACAGCCGGAAAGACTGTGTGCAGAGGTGAGTGGGGCTCTCCCGCCCTGTGC	61111
QY	2054	ArgAlaTySerPheTrPGIyGInSerSerThRGIuAlaGInGIuHiSerArGSeRHiS	20733
Db	6112	CGGGCTACTCTTTCTGGGGCCAGTCAAGTACCCAGGACAGACATCTCCCGGAGCCAC	61711
QY	2074	SerLySIIleSerLyHiMeThRProProAlaAPRoCySProGIyProGIuProAntTrp	20933
Db	6172	AGCAAGATCTCCAAACACATGACCCCGGACGCCCTTGGCCGAGGCCCAAGACCAACTGG	62311
QY	2094	GIyLySGIyProProGIyThRTrArGSeRSeRLeuGIuAspThGIuLeuSerTrIle	21133
Db	6232	GGCAAGGGGCTCTCCAGAGCCAAAGACGCTTAAGATTGGAACGAGAGCTGAGCTGAATT	62911
QY	2114	SerGIyAspLeuLeuProProGIyGIuGIuGIuGIuProProSeRProArGAspLeuLyS	21333

Accession	Gene	Protein	Species	Length (aa)	Length (bp)	Source
D8	6292	TCAGGACACCTCTCCGCCCCCTGGCGGCGAGAGAGCCCCCATCCCAAGGACCTGAAG	Human	2153	6489	GenBank
QY	2134	LYSCYSFYTSERVALGIUALAGINSERCYGLINHARGRPPOTHRSERTPLLEUASPGLU	Human	2153	6489	GenBank
Db	6352	AAGTGTCTACAGCGCTGAGAGGCCCCAGAGCTGCCAGCGCCGCGCTACGTCTTGCTGGATGAG	Human	6411	19233	GenBank
QY	2154	GLNHARGHISSERIIEALAVALSERCYLEUASPSESLYSEGLINPROHISLEUGLY	Human	2173	6519	GenBank
Db	6412	CAGAGGAGACCTCTATCGCCGTCACTGCCTGGACAGCGAGCTCCCAACCCCACTGGGC	Human	6471	19233	GenBank
QY	2174	THRASPPROSERHLENUGLYGLINPROLEUGLYGLYPROGLYSEERARGPROLYLVS	Human	2193	6551	GenBank
Db	6472	ACAGACCCCTCTAACCTTGGGGGGCCACCTCTGGGGGGGCTGGAGACCCGCCAAGAAA	Human	6531	19233	GenBank
QY	2194	LYLEUSERPROPROSERIIEHNLLEASPPROGLINSEGLINGLYPROARGTHPRO	Human	2213	6591	GenBank
Db	6532	AATCTTACGCCGCTTATATACCATATGACCCCCCGAGAGCCAAAGTCTCTGGACCCCG	Human	6591	19233	GenBank
QY	2214	PROSEPROGLIYLECYLEUARGARGARGALAPROSESEASPSERYASPPROLEU	Human	2233	6651	GenBank
Db	6592	CCGAGCCCTGGTATCTGCTCCGGAGGAGGCGTCCGTCCAGCGACTCCAAGATCCCTTG	Human	6651	19233	GenBank
QY	2234	ALASERGLYPROPROASPSEMETALALASERPROSEERPROLYSLYASPPVALLEUSER	Human	2253	6711	GenBank
Db	6652	GCCCTCTGGCCCCCTTGACAGCATGTGCTGCTCCGCCCTCCCAAGAAAGATGTGCTAGT	Human	6711	19233	GenBank
QY	2254	LEUSERGLYLEUSERSEASPPROALASPPLLEUASPPO	Human	2266	6750	GenBank
Db	6712	CTCTCCGATTATCTCTGACCCAGACGACTGGACCC	Human	6750	19233	GenBank

CC channels include short current time, slow activation kinetics near  
CC threshold, fast inactivation kinetics and slow tail current. The  
CC sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel  
genes from humans and rats. Each of the novel Ca-channels contains a  
CC putative IVS4 region comprising the amino acid sequence AAV14598. Cells  
CC expressing the T-type voltage-gated calcium channel proteins can be used  
CC to screen for drugs which affect calcium channels. Methods are also  
CC disclosed for treating a disease or disorder associated with a deficiency  
CC in a native T-type calcium channel nucleic acid, e.g. to treat  
CC cardiomyopathy, epilepsy, etc  
XX

Sequence 6783 BP; 1294 A; 2182 C; 1990 G; 1317 T; 0 U; 0 Other;

Alignment Scores:

Score:	11735.50	Length:	6783
Percent Similarity:	98.16%	Conservative:	2241
Best Local Similarity:	98.12%	Mismatches:	1
Query Match:	98.58%	Indels:	41
DB:	2	Gaps:	2

US-09-611-257A-37 (1-2266) x AAX83482 (1-6783)

QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20  
DB 1 ATGAGACGAGAGAGATGGAGCGGCGCGAGAGATCGGGACAGCCCGAGCTTCATG 60  
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluValAsp 40  
DB 61 CGGCTACACGACCTGTCGGGGGCGGGGGGCGGCGGGGCGGGGCTCAGACAGAAAAAGGAC 120  
QY 41 ProGlySerAlaAspSerGlyAlaGlyGlyLeuProTyrProAlaLeuAlaProVal 60  
DB 121 CCGGAGAGCGCGGACTCCAGGCGAGGGGCTCCCTACCCGCGCTGGCCCCGGTGGTT 180  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80  
DB 181 TTCTTCTACTTGAGCCAGGACAGCCGCCCGGAGCTGGGTCTCCGACGGGTCTTAAC 240  
QY 81 ProTyrPheGluArgGlyLeuSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
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QY 101 PheArgProCysGluAspIleAlaCysAspSerGlyArgCysArgTyrLeuGlnAlaPhe 120  
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QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValIlyMetValAlaLeuGly 140  
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QY 141 IlePheGlyValValCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal 160  
DB 421 ATCTTTGGGAAAAAGTTTACTCTGGGAGACACTTGGAGACCGGCTTCACTTTTTCATCGTC 480  
QY 161 IleAlaGlyMetLeuGluTyrTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
DB 481 ATGCGAGGAGATGCTGAGATCTGCTGAGACTGCAAGACCTCAGCTTCTCAGCTGTCAAG 540  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
DB 541 ACGAGTCGGTGTGTCGACCGGTCAGGGGCATTAAACCGGGTGCACGACATGGCATCTTT 600  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
DB 601 GTCACCTTGCTGCTGATACGCTGCCCATGCTGGGACACGTCCTGCTGCTGCTTCTTC 660  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuThrAlaGlyLeuLeuArgAsnArg 240  
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QY 241 CysPheLeuProGluAsnAspSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260

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QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
DB 781 AAGAGAAACGAGAGATGAGAGCCCTTCATCTGCTCCACGACCGGAGAAACGGATGGCG 840  
QY 281 SerCysArgSerValProThrLeuArgIleAspGlyGlyGlyProProCysGlyLeu 300  
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QY 301 AspTyrGluAlaTyrAsnSerSerAsnThrTyrCysValAsnTyrAsnGlnTyrTyr 320  
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QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheGlyValaIleAsnPheAspAsnIle 340  
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QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380  
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QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValIleIleAlaThrGlnPheSerGlu 400  
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QY 401 ThrIlyGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
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QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuValTyrLeu 440  
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QY 441 ValTyrIleLeuArgIlyAlaIleArgArgLeuAlaGlnValSerArgAlaIleGlyVal 460  
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QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnIlyThrGlnProSerSer 480  
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QY 501 HisIleHisIleTyrHisIleGluValAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
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QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540  
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QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
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QY 561 CysHisIleGluGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
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QY 581 GlyArgThrValGlySerGlyValValTyrProThrValHisThrSerProProProGlu 600  
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QY 601 ThrLeuValGluValAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620  
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 QY 641 ThrGlyAlaCysGlnSerSerCysIleValIleSerSerProCysIleuValIleAspSerGly 660  
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 QY 661 AlaCysGlyProAspSerCysProTyCysAlaArgAlaGlyIleGlyValGlnLeu 680  
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 QY 1001 SerGlnProAspPhePheSerProSerLeuAspGlyAspGlyAspArgIleValCysIleu 1020  
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DB 6592 GACCCCCCGAGAGCCAAAGTCTCGACCCCGCCGCTGTATCTCTCCCGGAGG 6651
QY 2223 ArgAlaProSerSerAspSerIleAspProLeuAlaSerGlyProProAspSerMetAla 2242
DB 6652 AGGCTCTCGTACAGCATCCAAAGATCCCTTGGCTTGGCCCCCTGACGATGGCT 6711
QY 2243 AlaSerProSerProIleValSerValLeuSerLeuSerGlyLeuSerSerAspProAla 2262
DB 6712 GCCTCGGCTCTCCCAAGAAAGATGTCTGAGTCTCTCCGGTTATCTCTGACCCAGCA 6771
QY 2263 AspLeuAspPro 2266
DB 6772 GACCTGAGACCC 6783

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RESULT 8  
AAK83483  
ID AAK83483 standard; cDNA; 6804 BP.

AAK83483;  
AC  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human T-type voltage-gated Ca channel alpha-1-G (hCAV1c) cDNA.  
XX  
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.  
XX  
XX Homo sapiens.  
OS  
PN WO9929847-A1.  
PD 17-JUN-1999.  
XX  
PF 30-OCT-1998; 98WO-US023161.  
XX  
PR 05-DEC-1997; 97US-00985809.  
XX  
PA (LOYO ) UNIV LOYOLA CHICAGO.  
XX  
PI Perez-Reyes E, Cribbs LL;  
XX  
DR WPI; 1999-394972/33.

```

DR P-PSDB; AAY14588.
XX New T-type voltage-gated calcium channels.
PT
XX
XX Disclosure; Page 49-58; 138pp; English.
PS
XX
CC This sequence represents the coding region for a human T-type voltage-
CC gated calcium (Ca) channel alpha-1G designated hCAV1c. Voltage gated
CC channels are membrane bound glycosylated proteins formed of several
CC subunits. The large alpha subunits form a pore in the membrane that is
CC selective for a given ionic species. Each alpha subunit contains 4
CC domains (I, II, III and IV) and each domain contains 6 putative
CC transmembrane helical segments (S1-S6). T-type Ca channels are activated
CC at a lower voltage than L- or N-type channels. Characteristics of T-type
CC channels include short current time, slow activation kinetics near
CC threshold, fast inactivation kinetics and slow tail current. The
CC sequences AAK83481-X83492 represent novel T-type voltage-gated Ca channel
CC genes from humans and rats. Each of the novel Ca-channels contains a
CC putative IYS4 region comprising the amino acid sequence AAY14598. Cells
CC expressing the T-type voltage-gated calcium channel proteins can be used
CC to screen for drugs which affect calcium channels. Methods are also
CC disclosed for treating a disease or disorder associated with a deficiency
CC in a native T-type calcium channel nucleic acid, e.g. to treat
CC cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6804 BP; 1301 A; 2186 C; 1998 G; 1319 T; 0 U; 0 Other;

```

Alignment Scores:

Pred.	No.:	Length:	Matches:
Score:	11727.00	6804	2240
Percent Similarity:	97.82%		
Best Local Similarity:	97.77%		
Query Match:	98.51%		
DB:	2	Gaps:	2

US-09-611-257a-37 (1-2266) x AAK83483 (1-6804)

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QY 1 MetAspGlnGlnGlnAspGlyAlaGlnGlnSerGlyGlnProArgSerPheMet 20
DB 1 ATGACAGAGAGAGAGATGAGCGGCGCGAGAGATCGGAGACAGCCCGACCTTCATG 60
QY 21 ArgLeuAspAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGlnVal 40
DB 61 CGGCTCAACGACCTGTGCGGGGCGGGGCGGGCCGGGGCTCAGCAAGAAAGAGAC 120
QY 41 ProGlySerAlaAspSerGlnAlaGlnGlyLeuProIleProAlaLeuAlaProVal 60
DB 121 CCGGGCAGCGCGGACTCCAGCGGAGGGGCTCCGATCCGGCGTGGCCCGGTTG 180
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
DB 181 TTCCTTACTTGAAGCAGGACAGCCCGCCGAGGCTGGGTCTCCGACAGGTCTGTAC 240
QY 81 ProTrpPheGlnArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
DB 241 CCTGGTTTAGGCGCATCAGCATGTGTATCTTCACTGCGTGAACCTTGGGATG 300
QY 101 PheArgProCysGlnAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
DB 301 TTCGGGCGCATGCGACATCGCTGTGACTCCAGGCGTCCGGGATCTGACAGGCTTT 360
QY 121 AspAspPheIlePheAlaPhePheAlaValGlnMetValIleValIleVal 140
DB 361 GATGACTTCATCTTGTGCTTCTTGGCTGTGAGATGTGTGAAAGATGGTGGCTTGGGC 420
QY 141 IlePheGlyValSerCysTrpLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160
DB 421 ATCTTGGGAAAAGTGTACTGAGAGACACTTGAACCGGCTTGACTTTTCATCTGTC 480
QY 161 IleAlaGlyMetLeuGlnArgTrpSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
DB 481 ATGCGAGGATGCTGAGTACTCGCTGACCTCGACAGAACTGACGCTTCAAGCTGTACAG 540

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QY ThrValArgValIleuArgProIleuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
DB ACGATCCGCTGCTGCGACCCGCTCAAGGCGCATTAACCGGGTGGCCAGCATGGCATCTT 600  
QY ValThrIleuIleuAspThrIleuProMetLeuGIYAsnValIleuIleuCysPhephe 220  
DB GTCACGCTGCTGCTGATACGCTGCGCATGCTGGGCAACGTCCTGCTGCTCTTCTTC 660  
QY ValPhePheIlePheGlyIleValGIYValIGlnLeuThrPalaGlyIleuIleuArgAnaArg 240  
DB GTCCTCTTATCTTCCGCATCGTCGGCGTCCAGCTGTGGGCAAGGGGTGCTTGGAAACCA 720  
QY CysPheLeuProGIYAsnPheSerIleuProLeuSerValAspLeuGIYArgTyrTyrGln 260  
DB TGCCTCTTACCTGAGAAATTCAGCTCCCTCCAGGCTGGACTGGAGCGCTTATTCAG 780  
QY ThrGIYAsnGlnAspGIYSerProPheIleCysSerGlnProArgGIYAsnGlyMetArg 280  
DB ACAGAGAAACGAGGATAGAGCCCTTCATCTGCTCCAGCCCAAGCGAGAACGGCATGGCG 840  
QY SerCysArgSerValProThrIleuArgGIYAspGIYGIYGIYProProCysGIYLeu 300  
DB TCCCTGCAAGAGCGTGGCCACGCTGCGGGGGAACGGGGGCGTGGCCACCTTGGCGGTCTG 900  
QY AspTyrGlnAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320  
DB GACTATGAGGCTTACAAACGCTCCAGCAACCACTGTGTCACTGGAACCAAGTATCAG 960  
QY ThrAsnCysSerAlaGlyIYIuhIAsnProPheIYsGIYAlaIleAsnPheAspAsnIle 340  
DB ACCAACTGCTCAGCGGGGAGCAACCCCTTCAAGGGCGCATCAACTTGAACAACAT 1020  
QY GIYTYrAlaIThrIleAlaIlePheGlnValIleThrLeuGIYGIYThrValAspIleMet 360  
DB GGCTATGCTGGAATCCCATCTTCCAGGTATCACTGAGGCGGTGGATTCAGCATCAG 1080  
QY TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuIleIle 380  
DB TACTTTGTATGGATGCTCATCTTCTTCACATTTCAATCTACTCTTCTCTCATCATC 1140  
QY ValGIYSerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGln 400  
DB GGGGCTCTCTTCATGATCAACCTGTGCTGTGATGGCCAGCATGTTCTCAGAG 1200  
QY ThrIYsGlnArgGlnSerGlnIleuMetArgGlnGlnArgValArgPheIleuSerAsnAla 420  
DB ACCAAACGACGGGAAAGCCAGCTGATGCGGAGACAGCGTGGGTCTGTCTCAACGCGC 1260  
QY SerThrLeuAlaSerPheSerGlnProGIYSerCysTyrGlnGlnIleuLeuIleTyrLeu 440  
DB AGCAACCTGGCTAGCTTCTCTAGACCCCGGCAAGCTGCTATGAGGAGCTGCTCAAGTACCTG 1320  
QY ValTyrIleuArgIYsAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
DB GGTATCATCTCTTGTAAAGCAGCCCGCAAGGCTGGCTCAGGTCCTCTGGCAGACGAGTGTG 1380  
QY ArgValGIYLeuIleuSerSerProAlaProIleuGIYGIYGlnGlnIleuThrGlnProSerSer 480  
DB CGGGTGTGGCTGTCTGACGACCCGACACCCCTCGGGGGCCAGGAGACCCAGCCACACAC 1440  
QY SerCysSerArgSerHisArgArgLeuSerValHisIleIleuValHisIleHisIleHis 500  
DB AGCTGCTCTCGCTCCACCGCCGCTATTCGCTCACCACTGTGTGACCAACCAACCAAC 1500  
QY HisIleHisIleIleTyrHisIleuGIYAsnGIYThrLeuArgAlaProArgAlaSerProGln 520  
DB CATCACCAACCACTACCACTGGGCAATGGGACGCTCAGGAGCCCGCCGGGCGACGCGGAG 1560  
QY IleGlnAspArgAspAlaAsnGlySerArgArgArgLeuMetLeuProProProSerThrPro 540  
DB ATCCAGGACGAGGATCCCAATGGGTCCCGCGGCTATGCTGCAACACCTTCGAGGCT 1620  
QY AlaLeuSerGIYAlaProProGIYGIYAlaGlnSerValHisSerPheTyrHisAlaAsp 560

DB GCCCTCCGGGGGCCCCCTGCTGTGGCCGAGAGTGTGGACAGCTTCTTACATGCCGAC 1680  
QY CysHisIleuGlnProValArgCysGlnAlaProProProArgSerProSerGIYAlaSer 580  
DB TGGCATTATGAGCCAGTCCGCTGGCCAGGCGCCCTCCAGGTCTCCATCTGAGGATCC 1740  
QY GIYArgThrValGIYSerGIYIYsValTyrProThrValHisIleThrSerProProGln 600  
DB GGCAAGACTGTGGGCAAGGGAGGTATTCACCGGTGCACACCAAGCCCTCCACCGAG 1800  
QY ThrIleuYsGIYValAlaIleuValGIYValAlaIleSerSerGIYProProThrLeuThr 620  
DB ACGTGAAGAGAAAGCACTAGTATGAGGTGGCTGCAGCTTGGGCGCCCAACCTCAC 1860  
QY SerLeuAsnIleProProGIYProTyrSerSerMetHisIYsIleuLeuGlnThrGlnSer 640  
DB AGCTTCAACATCCCAACCGGGGCTTACAGCTTCCATGACACAAAGCTTCTGGAGCACAGAT 1920  
QY ThrGIYAlaCysGlnSerSerCysIYsIleSerSerProCysLeuYsAlaAspSerGIY 660  
DB ACGGTGCTGCGCAAGGCTTGGCAAGATCTTCAGACCTTGTCTTAAGCAGACAGTGA 1980  
QY AlaCysGIYProAspSerCysProTyrCysAlaArgAlaGIYAlaGIYIleuIleu 680  
DB GCTGTGGTCCAGACAGCTGCCCTTACTGTGCCGGGCGGGGCGAGGGAGGTGAGCTTC 2040  
QY AlaAspArgGlnMetProAspSerAspSerGIYAlaValTyrGlnPheThrGlnAspAla 700  
DB GCCGACCGGAAATCCCTGACCTCAGACAGCGAGGAGTTTATGAACTTCAACAGGATGCC 2100  
QY GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGIYProAspAla 720  
DB CAGCACAGGCACTCCGGACCCCAACCGCGCGGCAACGAGCTGGGCCCAATGA 2160  
QY GlnProSerSerValIleuAlaPheTrpArgIleuIleCysAspThrPheArgIYsIleVal 740  
DB GAGCCAGCTGTGCTGCTGGCTTGGAGGCTAATCTGTGACACCTTCGAAAGATTGG 2220  
QY AspSerIYsTyrPheGlyArgGIYIleMetIleAlaIleIleuValAsnThrIleuSerMet 760  
DB GACCAACAGTACTTGTGGCGGGGAATCATGATCGGCATCTGTGTCAACACTTCAGCATG 2280  
QY GIYIleGlnTyrHisGIYGlnProGIYGlnIleuThrAsnAlaIleuGlnIleSerAsnIle 780  
DB GGCAATGATATCCAGAGCAGCCGAGAGGCTTACCAAGCCCTTGAATCGAATCAGATC 2340  
QY ValPheThrSerLeuPheAlaIleuGlnIleuIleuYsLeuIleuValTyrGIYProPhe 800  
DB GTCTCACAGGCTCTTGGCCCTGAGATGCTGTGAAGCTGCTGTGATGTGCTCTTT 2400  
QY GIYTYrIleYsAsnProTyrAsnIlePheAspGIYValIleValIleSerValTrp 820  
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QY GlnIleValGIYGlnGlnGIYGIYGIYLeuSerValIleuArgThrPheArgLeuMetArg 840  
DB GAGATCGTGGGCAACAGGGGGGCGGCTGTGTGTGTGTGGGACCTTCGCTGATGGCT 2520  
QY ValIleuYsLeuValArgPheLeuProAlaIleuGlnArgGlnIleuValIleuMetIYs 860  
DB GTGTGAAGCTGTGTGCTGCTTCTGCGGGGCTGACGCGGACGCTGTGTGTCTCATGAAG 2580  
QY ThrMetAspAsnValAlaThrPheCysMetLeuIleuMetLeuPheIlePheIleSer 880  
DB ACCATGAGCAAGTGTGCAACCTTCTGCAATGCTGTATAGCTTCTTATCTTCAATCTTCA 2640  
QY IleLeuGlnMetHisIleuPheGIYCysIYsPheAlaSerGlnArgAspGIYAspThrIleu 900  
DB ATCTGTGGCATCATCTTCTGTGGCTGCAAGTTTGTCTTGAAGCGGAGTGGGACACCTTG 2700  
QY ProAspArgIYsAsnPheAspSerLeuIleuThrAlaIleValThrValPheGlnIleLeu 920

Db 2701 CCAAGCCGGAAGATTGTAAGTCTGCTGGCCATCGTCACTGCTTTCAATCTCTG 2760  
Qy 921 ThrGlnIuAspTrpAenlyValLeuTyraSnGlyMeAlaSerThrSerSerTrpAla 940  
Db 2761 ACCCAGAGAGACTGGACCAAAAGTCTCTTACATGGTATGGCTCCAGCTGCTGGGCG 2820  
Qy 941 AlaLeuTyraPheIleAlaLeuMetThrPheGlyAsnTyraValLeuPheAsnLeuVal 960  
Db 2821 GCCCTTAATTCATTCCTCATATGCTTCGCAACCTACAGCTGCTTCAATTTGCTGTC 2880  
Qy 961 AlaIleLeuValGlnIuPheGlnAlaGlnIuIleSerLyraSgIuAspAlaSerGly 980  
Db 2881 GCCATTCTGGAGGAGGCTTCCAGGCGAG----- 2910  
Qy 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnIuGlyAspAlaAsnLySerGln 1000  
Db 2911 -----GGAGATGCGCAACAAATCCGAA 2931  
Qy 1001 SerGlnuProAspPhePheSerProSerLeuAspGlyAspAlaGlyValGlyCysLeu 1020  
Db 2932 TCAGAGCCCGGATTTCTTCTCAACCGCTGATGATGGGAGCAGGAAAGTGTCTTG 2991  
Qy 1021 AlaLeuValSerLeuGlyGlnHisProGlnuLeuArgLySerLeuLeuProProLeuIle 1040  
Db 2992 GCGTTGGTGTCTCGGAGAGACCCGAGCTGCGAAGAGCCTGTGCGCTCTCATC 3051  
Qy 1041 IleIleThrAlaAlaThrProMetSerLeuProLySerThrSerThrGlyLeuGlyGln 1060  
Db 3052 ATCCACACCGCGCCGACACCATCTCGTCCCAAGACACACACGCGGCTGGGCGAG 3111  
Qy 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGlnProGlyAlaAla 1080  
Db 3112 GCGCTGGAGCCCTGCGTGGCGCCGACACAGCAGCGGCTGGGAGAGCTGGGCGCGCC 3171  
Qy 1081 HisGlnuMetLySerProProSerSerAlaArgSerSerProHisSerProTmSerAlaAla 1100  
Db 3172 CACAGAGTGAAGTACCGCCGACGCGCCGACGCTCTCGCACAGCCCTGGAGGCGTGA 3231  
Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyAlaAlaProSerLeuLyS 1120  
Db 3232 AGCAGCTGGACACACAGCGCTCCAGCCGGAACAGCCTCGGCGCTGACCCAGCTGAAG 3291  
Qy 1121 ArgArgSerProSerGlyGlnArgArgSerLeuLeuSerGlyGlnGlnIuSerGln 1140  
Db 3292 CGAGAGAGCCCAATGGAGAGCGCGGCTCTGTGTTCGGAGAAAGGCGAGAGAGCGCAG 3351  
Qy 1141 AspGlnIuGlnIuSerSerGlnGlnIuArgAlaSerProAlaGlySerAspHisArgHis 1160  
Db 3352 GATGAAGAGAGAGCTCAGAAAGAGAGCGGCGCAGCCTCCGGGAGTGAACATGCGCAC 3411  
Qy 1161 ArgGlySerLeuGlnArgGlnAlaLySerSerPheAspLeuProAspThrLeuGlnVal 1180  
Db 3412 AGGGGGTCCCTCGAGCGGAGGAGCCAAAGATTCTTTGACCTGCCACACACCTCGAGGTG 3471  
Qy 1181 ProGlyLeuHisArgThrAlaSerGlyValArgGlySerAlaSerGlnHisGlnIuAspCysAsn 1200  
Db 3472 CCAAGGCTGACCTGCATGCGCAGTGGCGGAGAGGTCTCTTCTGAGCACCAAGACTGCAAT 3531  
Qy 1201 GlnLySerSerAlaSerGlyValArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220  
Db 3532 GGCAGAGTCGGCTTCAGGGGCGCTGGCGCCGCGGCTCGAGTGAAGACCCCGCACTGGAT 3591  
Qy 1221 GlnYAspAspAlaAspAspGlnGlyAsnLeuSerLyGlnIuArgValArgAlaTrpIle 1240  
Db 3592 GGGGATGACCGCGATGACGAGGCGCACTGACCAAAAGGAGACGGGTCCGGCGTGGATC 3651  
Qy 1241 ArgAlaArgLeuProAlaCysTyraLeuGlnArgAspSerTrpSerAlaTyraIlePhePro 1260  
Db 3652 CGAGCCGACTCCCTGCTGCTGCTCGAGCGAGACTCTGCTGATCAGCTTAATCTTCCCT 3711  
Qy 1261 ProGlnSerArgPheArgLeuLeuLeuCysHisArgIleIleThrHisLyMetPheAspHis 1280  
Db 3712 CCTCAGTCCAGGTTCCGCTCTCTGTGTCAACGAGATCATACCCCAAGATGTTGACACAC 3771

Qy 1281 ValValLeuValIleIlePheLeuAsnCyseIleThrIleAlaMetGlnuArgProLySile 1300  
Db 3772 GTGGTCTTGTCTATCATCTTCTTCACTGATCATACATCGCCATGGAGCGCCCAAAAT 3831  
Qy 1301 AspProHisSerAlaGlnArgIlePheLeuThrLeuSerAsnTyraIlePheThrAlaVal 1320  
Db 3832 GACCCCAACAGCCCTGAACCGCATCTTCTGACCCCTTCCAAATTACATCTTCAACCGCAGTC 3891  
Qy 1321 PheLeuAlaGlnuMetThrValLyValAlaLeuGlyTrpCysPheGlyGlnAla 1340  
Db 3892 TTTCTGGCTGAATGACAGTGAAGTGTGTGCACTGGGCTGTGTCTGGGGGAGCGGCG 3951  
Qy 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360  
Db 3952 TACCTGGAGAGCGATTGGAACGTGTGAGCGGCTGTGTGTCTCATCTCGATCATGAC 4011  
Qy 1361 IleLeuValSerMetValSerAspSerGlyThrLyIleLeuGlyMetLeuArgValLeu 1380  
Db 4012 ATTCTGGTGTCAATGTGTCTTGAACGCGGACCAAGATCTGGGCAATCGTAGGGTCTG 4071  
Qy 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnIuLeuLySleu 1400  
Db 4072 CGGCTGTGGAGACCTCGCGCCGCTCAGGGGTATCAGCGGCGCAGGGGCTGAAGCTG 4131  
Qy 1401 ValValGlnuThrLeuMetSerSerLeuLyProIleGlyAsnIleValValIleCysCys 1420  
Db 4132 GTGGTGAAGACGCTGTATGTCTCATCTGAACCATGGCAACATTTGAATCATCTGTGT 4191  
Qy 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLySgLySlyPhePheVal 1440  
Db 4192 GCGTCTTCAATCATTTTGGCATTTGGGGGTGCACTCTTCAAGGGAAGTTTTCGTG 4251  
Qy 1441 CysGlnIuGlnuAspThrArgAsnIleThrAsnLySerAspCysAlaGlnuAlaSerTyr 1460  
Db 4252 TGCCAGGCGAGATACAGAAATCATCACAATAATCGAGCTGTGCGAGCCAGCTTAC 4311  
Qy 1461 ArgTrpValArgHisLySlyTyraAsnPheAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480  
Db 4312 CGGTGGTCCGGGACAAATGTAACCTTGAACACTTGGCCAGGCGCTGATGCTCTGTTC 4371  
Qy 1481 ValLeuAlaSerLyAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500  
Db 4372 GTTTGGCTTCCAGATGTGTGGTGTGATCATATGATGGCTGTGATGCTGTGGC 4431  
Qy 1501 ValAspGlnIuProIleMetAsnHisAsnProTmPheLeuLeuTyraPheIleSerPhe 1520  
Db 4432 GTGACCAAGACGCCATCATGAACCAACACCCCTGATGCTGTACTTCATCTCGTTC 4491  
Qy 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValIleGlnuAsnPhe 1540  
Db 4492 CTGCTCATTTGGGCTTCTTGTCTTGAACATGTTGTGGGTGTGTGTGGAGAACTTC 4551  
Qy 1541 HisLySlyAsnArgGlnHisGlnIuGlnIuAlaArgArgArgGlnIuLySlyArgLeu 1560  
Db 4552 CACAAGTGTGGAGACCAAGAGAGAGAGAGGCGCGCGGAGAGAGAGCGGCTGA 4611  
Qy 1561 ArgArgLeuGlnuLySlyArgArg----- 1568  
Db 4612 CGAAGACTGGAGAAAGAGAGAGAGAGAGAGAGAGATGGCTGATTAATCTGAGAC 4671  
Qy 1569 -----LyAlaGlnCySlyAspProTyr 1575  
Db 4672 GATGTAATGTCTTCGCGACCTCAGCCGCTGCGTCAAGAGCCAGTCCAAACCTTAC 4731  
Qy 1576 TyrSerAspTyraSerArgPheArgLeuLeuValHisIleLeuCysThrSerHisTyraLeu 1595  
Db 4732 TACTCCACTACTCCCGCTTCGGCTCTGTCCACCACTTGTGCACCAAGCTACTACTG 4791  
Qy 1596 AspLeuPheIleThrGlyValIleGlyLeuAsnValIleThrMetAlaMetGlnHisTyra 1615  
Db 4792 GACCTTTCATCAACAGGTGTATGCGGCTGAAGTGTATCAATGCGCATGAGAGACTAC 4851



QY	1616	GlInGInPProGInIleLeuAspGluAlaLeuLysIleCyAsenTYrIlePheThrValIle	1635
Db	4852	CAGAGACCCCGAATTCGATGAGAGAGCTCTGAAGATCTGCAACATCACTTCACAGTCATC	4911
QY	1636	PheValLeuGInuSerValPheLysLeuValAlaPheGlyPheArgArgPheGluASP	1655
Db	4912	TTTGCTTGGAGTCAGTTTCAAACTTGGCCCTTTGGTTTCCGTGGTTCTTCCAGGAC	4971
QY	1656	ArgTrpAsnGInLeuAspLeuAlaIleValLeuSerIleMetGlyIleThrLeuGlu	1675
Db	4972	AGGTGAACCAAGCTGAGACTGGCCATCTGCTGTCTCATCATGGGATCAGCCTGGAG	5031
QY	1676	GluIleGluValaAsnAlaSerLeuProIleAsnProThrIleIleArgIleMetArgVal	1695
Db	5032	GAATTCGAGGTCAACGCTCCCTCCATCAACCCCAACATCCACCATCATAGAGGTG	5091
QY	1696	LeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMetArgValaLeuLeu	1725
Db	5092	CTGGCGATGGCCCGAGAGTCTGAAGGTGCTGAAGATGGCTGTGGCATATGGGCGCTGCTG	5151
QY	1716	AspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeu	1735
Db	5152	GACACGGTGATGACAGGCGCTGCCCCACAGTGGGAGAACCTGGGACCTTCTTCATGTGTGG	5211
QY	1736	PhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCyAspGluThr	1755
Db	5212	TTTTTCATCTTTGAGAGCTCTGGGGGTGGAGCTCTTTGGAGACTCTGGAGTGTGACGAGACA	5271
QY	1756	HisProCysGluGluLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeu	1775
Db	5272	CACCCCTGTAGGGCTGTGGCCGTCATGCCACTTTGGAACTTTGGCATGGCTTCTCTTA	5331
QY	1776	ThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArg	1795
Db	5332	ACCCCTTCGAGTCTCCAGTCTCCACAGGTGACAAATTGGAATGGCATTAAGAAAGAACCTCCGG	5391
QY	1796	AspCysAspGlnGluSerThrCysTrpAsnThrValIleSerProIleTYrPheValSer	1815
Db	5392	GACTGTGACCGAGGTCCACTGCTACAAACGGTCACTCTGCCATCTACTTGTGTGCC	5451
QY	1816	PheValLeuThrAlaGlnPheValLeuValaAsnValAlaIleAlaValLeuMetLysHis	1835
Db	5452	TTTCGGCTGACGGCCCGAGTGTGCTGATCAACGTGGTATGCGCGGTGATGAAGAC	5511
QY	1836	LeuGluGInuSerAsnLysGluAlaLysGluGluValaGluLeuGluValaGluLeuGluLeu	1855
Db	5512	CTGAGAGAGACCAACAAGAGGCCAAGAGAGAGGCCAGCTACAGAGCTGAGCTGAGACTG	5571
QY	1856	GluMetCysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro	1875
Db	5572	GAGATGAAGAACCTCTCAGGCCCCCAAGCCCACTCGGCACTGGGCAAGCCCTTCTCTGGCCT	5631
QY	1876	GlyValaGluGlyProAspSerProAspSerProLysProGlyAlaIleuHisProAlaAla	1895
Db	5632	GAGGGTCGAGGGCCCGGACAGCCCGACAGCCCAAGCCTGGGGCTCTGCAACCAAGCGACC	5691
QY	1896	HisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHisProThr	1915
Db	5692	CACGGGAAATCAGCTCCCACTTTTCCCTGGAGACACCCCAAGATGCAAGCCCAACCCACG	5751
QY	1916	GluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSer	1935
Db	5752	GAGCTGCAGAGACCACTTACTGTACTGTGCGAAGTCTGGGGGTCAAGCCCAACCACTCT	5811
QY	1936	LeuProAsnAspSerTYrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHis	1955
Db	5812	CTGCCCAATGACAGTCATATGTGTGCGATGGAGACCTGCCAGAGGGGCCCTTGGACAC	5871
QY	1956	ArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValIleAsnValHisSerGluPro	1975
Db	5872	AGGGGCTGTGGGGCTCCCGCAAAAGCTCAAGTCCGCTTGTCCGTTCACTCCCAAGCA	5931
QY	1976	AlaAspThrSerTYrIleLeuGlnLeuProLysAspAlaProHisIleLeuGlnProHis	1995

Db	5932	GCAGATACCAAGCTACATCTCTGACAGCTTCCAAAAGATACACTCATCTGCTCCAGCCCCAC	5991
Qy	1996	Sez1a1ProThrTrpGlyYThrIleProIysLeuProProGlyArgSerProLeuAla	2015
Db	5992	AGCGCCCAACCTGGGGCACACATCCCAAACTGGCCCCACAGAGAGGCTCCCTTGGCT	6051
Qy	2016	GlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeu	2035
Db	6052	CAGAGGCCACTCAGGGCCCGAGGACGAAATAGAGCTGACTCCCTTGACGCTTCAGGGCTCG	6111
Qy	2036	GlySerArgGlnAspLeuLeuAlaGlnValSerGlyProSerProProLeuAlaArgAla	2055
Db	6112	GGACGCCGGGAAGCCTGTCTGGCAGAGGTAGTGGGCTCTCCCGCCCTTGGCCCGGGCC	6171
Qy	2056	TyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnIlnHisSerArgSerHisSerLys	2075
Db	6172	TACTCTTCTGGGGCCAGTCAAGTACCAGGACAGCAGCAGCTCCGCAACAGCAG	6231
Qy	2076	IleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLys	2095
Db	6232	ATCTCCAAAGACATGACCCCGCCAGCGCCCTTGGCCAGGCCCAGAAACCAACTGGGGCAG	6291
Qy	2096	GlyProProGluThraGssSerSerLeuLeuAspThrGlnLeuSerTrpIleSerGly	2115
Db	6292	GGCCCTCCAGAGACAAACAGCTTGAAGTTGACACGGAGCTGAGCTGATTTCCAGGA	6351
Qy	2116	AspLeuLeuProProGlyGlyGlnGlnGluProProSerProArgAspLeuLysLysCys	2135
Db	6352	GACTCTCTGGCCCCCTGGCGGGCCAGAGAGAACCCCAATCCCAAGGACCTGGAAGACTGC	6411
Qy	2136	TyrSerValGlnAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlnGlnArg	2155
Db	6412	TACAGCTTGAGAGGCCAGACTGCGCAGCGCCGGCTGACTGCTGGCTGATGACAGAGG	6471
Qy	2156	ArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyYThrAsp	2175
Db	6472	AGACACTCTACGCGCTGACCTGCTGGAACAAGGGCTCCCAACCCCACTGGGACACAGC	6531
Qy	2176	ProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeu	2195
Db	6532	CCCTCTAACCTTGGGGGGCCAGCCCTCTTGGGGGGGCTGGAGCCGGCCCAAGAAAATCTC	6591
Qy	2196	SerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSer	2215
Db	6592	AGCCCGCTAGTATCACCATATAGACCCCCCGAGAGCCAAAGTCTCTCGGACCCCGCCAGC	6651
Qy	2216	ProGlyLysLeCysLeuAlaGArgArgAlaProSerSerAspSerLysAspProLeuAlaSer	2235
Db	6652	CTGTGATCTGCCCCCGAGAGAGGGCTCGTCCACGACATCCAAAGATCCCTTGGCTCT	6711
Qy	2236	GlyProProAspSerMetAlaAlaAspProSerProLysLysAspValLeuSerLeuSer	2255
Db	6712	GGCCCCCTCAGACAGCATGGCTGCTCCCTCCCAAGAAAAGATGTGCTGAGTCTCTCC	6771
Qy	2256	GlyLeuSerSerAspProAlaAspLeuAspPro	2266
Db	6772	GGTTTATCTCTGACCCAGCAGACCTGGAACCC	6804
RESULT 9			
AAH98402			
ID	AAH98402	standard; cDNA; 8002 BP.	
XX	AAH98402;		
XX	AC		
XX	12-OCT-2001	(first entry)	
DE	Human EST-derived coding sequence SEQ ID NO: 259.		
XX			
KW	Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;		
KW	tomato; monkey; dog; sea urchin; expressed sequence tag; BDT;		
KW	diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;		
KW	gene therapy; nutrition; ss.		

XX Homo sapiens.  
OS  
XX  
PN MO200154477-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001MO-US002687.  
XX  
PR 25-JAN-2000; 2000US-00491404.  
PR 17-JUL-2000; 2000US-00617746.  
PR 03-AUG-2000; 2000US-00631451.  
PR 15-SEP-2000; 2000US-00663870.  
XX  
XX (HYSB-) HYSBQ INC.  
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
XX WPI; 2001-476164/51.  
DR P-PSDB; AAM23743.  
XX  
PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
PT antibodies and research use.  
XX  
PS Claim 1; Page 369-371; 1275pp; English.  
XX  
CC The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
CC of the invention  
XX  
SQ Sequence 8002 BP; 1590 A; 2504 C; 2273 G; 1635 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 0 Length: 8002  
Score: 11627.50 Matches: 2238  
Percent Similarity: 97.73% Conservative: 1  
Best Local Similarity: 97.69% Mismatches: 4  
Query Match: 97.68% Indels: 48  
DB: Gaps: 2  
  
US-09-611-257a-37 (1-2266) x AAM98402 (1-8002)  
QY 1 MetAspGluGluGluAspGlyAlaGluGluSerGlyGlnProArgSerPheMet 20  
DB 496 ATGACGAGGAGGAGATGAGCGGCGCCGAGAGTGGGAGACGCCCGGAGCTTCATG 555  
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyValArgProGlySerAlaGluAsp 40  
DB 556 CGGCTCAACGACCTGTCCGGGGCCGGGGCCGGGGGTCAGCAAAAGAC 615  
QY 41 ProGlySerAlaAspSerGlyAlaGlyLeuProGlyArgProAlaLeuAlaProVal 60  
DB 616 CCGGGACCGCGGACTCCGAGCGGAGGGGCTGCCGTACCCGGGGCTGGCCCGGTG 675  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrGlyLeuArgThrValCysAsn 80  
DB 676 TTCTTCTACTTGAGCCAGGACGCGCGCGAGCTGTCTCCGACGCTCTTAAC 735  
QY 81 ProTyrPheGluArgGlyLeuSerMetLeuValIleLeuLeuAsnGlyValThrLeuGlyMet 100  
DB 736 CCGTGGTTTGAAGCGGATGAGATGTTGGTCACTCTTCACTGAGTACCTGGGACATG 795  
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
DB 796 TTCGGCCATGCGAGGACATCGCTGTACTCCAGCGCTGCGGATCTCTGACAGCCCTTT 855  
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValGlyMetValAlaLeuGly 140

DB 856 GATGACTTCATCTTTCCTTCCCTTGGCCGAGATGATGATGAATGATGGCTTGAGCC 915  
QY 141 IlePheGlyValArgCysTyrLeuGlyAspThrTTPAsnArgLeuAspPheIleVal 160  
DB 916 ATCTTTGGGAAAAAGTTTAACTGGGAGACATTTGGAAACCGGCTTACTTTTCACTGTC 975  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
DB 976 ATGCAGAGATGCTGAGTACTGCTGACCTGCAGAGCTCAGCTTCTCAGCTTCACAG 1035  
QY 181 ThrValArgValLeuArgProLeuAlaIleAsnArgValProSerMetArgIleLeu 200  
DB 1036 ACAGTCCGTGTGTCGACCGCTCAGGGCATTAACCGGGTGCACGATCGCATCTT 1095  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
DB 1096 GTCACGTTGCTGTGATACTCTGCCCATGCTGGGACAGCTCTGCTGCTGCTTCTTC 1155  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuThrAlaGlyLeuLeuArgAsnArg 240  
DB 1156 GTCTTCTTCATCTTCGACATGTCGCGTCCAGCTGAGGAGGCTGCTTCGAAACCGA 1215  
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
DB 1216 TGCTTCTACTAGATTAATTCAGCTTCCCTGAGGCTGAGCTTGAAGGCTATTACAG 1275  
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
DB 1276 ACAGAGAACAGAGATGAGAGCCCTTCATCTGCTCCAGACAGCAGAACCGCATGCGG 1335  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyLeuProCysGlyLeu 300  
DB 1336 TCTGCAAGAGCGTGTCCACAGCTGCGGGGAGCGGGGCGGTGACCACTTGCGGTCTG 1395  
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320  
DB 1396 GACTATGAGGCTTACAAAGCTCCAGACACACACCTGTGTCACTGAGAACGAGTACTAC 1455  
QY 321 ThrAsnCysSerAlaGlyGlyIleAsnProPheLeuGlyAlaIleAsnPheAspAsnIle 340  
DB 1456 ACCAAGTCTCAGCGGGGAGACAAACCTTCAAGGGCCCATCACTTGTGACACATT 1515  
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrPheValAspIleMet 360  
DB 1516 GGTATGCTCGATGATCGCATCTTCCAGTATCACTGAGGAGGCTGGGTGATGATATG 1575  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
DB 1576 TACTTTGTGATGATGCTCACTTCTTCAATTTTCACTTCACTTCACTTCACTATC 1635  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu 400  
DB 1636 GTGGGCTCTTCTTCAATGATCAACTGTGCTGGTGTGATGGCAGCGAGTTCTCAGAG 1695  
QY 401 ThrIleGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
DB 1696 ACCAAGCAGCGGGAACACAGCTGATGCGGAGAGGAGTGTGGGTTCGTCCAAAGCC 1755  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGlyGluLeuLeuLeuTyrLeu 440  
DB 1756 AGCACCTTGCTACTTCTTCAAGCCCGGACGCTGCTATAGAGAGCTCAAGTACTCTG 1815  
QY 441 ValTyrIleLeuArgGlyAlaIleArgArgLeuAlaGlnValSerArgAlaIleGlyVal 460  
DB 1816 GTGTACATCTCTGTGTAAGCAGCCGAGGCTGAGGCTCTCTCGGAGCAGCAGGTGTG 1875  
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
DB 1876 CGGGTGTGGCTGTCCAGACACCCAGCACTTCCGGGGGCAAGAGACACAGCCAGAGC 1935  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisIleHisIle 500

Db	1936	AGTGGCTCGCTCCACCGCGCCCTATCGTCCACCACTGTGTGCACCAACCAACCAAC	1995
Qy	501	HisHisHisHisTyrHisHisLeuGluValAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
Db	1996	CATACCAACCACTACCACTGGGCAATGGACGCTCAGAGGCCCCCGGGCCAGCCCGAG	2055
Qy	521	IlleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
Db	2056	ATCCAGGACAGAGGATGCCAAATGGGTCCCGCGGCTCATGTGTCACACCAACCTTCACACCTT	2115
Qy	541	AlaLeuSerArgValAlaProProGlyGlyValAlaGluSerValHisSerPheTyrHisAlaAsp	560
Db	2116	GCCCTCTCCGAGGCCCCCTCGTGTGGCCCAAGTCTGTGCACAGCTTCTACAGTCCGAC	2175
Qy	561	CysHisLeuGluProProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
Db	2176	TGCCACTTAAAGCCAGTCCGCTGCCAGGCGCCCTCCCAAGTCCCATCTGAAGCATCC	2235
Qy	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600
Db	2236	GGCAGAGACTGTGGGACGGGAGAGGTGATCCACCGTGACACACAGCCCTCCACCGAG	2295
Qy	601	ThrLeuLysGlyLysValAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
Db	2296	ACGCTGAAGGAGAAAGCACTAGTAAAGGTGGCTGGCACTTGAGGCCCAACCTCAAC	2355
Qy	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640
Db	2356	AGCTCAACATCCACCCGGGCGCTTACAGCTCCATGCACAAAGCTGTGGAGACACAGAT	2415
Qy	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660
Db	2416	ACAGGTGCTGTGCAAAGCTCTTGACAAATCTCCAGCCCTTGTAAGACAGACATGGA	2475
Qy	661	AlaCysGlyProAspSerSerCysProTyrCysAlaArgAlaGlyValAlaGluLeu	680
Db	2476	GCTGTGTGTCCAGAACGTGCGCCCTACACTGTGCGCGGCGGGAGAGAGTGGAGCTC	2535
Qy	681	AlaAspArgGluMetProAspSerAspSerGlnAlaValTyrGluPheThrGlnAspAla	700
Db	2536	GCCGACCTGTAAATGCTCTGACTCAGACAGCGAGGAGTTTATGAGTTCAACAGATGCC	2595
Qy	701	GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla	720
Db	2596	CAGACACAGCACTCCGGGACCCCCACAGCGGGGGCAACGAGGCTGGGCCACGATGCA	2655
Qy	721	GluProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPheArgLysIleVal	740
Db	2656	GAGCCCACTGTGCTGCTGCTTCGTGGAGGCTTAATCTGTGACACCTTCCGAAACATTTGTG	2715
Qy	741	AspSerLysTyrPheGlyArgGlyLysMetIleAlaIleLeuValAsnThrLeuSerMet	760
Db	2716	GACAGCAAGTACTTTTGCGGGGAAATCAATGCGCACTCTGTGTCAACACTCAGCATG	2775
Qy	761	GlyIleGlyTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle	780
Db	2776	GGCATCGAATACACGACGAGCGGAGGAGCTTACCAACGCGCTTAAGAAATCAGCAACTC	2835
Qy	781	ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe	800
Db	2836	GTCCTTCAACCAAGCTTGTGCGCTGTGAGATGTGTGTGAAAGCTGTGTGTATGTATGCTCTTT	2895
Qy	801	GlyTyrIleLysAsnProTyrAsnIlePheLeuGlyValIleValIleSerValTyr	820
Db	2896	GGCATCATCAAGAAATCCCTTACAACTTCCATGTGTCAATGTGTGTATCAGCGGTGG	2955
Qy	821	GluIleValGlyGlnGlnGlyGlyLysLeuValLeuArgThrPheArgLeuMetArg	840
Db	2956	GAGATCGTGGGCGACAGGGGGGCGGCTGTGTGCGTGTGGGCACTTCCGCTATGTGT	3015
Qy	841	ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys	860
Db	3016	GTGCTGAAGCTGTGTGCGCTTCTGCGCGGCGGTGCAGCGGACGCTGTGTCTCATGAAG	3075

QY	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer	880
Db	3076	ACCAATGACAAACGTGGCCACCTTCTGCATCTCTCTTAATGCTTCACTTCACTTCACTTCACTGAC	3135
QY	881	IleLeuGluIleMetHisLeuPheGluCysValPheAlaSerGluArgAspGlyAspThrLeu	900
Db	3136	ATCTGGAGCATGCACTCTTCCGGCTGCAGATTGGTTCCTTACGGCGGATGGGACACCTTG	3195
QY	901	ProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleLeu	920
Db	3196	CCAGACCGGAAGAATTTTGACTCCTTGGCTCTGGGGCCATCTGCATCTGCTTTCAGATCTCTG	3255
QY	921	ThrGlnGluAspTyrAsnLysValIleuTyrAsnGluMetLysAserHisSerSerTyrPala	940
Db	3256	ACCAAGAGAGACTGAACAAGTCTCTTACAAAGGATGGACCTTCCACAGTGTCTTGAGG	3315
QY	941	AlaLeuTyrPheIleAlaLeuMetThrPheGluYAsnTyrValLeuPheAsnLeuLeuVal	960
Db	3316	GCCCTTTATTTCAATGGCCCTTCATGACCTTGGGCACTAGTGCTCTTCAATTTGCTGGTCT	3375
QY	961	AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly	980
Db	3376	GCCATTTCTGGTGGAGGGCTTCCAGGCGGAG-----	3405
QY	981	GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyYAspAlaAsnLysSerGlu	1000
Db	3406	-----GGAAATGCCAACAAGTCCGAA	3426
QY	1001	SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu	1020
Db	3427	TCAAGAGCCCAATTTCTTCAACCCAGCTGGAATGGTATGGGAGACGAAGAATGCTTGG	3486
QY	1021	AlaLeuValSerLeuGluYuhIAspProGlnLeuArgLysSerLeuLeuProPoleuIle	1040
Db	3487	GCTTGGTGTCTTGGAGAGCACCCGAGACTGGGAAAGCTTGTGCGGCTTCTATCTC	3546
QY	1041	IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyLu	1060
Db	3547	ATCCACACGGGCGGCCACACCATGTGCTGCCCAAGACACACAGCGGCGCTGGGCGAG	3606
QY	1061	AlaLeuGluTyrAlaSerArgArgThrSerSerSerCysSerLysArgLysAlaProSerLeuLys	1080
Db	3607	GCGGTGGAGCCCTGGTGTGGCCCGGACGACGAGCAGCGGTGGCAGAGCTGTGGGCGGGC	3666
QY	1081	HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTyrSerAlaAla	1100
Db	3667	CACAGATGAAGTACCGCCCAAGGCGCCGAGCTCTTCGACAGCCCTCGAAGGCGTGA	3726
QY	1101	SerSerTyrThrSerArgArgSerSerArgAsnSerLeuGluArgAlaProSerLeuLys	1120
Db	3727	AGCAGCTGGACACGACAGACGCGCTCCAGCGGAAACAGCTCCGCGCGTGCACCACTGAAAG	3786
QY	1121	ArgArgSerProSerGluYuhArgArgSerLeuLeuSerGluYuhGluGlyGlnGluSerGln	1140
Db	3787	CGGAGAGCCCAATGTAGAGAGCGCGGATCCCTGTGTTCGGAGAAAGCCACGAGAGCCAG	3846
QY	1141	AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis	1160
Db	3847	GATGAAGAGGAGACTCAGAAAGAGAACCGGAGCCCTCCGGGCGAGTGAACATCCGCAC	3906
QY	1161	ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
Db	3907	AGGGGGTCCCTGGAGCGGAGGCGCAAGATGCTCTTGACTCCGCAAGACACACTGCAGGTG	3966
QY	1181	ProGlyLeuHisArgThrAlaSerGlyArgGlySerLysAserGluHisGlnAspCysAs	1200
Db	3967	CCAAGGCTGATCGCACTGCCAAGTGGCGCGAGGGTGTGCTTCTGAGCACCGAGGACTGCA	4026
QY	1200	nglyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProTyrLeuAs	1220
Db	4027	TGGCAAGTGTGGCTTCAAGGCGGCTGTGGCCGAGGCTTCGCGGCTGAATGACCCCCCACTGGA	4086

QY 1220 pgiYAspAspAlaAspAspGluGluYAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240  
DB 4087 TGGGGATGACGGCGGATGACAGAGGCAACTGAGCAAGGGAAACGGGTCCGCGGTGAT 4146  
QY 1240 eAGsAlaArgLeuProAlaCysTrpLeuGluArgAspSerTrpSerAlaTrpIlePhePr 1260  
DB 4147 CCGAGCCCGACTCCCTGCTGCTGCTGCTGAGCGAGACTCTCGTGCACCTTCTCC 4206  
QY 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280  
DB 4207 TCTCAGTCCAGGTTCCGCTCCGTGTCAACCGGATCATCACCAAGAAAGTTCCAGCA 4266  
QY 1280 sValValLeuValIleIlePheLeuAsnGlyIleThrIleAlaMet-GluArgProLysI 1300  
DB 4267 CGTGAGCTCTGATCATCTTCTCTTAACATCATCACATCGCCATGGAGACGCCCAAAA 4326  
QY 1300 le-AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTrpIlePheThrAla 1319  
DB 4327 TTTGACCCCAACGCTTGAACGCACTTCTGACCTTCTCCAAATTACATTTACCCGCA 4386  
QY 1320 ValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGln 1339  
DB 4387 GTCTTTCTGGCTGAATGACAGTGAAGTGTGGCATCTGGGCTGTGCTTCGGGAGACAG 4446  
QY 1340 AlaTrpLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIle 1359  
DB 4447 GCGTAACTCGCGAGAGTGGAAAGTGTGAGCGGCTGTGGTGCATCTCCGTATC 4506  
QY 1360 AspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgVal 1379  
DB 4507 GACATTTGTGGTGTCAATGATGTTCTGACAGCGGACCAAGATCTTGAGGACATGAGGAGT 4566  
QY 1380 LeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLys 1399  
DB 4567 CTGGGGTGTGTGGCGGCGCTGGCGCGCTCAGGTTGATCAGCGGGGCGAGGGCTGAG 4626  
QY 1400 LeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCys 1419  
DB 4627 CTGTGTGTGAGAGAGCTGATGTCTCTCACTGMAACCCATCGGCAACATTTGAATCATCTGC 4686  
QY 1420 CysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePhe 1439  
DB 4687 TGTGCTCTTTCATCATTTTGGCATCTTGGGGTGGAGCTTTCAAGGGAACTTTTTC 4746  
QY 1440 ValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSer 1459  
DB 4747 GTGTGCCAGGGCGAGATCACAGGACATCACCAATTAATCGACTGTGGCGAGCCAGT 4806  
QY 1460 TyrArgTrpValArgHisLysTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeu 1479  
DB 4807 TACCGGTGGGTCCGGCAAGTACCACTTTGACAACTTGGCCAGGCGCTGATCTCCCTG 4866  
QY 1480 PheValLeuAlaSerLysAspGlyTrpValAspIleMetTrpAspGlyLeuAspAlaVal 1499  
DB 4867 TTTGCTTTTGGCTTCAAGAGATGTTGGTGGACATCATGATGAGTGGTGGTGGAGAAC 4926  
QY 1500 GluValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTrpPheIleSer 1519  
DB 4927 GGCGTGCACGAGCCCATATGATACCAACCCCTGGAGTGTGCTGATCTTCTG 4986  
QY 1520 PheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsn 1539  
DB 4987 TTTCTGTCTCATTTGGCTTCTTGTCTCTGAAACATGTTTGTGGTGTGGTGGTGGAGAAC 5046  
QY 1540 PheHisLysCysArgGlnHisGlnGluGlnGluAlaArgAspGlyGlnGluLysArg 1559  
DB 5047 TTTCCACAAGTGTCCGACACACAGAGAGAGAGGCGCGGCGGAGAGAGAGAGGCGC 5106  
QY 1560 LeuArgTrpLeuGlnLysLysArgArg----- 1568  
DB 5107 CTAGAGAGACTGAG 5166  
QY 1569 -----LysAlaGlnCysLysProTrpTrpSerAspTrpSerArg 1581

DB 5167 AGCTCAGCCAGCGCTGCTGACAGAGCCAGTGAACCTTACTACTCCAGTACTCCCGC 5226  
QY 1582 PheArgLeuLeuValHisHisLysCysTrpSerHisTrpLeuAspLeuPheIleThrGly 1601  
DB 5227 TTTCCGCTCTCTGTCCACCATTTGTGACACAGCACTTACTGTGAGCTTCTTCAACAGGT 5286  
QY 1602 ValIleGlyLeuAsnValValThrMetAlaMetGluHisLysTrpGlnInProGlnIleLeu 1621  
DB 5287 GTCATGGGCTGAACCTGTGCATCATGAGCAATGAGACACTTACAGAGCCCGCATTTCTG 5346  
QY 1622 AspGluAlaLeuLysIleCysAsnTrpIlePheThrValIlePheValIleuGlnSerVal 1641  
DB 5347 GATGAGCTCTGAAGATCTGCATCATCTTCACTGTATCTTTGTCTTGGAGTCAAGTT 5406  
QY 1642 PheLysLeuValAlaPheGlyPheArgArgPheGlnAspArgTrpAsnGlnLeuAsp 1661  
DB 5407 TTTCAACTGTGGCTTTGGTTCCGTGGTCTTCCAGGACAGTGGAACTGAGTGCAGC 5466  
QY 1662 LeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGluIleGluValAlaAspAla 1681  
DB 5467 CTGGCATTTGTGTGCTGTCCATCATGAGGCAATGAGGCAATGAGGAAATCAGAGTCAACGCC 5526  
QY 1682 SerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgVal 1701  
DB 5527 TCGTGCCATCAACCCCACTCATCTCCGATCATAGAGGTGTGGCATTTGCCCGAGT 5586  
QY 1702 LeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAla 1721  
DB 5587 CTGAAGCTGTGAAGATGGCTGTGGCATATGGGCGCTGTGGACACGGGTGACAGGCC 5646  
QY 1722 LeuProGlnValGlyLysLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaIle 1741  
DB 5647 CTGCCCCAGGTGGGAACCTGGGACTTCTTATGTGTGTTTTCATCTTTGAGCT 5706  
QY 1742 LeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGlnGlyLeu 1761  
DB 5707 CTGGCGGTGAGGCTCTTTGGAGACTTGGAGTGTGAGAGACACACCCCTGTGAGGGCTG 5766  
QY 1762 GlyArgHisAlaIleThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSer 1781  
DB 5767 GGGCGTATGCCACCTTTGGAACTTTGGCATGGCTTCTTCAACCTTCCGAGTCTCC 5826  
QY 1782 ThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlnUser 1801  
DB 5827 ACAGGTGACAAATGGATGATGATGAGAGACACCTCGGAGACTGTGACAGGAGTCC 5886  
QY 1802 ThrCysTrpAsnThrValIleSerProIleTrpPheValSerPheValLeuThrAlaGln 1821  
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QY 1822 PheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlnGlnUserAsnLys 1841  
DB 5947 TTTGCTGTATCTCAACGTGTGATGCGCGTGTATGAGACACTGGAGAGAGACAAAG 6006  
QY 1842 GluAlaLysGlnGluAlaGluLeuGluAlaGlnLeuGluLeuGlyLysThrLeuSer 1861  
DB 6007 GAGGCCAAGAGAGAGCGGAGTGAAGCTGAGAGCTGAGATGAAAGACCTTCAGC 6066  
QY 1862 ProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAsp 1881  
DB 6067 CCCAGGCCCACTGGCACTGGGCAAGCCCTTCTCTGCTGGGTGAGGGCCCCAGC 6126  
QY 1882 SerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArg-SerAlaSer 1901  
DB 6127 AGCCCGAGACGCCCAAGCTGGGGCTGTGACCAAGCGGCCCAAGAGATCAGCTTC 6186  
QY 1901 TrpHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGlyProAs 1921  
DB 6187 CCACTTTTCCCTGAGAGACCCCAAGTGCAGGCCCAACCCCAAGAGACTGACAGAGACAGA 6246  
QY 1921 PheLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu-ProAsnAspSerTr 1941

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Db      6247 CTACTGACTGTGGGAGAGTCTGGGTCAGCCGAAGCACTCTGCCCCCAATGACAGCT 6306
QY      1941 yMecCySaRgh's-GlySerThrAlaGluGlyProLeuGlyHisArgGlyTTPGlyLeu 1960
Db      6307 ACATGTGTGGGATGGGAGGACATGCGAGGGGCCCCCTGGGACACAGGGGCTGGGGGCTC 6366
QY      1961 ProLYsAlaGlnSerGlySerValIleuSerValHisSerGlnProAlaAspThrSerTyr 1980
Db      6367 CCCAAGCTCAGTCAGGCTCCGCTTGTCCGTTCACTCCACGACGACAAATACAGCTAC 6426
QY      1981 IleuGlnLeuProLYsAspAlaProHisIleuLeuGlnProHisSerAlaProThrTTP 2000
Db      6427 ATCTGCACTTCCCAAGATGCACTCATCTGCTCAGGCCCAAGGCCCAACTGG 6486
QY      2001 GlyThrIleProLYsLeuProPProLYsArgSerProLeuAlaGlnArgProLeuArg 2020
Db      6487 GGGACCATCCCCCAAGCTGCCCCCAGCAGACGCTCCCTTTGGCTCAGAGGCCACACAG 6546
QY      2021 ATGGAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAsp 2040
Db      6547 CGCCAGGACAGCAATAGAGATGACTCTTGGAGCTTCAAGGCTGGGCAAGCCGGAAAGAC 6606
QY      2041 LeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTTPGly 2060
Db      6607 CTGCTGGCAGAGGTGAGTGGGCTCCCTCCGCCCCCTGGGCCCTACTTCTTGGGGC 6666
QY      2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerTyrIleSerTyrHisMet 2080
Db      6667 CAGTCAAGAACCCAGGACACAGCAGCACTCCGAGCAGCAGCAAGATCTCCAAAGCAAG 6726
QY      2081 ThrProAlaProLYsProLYsProLYsProLYsProLYsProLYsProLYsProLYs 2100
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QY      2100 rArgSerSerLeuGlnLeuAspThrGluLeuSerTTPIleSerGlyAspLeuLeuPro 2120
Db      6787 CAGAAACAGCTTGAAGTGGACACGAGCTGAGCTGATTTGACGAGACCTCTGCCCC 6846
QY      2120 OGlyGlyGlnGluGluProProSerProArgAspLeuLYsGlySerValGluAla 2140
Db      6847 TGGCGGCCAGAGAGACCCCAATCCCAAGGACCTGAAGATGCTTACAGCTGAGAGC 6906
QY      2140 aglnSerCySGlnArgArgProThrSerTTPLeuAspGluGlnArgArgHisSerIleAla 2160
Db      6907 CCAAGACTGCCAGGCCCGGCCCACTCTGCTGAGTGAAGAGAGACACTTATCC 6966
QY      2160 aValSerCyLeuAspSerGlySerGlnProHisIleuGlyThrAspProSerAsnLeuG 2180
Db      6967 CGTCACTGCTGGAGACAGCGGCTCCCAACCCCACTGGGACAGACCCCTTAACTTGG 7026
QY      2180 yGlyGlnProLeuGlyGlyProGlySerArgProLYsLYsLYsLeuSerProProSerI 2200
Db      7027 GGGCCAGCCTCTTGGGGGCTGAGAGCCGGCCCAAGAAAAAACTAGCCCGCTAGTAT 7086
QY      2200 eThrIleAspProProLYsSerGlnGlyProArgThrProProSerProGlyIleCysLe 2220
Db      7087 CACCAATAGACCCCCCGAGAGCCAAAGTCTCCGAGACCCCGCCACTGATCTCGCT 7146
QY      2220 uArgArgArgAlaProSerSerAspSerLYsAspProLeuAlaSerGlyProProAspSe 2240
Db      7147 CCGAGAGAGGGGCTCCGTCAGCACTCCAAGAGATCCCTTGGCTTGGGCCCTTACAG 7206
QY      2240 tMetAlaAlaSerProSerProLYsLYsAspValIleuSerLeuSerGlyLeuSerSer 2260
Db      7207 CAGTGTGCTCCCTCCCTCCCAAGAAAGATGTGTGAGTCTCTCGGTTATCTCTGA 7266
QY      2260 pProAlaAspLeuAspPro 2266
Db      7267 CCCAGCAGACTGGAACCC 7285

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RESULT 10  
AAZ52309  
id AAZ52309 standard; cDNA; 7286 BP.

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XX      XX      AAZ52309;
AC      AC      18-JUL-2000 (first entry)
XX      XX      Rat pancreatic T-type calcium channel cDNA.
XX      XX      Rat: pancreatic T-type calcium channel alpha subunit; insulin;
XX      XX      pancreatic beta cell; alphaIG; low voltage activated Ca2+ channel family;
XX      XX      anti-diabetic; calcium influx; L type calcium channel; NIDDM;
XX      XX      type II diabetes; non-insulin dependent diabetes mellitus; ss.
XX      XX      Rattus sp.
XX      XX      Location/Qualifiers
FH      FH      1..157
FT      FT      misc_feature
FT      FT      /tag= b
FT      FT      /note= "Region upstream to the coding region of
FT      FT      pancreatic T-type calcium channel protein"
FT      FT      2..7285
FT      FT      /tag= a
FT      FT      /product= "Pancreatic T-type calcium channel alpha
FT      FT      subunit"
FT      FT      /transl_except= (pos:11..13, aa:Xaa)
FT      FT      /transl_except= (pos:7022..7024, aa:Xaa)
FT      FT      /transl_except= (pos:7112..7114, aa:Xaa)
FT      FT      /note= "Xaa corresponds to in-frame stop codon. This
FT      FT      region includes sequence upstream to the coding region of
FT      FT      pancreatic T-type calcium channel protein. Does not
FT      FT      include stop codon"
FT      FT      /partial
FT      FT      158..7285
FT      FT      /tag= c
FT      FT      /product= "Pancreatic T-type calcium channel alpha
FT      FT      subunit"
FT      FT      /note= "This region is claimed as SEQ ID NO: 1"
PN      PN      WO200015845-A1.
PD      PD      23-MAR-2000.
XX      XX      26-AUG-1999; 99WO-US019675.
PF      PF      26-AUG-1998; 98US-0098004P.
XX      XX      26-AUG-1998; 98US-0098004P.
PR      PR      27-JAN-1999; 99US-0117399P.
XX      XX      (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
PA      PA      LI M;
XX      XX      MPI: 2000-271475/23.
XX      XX      P-PSDB; AAY70720.
DR      DR      Novel nucleic acids encoding pancreatic T-type calcium channels used for
DR      DR      regulation of T-type calcium channels and treatment of type II diabetes.
XX      XX      Example 1; Page 114-119; 124pp; English.
XX      XX      The present cDNA encodes a protein that includes pancreatic T-type
XX      XX      calcium channel alpha subunit derived from rat insulin secreting beta
XX      XX      cell line, INS-1. The protein shows 96.3 % identity to the neuronal T-
XX      XX      type calcium channel alpha subunit (alphaIG). The T-type Ca2+ channel
XX      XX      from INS-1 (alphaIG-INS) and neuronal alphaIG are alternative splice
XX      XX      isoforms of the same gene. The INS-1 isoform is also expressed in brain,
XX      XX      neonatal heart and kidney besides pancreatic beta cells. T-type Ca2+
XX      XX      channel belongs to the family of low voltage activated Ca2+ channels. The
XX      XX      present sequence is used for treating diseases associated with abnormal
XX      XX      expression or function of T-type calcium channels. They are especially
XX      XX      used for treating type II diabetes. Modulators of pancreatic T-type Ca2+
XX      XX      channel e.g. antisense oligonucleotides, ribozymes and inhibitors are
XX      XX      used in methods for modifying insulin secretion by pancreatic beta cells,
XX      XX      basal calcium levels, potential L type calcium channel activity,
XX      XX      pancreatic cell death, pancreatic beta cell proliferation and calcium

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CC Influx through L type calcium channels in cells  
XX Sequence 7286 BP; 1467 A; 2224 C; 2064 G; 1531 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	7286
Score:	11111.00	Matches:	2135
Percent Similarity:	94.80%	Conservative:	35
Best Local Similarity:	93.27%	Mismatches:	95
Query Match:	93.34%	Indels:	24
DB:	3	Gaps:	5

US-09-611-257A-37 (1-2286) x AA252309 (1-7286)

1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20  
158 ATGGACAGAGAGAGAGATGGAGCGGGCCGAGAGAGTCGGGACACGCCCGTAGCTTCACG 217  
21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGlyLysAsp 40  
218 CAGCTCAACGACCTGTCGGGGGGCCGGGGCCGGCAGGGGGCCGGGGTCCAGCGAAMAAGAC 277  
41 ProGlySerAlaAspSerGlyAlaGlyGlyLeuProGlyProAlaLeuAlaProValVal 60  
278 CCGGGCAGCGGAGCTCCGAGCGGAGGGGCTGCTGTAACCGGCGTAAAGCCCGGTGTT 337  
61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80  
338 TTCTTCTTACTTGAACCGAGACGCCGCCCGGAGCTGTGTCTCCGACCGCTGTATAC 397  
81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnGlyValThrLeuGlyMet 100  
398 CCGGAGTTCCAGGACAGTACGATAGTGTCTTCTTCAACTGTGTGACTCTGGGTATG 457  
101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
458 TTCAAGGCGGTGGAGCATTGCTGTGACTCCAGCGGCTGCGGATCTGGACGGCTTC 517  
121 AspAspPheIlePheAlaPheAlaValGluMetValIlyMetValAlaLeuGly 140  
518 GATACATTCATCTTTCCTCTTCTTCTGCTGTAATGTGTGAAGATGTGTGGCTTGGCC 577  
141 IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal 160  
578 ATCTTTGGGAAGAATGTATCTGAGGACACTTGGAAACCGGCTTGTGCTTTTCACTTGC 637  
161 IleAlaGlyMetLeuGlnTyrSerIleAspLeuGlnAsnValSerPheSerAlaValArg 180  
638 ATTCAGGGAGTGTGAGTATTCCTGCTGACCTGCAGAACTGCACCTTCTCCGACGTACG 697  
181 ThrValArgValLeuAspGluProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
698 ACAGTCCGTGTGCTGCAGCCGCTCAGGCGCATTTAAACCGGGTCCGACGATCGCATTC 757  
201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValIleLeuLeuCysPhePhe 220  
758 GTCACTTATCTGCTGGACACCTTGGCTATGTGGGCAACGTCTGCTCTCTGTTTCTTC 817  
221 ValPhePheIlePheGlyIleValGlyValGlnLeuThrPalaglyLeuLeuAspArg 240  
818 GTCTTTTTCATCTTTGGCATGTGGGCGTCCAGCTGTGGGAGAGACGTCTTCGCAACCGA 877  
241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
878 TGCTTCTCTCCCGAGAACTTCAAGCTCCCTCTGAGCGTGGACCTTGACCTTATTAACAG 937  
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938 ACAGAGAAATGAGAGAGAGGCCCTTCACTGTCTCTCAGCCCTGGGAAATGCGCATGAGA 997  
281 SerCysArgSerValProThrLeuArgIlyAspGlyGlyGlyGlyProProCysGlyLeu 300  
998 TCCTGCAAGAGTGTCCCACTGCTGTGGGAAAGCGGTGTGTGCGCCACCTTCGACGTCTG 1057

301 AspTyrGluAlaTyrAsnSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyr 320  
1058 GACTATGAGACCTATAACAGTTCCAGCAACACCACTGTGTCACTGAGAACCACTATCTAT 1117  
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341 GlyTyrAlaThrIleAlaIlePheGlnValIleThrLeuGlnGlyTyrValAspIleMet 360  
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1238 TACTTGATGAGACCTCACTCTTCACTCACTTCACTTCACTTCACTTCACTTCACTTCA 1297  
381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
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401 ThrLeuGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
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421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGlnGluLeuLeuLysTyrLeu 440  
1418 AGCACCTGTGCAAGCTTCTGTGAGCCAGGCGTGTATGAGAGGCTCACTCAAGTACCTG 1477  
441 ValTyrIleLeuArgLysAlaIleArgArgLeuAlaGlnValSerArgAlaIleGlyVal 460  
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461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGlnThrGlnProSerSer 480  
1538 CCGGCTGGGCTGTCCAGCAAGCCAGTGGCCCGTATGAGGAGAGGCCAGCCAGTGGC 1597  
481 SerCysSerArgSerHisArgArgLeuSerValHisIleValHisIleHisIleHis 500  
1598 AGCTGACCTGCTCACCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1567  
501 HisHisHisIleTyrHisIleGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
1658 CACCATACCACTACCACTGCGGTATGGACCTCAGATTCCTCCGGGCGACGCCAGAG 1717  
521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540  
1718 ATCCAGGACAGGAGATGCATGGGTCTCGCGGCTCATGCTACCAACACCTTACACACC 1777  
541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560  
1778 ACTCCCTGTGGGGCCCTCCGAGGGGGTGGAGTGTGTACACAGCTTCTACCACTGTGAC 1837  
561 CysHisIleGlnGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
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581 GlyArgThrValGlySerGlyLysValTyrProThrValHisIleThrSerProProGlu 600  
1898 GGTAGCATGTGGGTATGGGAAGTGTACCCCATGTCATACCACTCCACAGAG 1957  
601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620  
1958 ATACTGAAGATTAAGACATGAGAGTGGCCCCCAGCCCTGGGCCCCACCTTAC 2017  
621 SerLeuAsnIleProProGlyProTyrSerSerMetHisIleLysLeuLeuGlnThrGlnSer 640  
2018 AGCTTCAACATCCCACTGGGCCCTTCAAGCTTCATGACACAGCTCTGGAGACACAGT 2077  
641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
2078 ACGGAGCGCTGCATTACTCTCTGCAAAATCTCCAGGCTTGTCTCAAGGAGACAGTGTGA 2137

QY	661	AlAcysglYProAspSerCYsProTYrCYsAlAArgAlaGlyAlaGlyValGlnLeu	680
Db	2138	GCCGCGGGCGCGGACAGTTGTCCTTACTGTGCGCGGACAGAGCAGAGAGCCAGATCC	2197
QY	681	AlAspArgrgluMetProAspSerAspSerGlnAlaValTYrGlnPheThrGlnAspAla	700
Db	2198	GCTAACCATGTCAATGCTTGACTCAGACAGCAGGCTGTGTRTAGTTCAACAGAGCGCT	2257
QY	701	GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp	719
Db	2258	CAGACAGATGACTCCGGGATCCCAACAGCGGGGGGAGCAGCGGAGCGTGGGCCAGAT	2317
QY	720	AlaGlnProSerSerValLeuAlaPheTrpArgLeuIleCYsAspThrPheArgLysIle	739
Db	2318	GCAAGAGCTAGTTCTGTGCTGGCTTTTCGGAGGCTGATCTGTGACAAATTCGGAAATGC	2377
QY	740	ValAspSerLysTYrPheGlyArgGlyTLeuMetIleAlaIleLeuValAsnThrLeuSer	759
Db	2378	GTAATATGCAAAATCTTTGGCCGGGGAATCATGATCGCATCTGGTGTCAATATCACTAGC	2437
QY	760	MetGlyIleGlnTYrHisGlnGlnProGlnGlnLeuThrAsnAlaLeuGlnLysSerAsn	779
Db	2438	ATGGGCACTCAGTACACAGAGCAGCCGAGGAGCTCAACAAAGCCCTGGAAATCAGACAC	2497
QY	780	IleValPheThrSerLeuPheAlaLeuGlnuMetLeuLeuLysLeuLeuValTYrGlyPro	799
Db	2498	ATGCTCTTCAACAGCGCTTCTGGCTTGGAGATGCTGTAAGAACTGTGTCTTACGGTCCC	2557
QY	800	PheGlyTYrTyrIleLysAsnProTYrAsnIlePheAspGlyValIleValIleSerVal	819
Db	2558	TTTGGCTACATTAAGAAATCCCTACAACTTTTAATGTGTGTCATTTGTGTCATCAGTGTG	2617
QY	820	TrpGlnIleValGlyGlnGlnGlyGlyGlyLysLeuSerValLeuArgThrPheArgLeuMet	839
Db	2618	TGGAGAGATTTGGCGCCAGCAGGAGAGTGCGCTGTGCGTGGCGGACCTTCGGCTAGTG	2677
QY	840	ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValIleuMet	859
Db	2678	CGGGTGTGAAGCTGTGTGCGCTTCTCGTCCGGCCCTGCAAGCCAGCTCGTGTGTCATGT	2737
QY	860	LysThrMetAspAsnValAlaThrPheCysMetLeuMetLeuPheIlePheIlePhe	879
Db	2738	AAGACCAAGACAACGTTGCCACCTTCTGCATGCTCTCAATGCTGTCATCTTCACTCTTC	2797
QY	880	SerIleLeuGlyMetHisLeuPheGlyCYsLysPheAlaSerGlnArgAspGlyAspThr	899
Db	2798	AGCATCTCTGGGCAATGCATCTCTTTGGTTGGCAAGTTCCGATCTGAAACGGGATGGGGACAG	2857
QY	900	LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle	919
Db	2858	TTGCGACAGCCGAAAGAAATTTGCACTCCCTGCTGTGGGCCATCGTCACTGTCTTCAAGATT	2917
QY	920	LeuThrGlnGlnAspTrpAsnLysValLeuTYrAsnGlyMetAlaSerThrSerSerTrp	939
Db	2918	CTGACTCAGGAAGACTGGAAATTAAGTCTCTTCAACACGGCAATGGGCTCCACATCGCTTGG	2977
QY	940	AlaAlaLeuTYrPheIleAlaLeuMetThrPheGlyAsnTYrValLeuPheAsnLeuLeu	959
Db	2978	GCTGCTCTTAACTTCATGACCCCTCATAGACTTTTGGCACTATGTGCTCTTTAACTGCTG	3037
QY	960	ValAlaIleLeuValGlnGlyPheGlnAlaGlnGlnLysLeuLysSerLysGlnAspAlaSer	979
Db	3038	GTGGGCCATTTCTTGTGGAAGATTTCCAGGCAAGGAAATCGGCAAAACGGGAAGATCGAGT	3097
QY	980	GlyGlnLeuSerCYsIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer	999
Db	3098	GGACAGTTAAGCTGATATCAGGTGCTTCAACTTCAGGGGGGAGAGCCACCAAGCTT	3157
QY	1000	GlnSerGlnProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCYs	1019
Db	3158	GAGTAGAGCCCTGATTTCTTTTGGCCAGGTGGTGAATGGGGAAGAAAGAGCCG	3217
QY	1020	LeuAlaLeuValSerLeuGlyGlyLysProGlnLeuArgLysSerLeuLeuProLeu	1039

[illegible]



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Db 4418 TGGTGTCCTCTTCATCATTTTGGAAATTCGCGGGTGACGCTTCCTCAAGGGAAGTTC 4477  
Qy 1439 PheValCysGlnGlyLysAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla 1458  
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Qy 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518  
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Qy 1559 ArgLeuArgArgLeuGlnLysLysArgArg----- 1568  
Db 4838 CGACTACGAGAGCTGAGAGAAAGAGAGATCTTAATGTTGACGATGTAATTCCTCC 4897  
Qy 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSer 1580  
Db 4898 GGCAGCTCAGCCAGCGCGCTGAGAAAGCCAGTGCAGAGCCCTCATCTGATCTACG 4957  
Qy 1581 ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1600  
Db 4958 AGATTCCGGCTCTTGTGCCACACCTGTGTACAGCACTACGACCTCTTATCATCT 5017  
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Qy 1621 LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGlnSer 1640  
Db 5078 CTGACAGAGGCTCGAAGATCTGCATTACATCTTTACCGTCATCTTTGTGTTGAGTCA 5137  
Qy 1641 ValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeu 1660  
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Qy 1681 AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1700  
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Qy 1701 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln 1720  
Db 5318 GTTCTGAAGCTGTTGAGATGCTGTGGGCACTGGGCACTGCTGGACACCGTATGAG 5377  
Qy 1721 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1740  
Db 5378 GCCCTGCCCCAGGTGGGGAACCTGGACTTCTTTCATGTTATGTTTTCATCTTTCGA 5437  
Qy 1741 AlaLeuGlyValGlnLeuPheGlyLysAspLeuGlnCysAspGluThrHisProCysGlnGly 1760  
Db 5438 GCTCTGGCGGTGAGGCTCTTTGGAGACTGGAGTGTGAAGAGACACCCCTGTGAGGGC 5497  
Qy 1761 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780  
Db 5498 TTGGGTGGGATGCCACTTTAGGAACCTTTGGATGGCTTTTGTACCCCTTCCGAGTCC 5557  
Qy 1781 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu 1800  
Db 5558 TCCACTGTGACACATCGAATGTTATTAAGAAGACACCTCCGGGACTGTGACGAGAG 5617  
Qy 1801 SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla 1820  
Db 5618 TCCACTGTGACACATCGAATGTTATTAAGAAGACACCTCCGGGACTGTGACGAGAG 5677  
Qy 1821 GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlnGlnSerAsn 1840  
Db 5678 CAGTTTGTGCTGTCAACGTGTCTATAGCTGTCTGTATGATGAGACCTGGAAAGAACAC 5737  
Qy 1841 LysGluAlaLysGlnGluAlaGlnLeuGlnAlaGlnLeuGlnLeuMetLysThrLeu 1860  
Db 5738 AAAGAGCCCAAGAGAGGCGGAGCTCGAGCCGAGCTGAGAGTGAAGACGCTC 5797  
Qy 1861 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGlnGlyPro 1880  
Db 5798 AGCCCGACGCCACATCCCGCTGGGAGCGCTTCCTCTGCGCGGGTGGAGGTTGTC 5857  
Qy 1881 AspSerProAspSerProLysProGlyAlaLeuHisProAlaHisAlaArgSerAla 1900  
Db 5858 AACAGTCTGACAGCCCTTAAGCTGGGGCTCCACACACCACTGCCACATTTGAGACAGCC 5917  
Qy 1901 SerHisPheSerLeuGlnHisProThrMetGlnProHisProThrGlnLeuPro----- 1918  
Db 5918 TCGGGCTTCCTCCCTTGAGACCCCAAGATGTACCCACCCGAGAGGAGGACAGTCCCC 5977  
Qy 1919 ---GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937  
Db 5978 CTAGACACCAAGCTGTGACTGTGAGGAAGTGTGGGTGACGCGGAGCACTCTGCCCC 6037  
Qy 1938 AsnAspSerTyrMetCysArgHisGlySerThrAlaGlnGlyProLeuGlnHisArgGly 1957  
Db 6038 AATGACAGCTTACATGTGGCCCAATGGAGACACTGTGAGAGATCCCTTAGACACAGGGCC 6097  
Qy 1958 TrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAsp 1977  
Db 6098 TGGGGGCTCCCAAGCCAGTCAAGGCTCATCTTGTCCGTTCACTCCCAACAGCAGAC 6157  
Qy 1978 ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAla 1997  
Db 6158 ACCAGCTGCATCTTACAGCTTCCCAAGATGTCACTGTGTCCAGCTCATAGGGGCC 6217  
Qy 1998 ProThrTrpGlyThrIleProLysLeuProProGlyValArgSerProLeuAlaGlnArg 2017  
Db 6218 CCACTGGGGGCCCATCCCTTAATCAACCCCACTGGCGCTCCCTCTGGCTCAGAGG 6277  
Qy 2018 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2037  
Db 6278 CTTCTAGAGGCGCAGGAGCAATGAGACTGATCCCTGGATGTGACAGGGCTGGGTAGC 6337  
Qy 2038 ArgGlnAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSer 2057  
Db 6338 CCGGAAGACCTGTGTGAGAGTGAAGTGGGCTCTCTGCTGTGACCCGCTCTCAATCC 6397  
Qy 2058 PheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSer 2077  
Db 6398 TTCTGGGGCGGGTCAAGCATCCAGTGCACAGCCTTCCGACATCCAGACAAAGTCTCC 6457  
Qy 2078 LysHisMetThrProProAlaProCysProGlyProGlnProAsnTrpGlyLysGlyPro 2097  
Db 6458 AAGACATTCGCGCTGAGGCTCTTGTCCAGGCTGTGAACCCAGCTGGGCAAGGACCTT 6517

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QY      2098 ProGluThrArgSerSerLeuLeuAapThruGluLeuSerTrpIleSerGlyAspLeu 2117
      |||
Db      6518 CCGAGAACCGAAGACGCTTAGAGCTGACACGAGACTGAGCTTCAAGAGACCTC 6577
QY      2118 LeuProGlyIyGlyIngluProProSerProArgAspLeuYslyCytyrSer 2137
      |||
Db      6578 CTT---CCGAGCAGCCAGGAGAAACCCCTGCTCCCAACGGGACCTGAAGAAGTCTACAGT 6634
QY      2138 ValGluAlaGlnSerCysGlnAArgProThrSerTrpLeuAspGluGlnAArgHis 2157
      |||
Db      6635 GTTAGAACCCAGAGCTGACGAGCCGACGCTGGGTCTGCTAGATGAAACGCGAGACAC 6694
QY      2158 SerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSer 2177
      |||
Db      6695 TCCATTGCTGTACGCTGTCTGACACGCGGCTCCCAACCCCGCTTAGTCCAGACCCCTCA 6754
QY      2178 AsnLeuGlyGlyInProLeuGlyIyGlyProGlySerArgProIyAspLeuSerPro 2197
      |||
Db      6755 AGCCTCGGGGCGCAACCTTGGGGGCTCTGGAGCGGCGCTAAGAAAAAACTCAGCCCA 6814
QY      2198 ProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSerProGly 2217
      |||
Db      6815 CCCAGATATCTATATGAAACCCCGAGAGCCAGGCGCTCTCGGCCCATGCACTCTGAT 6874
QY      2218 IleCysLeuArgArgArgAlaProSerSerAspSerIyAspProLeuAlaSerGlyPro 2237
      |||
Db      6875 GTCTGCTCAGAGAGAGGGGCGCGCCAGTGACTTAAGATCCCTCGGCTCCACCCC 6934
QY      2238 ProAspSerMetAlaAlaSerProSerProIyAspValLeuSerLeuSerGlyLeu 2257
      |||
Db      6935 CTTCAGACAGCAGCGCTGCTCACCCCTCCCAAGAAAGACACGCTGAGTCTCTGCTTTG 6994
QY      2258 SerSerAspProAlaAspLeuAspPro 2266
      |||
Db      6995 TCTTTCGACCCACAGACATGAGACCCC 7021

RESULT 11
AAx83488
ID      AAx83488 standard; cDNA; 6741 BP.
AC      AAx83488;
DT      07-DEC-1999 (first entry)
DE      Rat T-type voltage-gated Ca channel alpha-1-G (rCav1d) cDNA.
XX      Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW      activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX      Ratus sp.
OS
XX      MO9929847-A1.
PN      PD
XX      17-JUN-1999.
XX      30-OCT-1998; 98MO-US023161.
PF      05-DEC-1997; 97US-00985809.
PR      (LOYO ) UNIV LOYOLA CHICAGO.
PA      Perez-Reyes E, Cribbs LL.
PI      WPI, 1999-394972/33.
XX      DR
XX      P-PSDB; AAY14593.
XX      PT
XX      New T-type voltage-gated calcium channels.
XX      Disclosure, Page 94-103; 138pp; English.
CC      This sequence represents the coding region for a rat T-type voltage-gated
Cc      calcium (Ca) channel alpha-1-G designated rCav1d. Voltage gated channels
Cc      are membrane bound glycosylated proteins formed of several subunits. The

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Cc      large alpha subunits form a pore in the membrane that is selective for a
Cc      given ionic species. Each alpha subunit contains 4 domains (I, II, III
Cc      and IV) and each domain contains 6 putative transmembrane helical
Cc      segments (S1-S6). T-type Ca channels are activated at a lower voltage
Cc      than L- or N-type channels. Characteristics of T-type channels include
Cc      short current time, slow activation kinetics near threshold, fast
Cc      inactivation kinetics and slow tail current. The sequences AAx83488-
Cc      X83492 represent novel T-type voltage-gated Ca channel genes from humans
Cc      and rats. Each of the novel Ca-channels contains a putative IVS4 region
Cc      comprising the amino acid sequence AAY14598. Cells expressing the T-type
Cc      voltage-gated calcium channel proteins can be used to screen for drugs
Cc      which affect calcium channels. Methods are also disclosed for treating a
Cc      disease or disorder associated with a deficiency in a native T-type
Cc      calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
Cc      XX
SQ      Sequence 6741 BP; 1355 A; 2041 C; 1908 G; 1437 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      0      Length:      6741
Score:      10962.50      Matches:      2108
Percent Similarity: 94.28%      Conservative: 33
Best Local Similarity: 92.82%      Mismatches: 101
Query Match:      92.09%      Indels: 29
DB:      Gaps: 5

US-09-611-257a-37 (1-2266) x AAx83488 (1-6741)

QY      1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
      |||
Db      1 ATGGACGAGAGAGAGATGAGACGGGGCGCCGAGAGTGGGACACGCCCGTAGTTCACG 60
QY      21 ArgLeuAsnAspLeuSerGlyAlaGlyIyArgProGlyProGlySerAlaGluIyAsp 40
      |||
Db      61 CAGCTCAACGACTGTCCGGGCGCGGGGCGGACGGGCGGGGTCCACGAGAAAGAC 120
QY      41 ProGlySerAlaAspSerGlyAlaGluGlyLeuProIyProAlaLeuAlaProValVal 60
      |||
Db      121 CCGGGAGCGCGGACTCCGAGCGGAGGGGGCTGCCGTACCCGGCGCTAGCCCGGTGTT 180
QY      61 PhePheTyrlLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
      |||
Db      181 TTCTTCTTACTTAGCCAGGACAGCCCGCGGACGTGTCTCCGACGGGTCTGTAAAC 240
QY      81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
      |||
Db      241 CCGTGGTTGACGACGATGATGCTGTGTCATTTCTTCAATGTGTGACTCTGGGTAAG 300
QY      101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
      |||
Db      301 TTCAGGCGGTGAGAGACATTGCTGTGACTCCAGCGCTGCCGATCCTGACAGGCTTC 360
QY      121 AspAspPheIlePheAlaPhePheAlaValGluMetValValIyMetValAlaLeuGly 140
      |||
Db      361 GATGACTTATCTTGTGCTTCTTGTCTGTGAAATAGTGAGAAAGTGGGCTTTGGGC 420
QY      141 IlePheGlyIyLeCysTyrlLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160
      |||
Db      421 ATCTTTGGGAAGAAATGTTAAGTGGAGACACTTGGAAACGGCTTGACTTTTCAATTGC 480
QY      161 IleAlaGlyMetLeuGluIyTrpSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
      |||
Db      481 ATTGCAAGGATGCTGAGATATTGCTGGACCTCGAAGACGTCACTTCCGACAGTCAAG 540
QY      181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
      |||
Db      541 ACAGTCCGCTGTCTGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGGGCAATTC 600
QY      201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
      |||
Db      601 GTACATTTACTCTGGACACTTGGCTTATGCTGGGCAACGCTCTGCTGCTTCTTC 660
QY      221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
      |||

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Db 661 GTCCTTTTCATCTTGGCATCGTGGCGCTCAGCTGTGGCAGAGACTGCTTCCGCAACCG 720  
Qy 241 CysPheLeuProGluAenPheSerLeuProLeuSerValAspLeuGluAryTyrTyrGln 260  
Db 721 TGCTTCTCCCGAGAACTTCAAGCTCCCTGTAGCGGTGACCTGGAGCCTTATTCACAG 780  
Qy 261 ThrGluAsnGluAenGluSerProPheIleCysSerGlnProAryGluAenGlyMetAry 280  
Db 781 ACAGAAATATGAGCGAGAGCCCTTTCATCTGCTCAGCCTCGGGAATGGCATGAGA 840  
Qy 281 SerCysArySerValProThrLeuAryGlyAspGlyGlyGlyProProCysGlyLeu 300  
Db 841 TCCGCAAGAGGTGGCCACATCGCTGGGGAGGCGGTGGTGGCCACCTCGACGCTG 900  
Qy 301 AspTyrGluAlyAryAenSerSerSerAsnThrCysValAenTyrAsnGlnTyrTyr 320  
Db 901 GACTATAGACCTTAAACAGTTCCAGCAACCACTGTGTCACTTGTGAAACAGATCAT 960  
Qy 321 ThrAenCysSerAlaGlyGlyLysAsnProPheIleGlyAlaIleAenPheAspAsnIle 340  
Db 961 ACCAATGCTCTGGCGGCGAGCAACCCCTTCAAAAGCGCCATCAACTTTCACACATT 1020  
Qy 341 GlyTyrAlaTrrPheIleAlaIlePheGlnValIleThrLeuGluGlyTrrPValAspIleMet 360  
Db 1021 GGCATATGCTGATCGCATCTTCCAGGTCACTCACTGAGGGCTGGGTGCATCATATG 1080  
Qy 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380  
Db 1081 TACTTCGTATAGACGCTCACTCTTCTACAACTTCACTTCACTTCTTCTCATCATC 1140  
Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
Db 1141 GTGGGCTCTCTCTTCATGATCAACCTGGCTGGTGGATGGCAGAGTTCTCCGAG 1200  
Qy 401 ThrTyrGlnAryGluSerGlnLeuMetAryGluGlnAryValAryPheLeuSerAsnAla 420  
Db 1201 ACCAAACAGCGGAGAGTCAGCTATGCGGAGAGCGGTGTACATTCCTGTCCAAAGCT 1260  
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuTyrLeu 440  
Db 1261 AGCACTCTGGCAACTTCTCTGACCCAGCGAGCTGTATGAGGACTACTCAATCACTG 1320  
Qy 441 ValTyrIleLeuAryGlyAlaIleAryAryGlyLeuAlaGlnValSerAryAlaIleGlyVal 460  
Db 1321 GTGTACATCTCCGAAAGAGAGCCGGAAGGCTGGCCAGCTCTTAGGGCTATGGGCTG 1380  
Qy 461 AryValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
Db 1381 CGGGCTGGGCTGTCAAGCAGCCAGTGGCCGTAGTGGGAGAGCCCAAGCCAGTGGC 1440  
Qy 481 SerCysSerArySerHisAryAryLeuSerValHisHisLeuValHisHisHisHis 500  
Db 1441 AGCTGCACTCTCTCAACCGCTGTCTGTCTGTCTCAACCACTGTGTCAACCACTACAC 1500  
Qy 501 HisHisHisHisAryTyrHisLeuGlyAsnGlyThrLeuAryAlaProAryAlaSerProGlu 520  
Db 1501 CACCATCAACCACTCACTGGGTAAATGGACGCTCAAGATTCCCGGGGCGAGCCAGAG 1560  
Qy 521 IleGlnAspAryAspAlaAsnGlySerAryAryGlyMetLeuProProProSerThrPro 540  
Db 1561 ATCCAGGACAGAGGATGCCAATGGGTCTGCGCGGCTCAATGCCAACCCTGTACACCC 1620  
Qy 541 AlaLeuSerGlyAlaProProGlyValIleGlySerValHisSerPheTyrHisAlaAsp 560  
Db 1621 ACTCCCTCTGGGGGCGCTCCAGAGGGGTGGAGTCTGTACACAGTTTTCACATGCTGAC 1680  
Qy 561 CysHisLeuGluProValAryCysGlnAlaProProProArySerProSerGluAlaSer 580  
Db 1681 TGCCACTTGGAGCGAGTCCGTTGGCAGGCAACCCCTCCAGATGCCATCCGAGAGCACT 1740  
Qy 581 GlyAryGlnThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600  
Db 1741 GGTAGAGACTGTGGGTAGTGGAGGTGTACCCCACTGTGCATACAGCCCTTCACAGAG 1800

Qy 601 ThrLeuLysGlyLysValAlaLeuValAlaAlaSerSerGlyProProThrLeuThr 620  
Db 1801 ATACTAGAGATTAACACTAGTGGAGGTGGCCCCAGGCTTGGGGCCCCCACTTACAC 1860  
Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGlnThrGlnSer 640  
Db 1861 AGCTTCAACATCCCACTCTGGGCTTTCACCTCCATGTACACAGTCTCTGGAGACAGAGT 1920  
Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660  
Db 1921 ACCGAGCGCTGCATGCTCTGTCAAAATCTCCAGCCCTTGTCTCCAAAGCAGACATGGA 1980  
Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaAryAlaGlyValaGlyGluValGluLeu 680  
Db 1981 GCTTGGGGCGGCAAGTGTCTCTACTGTGCCCCGACAGAGACAGAGACAGAGGATCC 2040  
Qy 681 AlaAspAryGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700  
Db 2041 GCTGACCATGTCTATGCTCTGACTGACAGAGAGGCTGTGTATGATTCACACAGACGCT 2100  
Qy 701 GlnHisSerAspLeuAryAspProHisSer--AryAryGlnArySerLeuGlyProAsp 719  
Db 2101 CAGCAGATGACTCTCGGGATGCCCAAGCGGCGGCGACAGCGAGGCTGGGCGCCAGAT 2160  
Qy 720 AlaGluProSerSerValLeuAlaPheTrrPArgLeuIleCysAspThrPheAryGlyIle 739  
Db 2161 GCAGAGCTTATGTTCTGTGGCTTCTGTGAGGCTATGTGTACATTCCTGGAAAGATC 2220  
Qy 740 ValAspSerTyrTyrPheGlyAryGlyIleMetIleAlaIleLeuValAenThrLeuSer 759  
Db 2221 GTAGATAGCAAAATCTTGGCCGGAGATCATATGTGCCATCTGTGATACACTCAGC 2280  
Qy 760 MetGlyIleGlyTyrHisGlyGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779  
Db 2281 ATGGGATGAGTACACAGCAGAGCCGAGAGACTCACCAACCCCTGGAAATCACAAAC 2340  
Qy 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPro 799  
Db 2341 ATGCTCTTCAACAGCCTCTTGGCTTGGAGATCTGTGAATCGCTGTGTACGGGCC 2400  
Qy 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819  
Db 2401 TTTGGCTACATTAAGATCTCTCAACATCTTTGATGTGTCTATGTGGTCAATCAGTGTG 2460  
Qy 820 TrrGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuAryThrPheAryGlyMet 839  
Db 2461 TGGAGATTTTGGGCCAGCAGAGGAGGTGGCTGTCCGTGTGCGGACCTTCCGCTGATG 2520  
Qy 840 AryValLeuLysLeuValAryPheLeuProAlaLeuGlnAryGlnLeuValIleLeuMet 859  
Db 2521 CGGGTGTGAAGCTGGGTGCTTCTGCTGCGCCCTGAGGCGCAGCTCGTGGTGCATG 2580  
Qy 860 LysThrMetAspAsnValAlaThrPheCysMetLeuMetLeuPheIlePheIlePhe 879  
Db 2581 AAGACATGACACACGGGCGACCTTGTGATGTCTCATAGCTGTTCATCTTCACTTTC 2640  
Qy 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluAryAspGlyAspThr 899  
Db 2641 AGCATCTCTGGGCAATGATCTCTTTGGTTGCAAGTTGCACTGAACGGGATGGGAGACG 2700  
Qy 900 LeuProAspAryLysAsnPheAspSerLeuLeuTrrPAlaIleValThrValPheGlnIle 919  
Db 2701 TTGCCAAGCCGGAAGATTCGACTCCCTCTGCGGCCATCGCACCTGTTCACATTC 2760  
Qy 920 LeuThrGlnGluAspTrrPAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrr 939  
Db 2761 CTGACTAGAGAGCTGGAATTAAGTCTCTTCAACCGGACTGGCTTCAATGCTCTGG 2820  
Qy 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeu 959  
Db 2821 GCTGCTCTTAACTTCACTGCGCTCATGACTTTTGGCAATATGTGTCTTAACTGCTG 2880

QY 960 ValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSer 979  
 |||||  
 Db 2881 GTGGCAATCTTTGGAAAGGATTCAGGCAAG----- 2913  
 QY 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer 999  
 |||||  
 Db 2914 -----GGAGATGCCACCAAGTCT 2931  
 QY 1000 GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyLysArgLysCys 1019  
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 Db 2932 GAGTCAGAGGCTTAATCTTTTGCCCAAGTGGATGTGATGGAGAGAAAGAGCCG 2991  
 QY 1020 LeuAlaLeuValSerLeuGlyGlnHisProGluLeuArgLysSerLeuLeuProLeu 1039  
 |||||  
 Db 2992 TTGGCCCTGGTGGCTTTGGAGAAACAGCGGAATCTACGAAAGAGCTTTTGGCAACCCCTC 3051  
 QY 1040 IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly 1059  
 |||||  
 Db 3052 ATCATCATACGGCTCGGACACCAATGTCAACCCCAAGAGCTCCAGCACAGGTGTGGGG 3111  
 QY 1060 GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla 1079  
 |||||  
 Db 3112 GAAGCACTGGGCTCTGGCTCTCGACGTACCAAGTAGAGTGGTCCGCTGAGCCTGAGGCT 3171  
 QY 1080 Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098  
 |||||  
 Db 3172 GCCCACCATTAGATGAATATCTCCGCCAAGTCCCGCAGCTCCCGCACAGTCCCTGGAGT 3231  
 QY 1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118  
 |||||  
 Db 3232 GCGGCAAGCAGCTGGACACAGCAGGCGCTCCAGCAGAGAACGCTGGGGCCGGGCCCCCAG 3291  
 QY 1119 LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGlu 1138  
 |||||  
 Db 3292 CTAAAGCGAGAGGAGCCCGAGCGAGCGAGGTCCTGCTGTCTGGAGAGGCGCAGAG 3351  
 QY 1139 SerGlnAspGluGlnGlnSerSerGluGluGluArgAlaSerProAlaGlySerAspHis 1158  
 |||||  
 Db 3352 AGTCAGATAGAGAGAGAAATTCAGAAAGAGACCGGGCCACCCAGCAGGCAATGACAT 3411  
 QY 1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178  
 |||||  
 Db 3412 CGCCACAGGGGCTTCCTTGGAACTGAGGCGCAAGAGTCTTGTGACCTGCTGACACTGT 3471  
 QY 1179 GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGlnHisGlnAsp 1198  
 |||||  
 Db 3472 CAGGTGCCGGGGCTGCACCGCACAGCGCGCGGAGCTGCTCTGTGAGCAACAAGAC 3531  
 QY 1199 CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro 1218  
 |||||  
 Db 3532 TGTAAATGGCAAGTCCGCTTCAGGGCGTTGGCCCGCACCTGAGGACTGATGACCCCA 3591  
 QY 1219 LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla 1238  
 |||||  
 Db 3592 CTGGATGGGATGATGACATGATGAGGAAATCTGAGCAAGGGGAAACCATATCAAGAC 3651  
 QY 1239 ThrIleArgAlaArgLeuProAlaCysTyrlLeuGluArgAspSerTrpSerAlaTyrlIle 1258  
 |||||  
 Db 3652 TGGGTTCAGATCCGGCTTCCTGCTGTTCGCGAGAGGAGATTCCTGTGGCGCTTAATC 3711  
 QY 1259 PheProGlnSerArgPheArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278  
 |||||  
 Db 3712 TTTCTCTCTCAAGTCAGAGTTTGGTCTCTCTGTGTACCGGATCATACCCCAAGAGTTT 3771  
 QY 1279 AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro 1298  
 |||||  
 Db 3772 GACCATGTGGTCTCTCGCATCATCTTCTCAACTGTATCACATCGCTATGAGAGCGGCC 3831  
 QY 1299 LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrlIlePheThr 1318  
 |||||  
 Db 3832 AAAATTTGACCCCAACAGCGCTGAGCGCATTTCTCTGACCTCTTCCAACTACATCTTCAC 3891  
 QY 1319 AlaValPheLeuAlaGluMetThrValLysValAlaLeuGlyIleTrpCysPheGlyGlu 1338

Db 3892 GCAGTCTTTCTAGCTGAATGACATGAAAGTGTGGCAGCTTGGCTTGGGGAG 3951  
 QY 1339 GlnAlaTyrlLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal 1358  
 |||||  
 Db 3952 CAGGCTTACCTCGGAGCAGCTGGAATGTGTGAGCGGCTGTGGTCTCATCTCCGTC 4011  
 QY 1359 IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg 1378  
 |||||  
 Db 4012 ATCGACATCTTGTTCTTCATGTGTCCAGACGGGACCAAGATCTTGGCATGTGTAGG 4071  
 QY 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398  
 |||||  
 Db 4072 GTGCTCGGCTGCTCGGAGCCTGCGTCACATCAGGTCATCAGCCGGGCCAGGAGACTG 4131  
 QY 1399 LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle 1418  
 |||||  
 Db 4132 AAGCTGTGTGAGAGCTCTGATGTATCCCTCAAAACCATTTGGCAACATGTGTGATTT 4191  
 QY 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe 1438  
 |||||  
 Db 4192 TCTGTGCTCTTTCATCATTTTGGAAATCTCGGGGTGCAGCTCTTCAAAGGAAATTC 4251  
 QY 1439 PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla 1458  
 |||||  
 Db 4252 TTCGTGTGCAGGTTGAGGACACACAGAAATCATCTAACAATCCGACTGCGCTGAGGCC 4311  
 QY 1459 SerTyrlArgTrpValArgHisLysTyrlAsnPheAspAsnLeuGlyAlaLeuMetSer 1478  
 |||||  
 Db 4312 AGCTACCGATGGGTCCGGCAAGATACACTTGTGAACCTGGGCGAGGCTGTGATGTCC 4371  
 QY 1479 LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrlAspGlyLeuAspAla 1498  
 |||||  
 Db 4372 CTGTTTGTCTGTGCTCCAGAGATGTTGGTGTGACATCATATGATGGCTGTGATGCT 4431  
 QY 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrlPheIle 1518  
 |||||  
 Db 4432 GTGGGTGTGATCACAGGCCCATCATGAACCAACCCCTGGATGCTGTATATCATTC 4491  
 QY 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu 1538  
 |||||  
 Db 4492 TCTTTCCTCTCATGTGGCTTCTTGTTCCTGAACATGTTGTGGCGCTGTGGAG 4551  
 QY 1539 AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLys 1558  
 |||||  
 Db 4552 AACTTCATTAAGTCAGACAGACCAAGAGAGAGAGCGAGCGGCTGAGAGAGAG 4611  
 QY 1559 ArgLeuArgArgLeuGluLysLysArgArgLysAlaGlnCysLysAspProTyrlTyrlSerAsp 1578  
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 Db 4612 CGACTACGAGGCTGGAGAAAGAAAGAAAGAACCCAGTGCAGACCTTACTACTGCAC 4671  
 QY 1579 TyrlSerArgPheArgLeuLeuValHisHisLysCysThrSerHisTyrlLeuAspLeuPhe 1598  
 |||||  
 Db 4672 TACTCGAATTCCTGGCTCTTGTTCACCACTGTGTACCAAGCAGCTTGAACCTCTTC 4731  
 QY 1599 IleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrlGlnGlnPro 1618  
 |||||  
 Db 4732 ATCACTGTGTATCGGGCTGAACGTGTCACTATAGCGCATTAAGCAACAGACGCC 4791  
 QY 1619 GlnIleLeuAspGluAlaLeuLysIleCysAsnTyrlIlePheThrValIlePheValLeu 1638  
 |||||  
 Db 4792 CAGATCTGAGAGAGGCTGGAAGATCTGCAATTCATCTTTAACGTCATCTTGTGCTTT 4851  
 QY 1639 GluSerValPheLysLeuValAlaPheGlyPheArgArgPhePheGluAspArgTrpAsn 1658  
 |||||  
 Db 4852 GAGTCAGTTTAAACTGTGTGGCTTGTGGCTTCCGCGTTTCTTCCAGGACAGGTGGAAAC 4911  
 QY 1659 GlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGluIleGlu 1678  
 |||||  
 Db 4912 CAGCTGACCTGGCTATTTGTCTTCTGTCCATCATGGGATACACATGAGAGATTTGAG 4971  
 QY 1679 ValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIle 1698

Db 4972 GTCAATCTGCTGCTCCCATCAACCCACCATATCCGATCATGAGGGTCTCCGATT 5031  
 Qy 1699 AlArgValIleuIysLeuIleuIysMetAlaValIleuMetArgAlaIleuLeuAspThrVal 1718  
 Db 5032 GCTCGAGTTCTGAAGCTGTTGMAAGATGGCTGTGGGCACTGGGGACACTGCTGCACACGGGTG 5091  
 Qy 1719 MetGlnAlaLeuProGlnValIleuValAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIle 1738  
 Db 5092 ATCAGAGCCCTGCGCCCGAGGTGGGGAACTTGGGACTTCTCTTCAATGTTATGTTTTCATC 5151  
 Qy 1739 PheAlaAlaIleuGlyValIleuLeuPheGlyAspLeuGluCysAspGluThrHisProCys 1758  
 Db 5152 TTTGCACTCTGGGGCTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCTTGT 5211  
 Qy 1759 GluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPhe 1778  
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 Qy 1799 GlnGluSerThrCysTrpAsnThrValIleSerProIleTrpPheValSerPheValLeu 1818  
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 Qy 1819 ThrAlaGlnPheValLeuValAsnValValIleAlaValIleuMetLysHisLeuGluGlu 1838  
 Db 5392 ACCGCCAGTTTGTGTGTCTGCTCACTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 5451  
 Qy 1839 SerAsnIysGluAlaIysGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1858  
 Db 5452 AGCAACAAGAGGCGCAAGAGAGAGGCGGAGCTCGAGCCGAGCTGAGCTGAGATAG 5511  
 Qy 1859 ThrIleuSerProGlnIleProHisSerProLeuGlySerProPheLeuThrProGlyValGlu 1878  
 Db 5512 ACCTCTACCCCGGAGCCCACTCCCGCTGGGCGAGCCCTTCTCTGCGCGGGGTGAG 5571  
 Qy 1879 GlyProAspSerProAspSerProIysProGlyAlaLeuHisProAlaAlaHisAlaArg 1898  
 Db 5572 GGTTCTCAACAGTACTGACAGCCCTTACGCTGGGCTCCACACACACACTGCCCAATTGGA 5631  
 Qy 1899 SerAlaSerHisPheSerLeuGlnHisProThrMetGlnProHisProThrGlnLeuPro 1918  
 Db 5632 GCACGCTCGGGCTTCTCCCTTGAGCACCCCGAGTGTACCCCAACCCCGAGAGAGTCCCA 5691  
 Qy 1919 -----GlyProAspLeuLeuThrValArgIysSerGlyValSerArgThrHisSer 1935  
 Db 5692 GTCCCTCCATGAGACGACCTGTCTGATGTGAGAACTGTGTGTGACGCCGAGCCACTCT 5751  
 Qy 1936 LeuProAsnAspSerTrpMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHis 1955  
 Db 5752 CTGCCCAATGACAGTACTGATGTGCGGCAATGGAGCACTGCTGAGAGATCCCTTAGACAC 5811  
 Qy 1956 ArgGlyTrpGlyLeuProIysAlaGlnSerGlySerValLeuSerValHisSerGlnPro 1975  
 Db 5812 AGGGGCTGGGGGCTCCCAAGGCCAGTCAAGGCTTCACTTGTCCGTTCACTCCCAACA 5871  
 Qy 1976 AlaAspThrSerTrpIleLeuGlnLeuProIysAspAlaProHisIleLeuGlnProHis 1995  
 Db 5872 GCAACACACAGCTGATCTTCAAGCTTCCCAAGATGTGCACTATGTGCTCAGACTCAT 5931  
 Qy 1996 SerAlaProThrTrpGlyThrIleProIysLeuProProGlyArgSerProLeuAla 2015  
 Db 5932 GGGGCTCCCACTGGGGGCGGCATCCCTTAACCTAACCCCACTGGCGGCTCCCTCTGGCT 5991  
 Qy 2016 GlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeu 2035  
 Db 5992 CAGAGGCTCTTCAAGGCGCGCAGGCAATAAGAACTGATCCCTGGATGTGACAGGGCTGTG 6051  
 Qy 2036 GlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAla 2055  
 Db 6052 GGTAGCCGGGAGAACTGTTGTCAAGAGTGAAGTGGGCCCTCTCGCTCAACCCCGGTCC 6111

Qy 2056 TyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerIys 2075  
 Db 6112 TCATCTCTCTGGGGCGGGTGCAGATCCAGTGCAGACAGCTTCCGGCATCCAGACCAAA 6171  
 Qy 2076 IleSerIysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLys 2095  
 Db 6172 GTCTCCAGGACATCCGCTGCGAGCCCTTGGCCCAAGGCTGGAAACCAAGCTGGCCAG 6231  
 Qy 2096 GlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGly 2115  
 Db 6232 GACCTCCAGAGACCAAGAGAGCTTAGAGCTGACACCGAGCTGAGTGAATTCAGGA 6291  
 Qy 2116 AspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuIysCys 2135  
 Db 6292 GACCTCCCT---CCCAAGCAAGCAAGAAACCCCTGTTCCACAGGGACTGAAGAAATGC 6348  
 Qy 2136 TyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlnAlaArg 2155  
 Db 6349 TACAGGTGAGAGCCAGAGACTGCAGAGCCGAGGCTGGGTCTGGCTAATGAAACAGCG 6408  
 Qy 2156 ArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAsp 2175  
 Db 6409 AGACACTTCATGCTGTCAAGCTGTGTGACAGGCGCTCCCAACCCGCTATGTCCAAC 6468  
 Qy 2176 ProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProIysIysLeu 2195  
 Db 6469 CCTCAAGCTCTCGGGGCCCAACTCTTGGGGGTCTCGGAGCGCGGCTTAAGAAAAATCT 6528  
 Qy 2196 SerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSer 2215  
 Db 6529 AGCCCAACCAAGTACTCTATAGACCCCGAGAGCCAGGAGCTTGGCCCCCATGCACT 6588  
 Qy 2216 ProGlyIleCysLeuArgArgArgAlaProSerSerAspSerIysAspProLeuAlaSer 2235  
 Db 6589 CTGGGTGTGCTCTCAGAGAGAGGGCGCGGCAAGTACTTAAGATCCCTCGTCTCC 6648  
 Qy 2236 GlyProProAspSerMetAlaAlaSerProSerProIysIysAspValLeuSerIleuSer 2255  
 Db 6649 AGCCCCCTTGACGACAGCGGTGCTCACTCCCAAGAAAGACAGCTGAGTCTCT 6708  
 Qy 2256 GlyLeuSerSerAspProAlaAspLeuAspPro 2266  
 Db 6709 GGTTGTCTTCAACCAAGACATGACCCC 6741  
 Db  
 RESULT 12  
 AAX83485  
 ID AAX83485 standard; cDNA; 6762 BP.  
 AC AAX83485;  
 AT 07-DEC-1999 (first entry)  
 DE Rat T-type voltage-gated Ca channel alpha-1-G (rcavtra) cDNA.  
 KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;  
 KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.  
 OS Rattus sp.  
 PN W09929847-A1.  
 PD 17-JUN-1999.  
 PF 30-OCT-1998; 98MO-US023161.  
 PR 05-DEC-1997; 97US-00985809.  
 PA (LOYO ) UNIV LOYOLA CHICAGO.  
 PI Perez-Reyes E, Cribbs LL;  
 WP1; 1999-394972/33.



Db 1621 ACTCCCTCTGGGGGCGCTCCGAGGGGTCCGAGTCTGTACACAGCTTCTACATGCTGAC 1680  
 Qy 561 CyshisLeuGluProValaIrgCyeglnAlaProProProArgSerProSerGluAlaSer 580  
 Db 1681 TGCCACTTGGAGCCAGTCCGTTGGCCAGGCAACCCCTCCAGATGCCATCGAGGCACTCT 1740  
 Qy 581 G1YArgrHValG1ysSerG1yLysValaIYrProHrHValH1srHsrProProGlu 600  
 Db 1741 GGATGGACTGTGGGTAGTGGGAGAGGTGTACCCCACTGTGCATACACCCCTCCACAGAG 1800  
 Qy 601 ThreLeuysGluYsaAlaLeuValG1uValAlaAlaSerSerG1yProProHrHLeuThr 620  
 Db 1801 ATACTGAAGATTAAGACACTAGTGAAGTGGCCCCCAGCCCTGGGCCCCCACCCTTACC 1860  
 Qy 621 SerLeuasnileProProG1yProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640  
 Db 1861 AGCTTCAACATCCACCTGGGCGCTTCAGCTCCATGCAAGACTCTCGAGACACAGAGT 1920  
 Qy 641 ThrG1yAlaCygsGlnSerSerCyalyel1eSerSerProCySLeuYsaAlaAspSerG1y 660  
 Db 1921 ACCGGAGCTGTCCATAGCTCTGTCAAAATCTCCAGCCCTGTCTCAAGGCGACAGTGA 1980  
 Qy 661 AlaCyeg1yProAspSerCyProTyrcySaAlaArgAlaG1yAlaG1yGluValG1uLeu 680  
 Db 1981 GCTTGGGGCCGAGCACTTGTCTCTACTGTCTCCGAGACAGAGACAGAGCCAGAGTCC 2040  
 Qy 681 AlaAspArgG1uMetProAspSerAspSerG1uAlaValIYrgluPheHrGlnAspAla 700  
 Db 2041 GCTACCATGTCATGCTGCTGATCAGACAGAGGCTGTGTATGATTACACAGAGCGCT 2100  
 Qy 701 GlnHisSerAspLeuAArgAspProHisSer---ArgArgGlnArgSerLeuG1yProAsp 719  
 Db 2101 CAGACAGGTGACCTCCGGGATCCCAACGCGCGGACAGCGAGCTGTGGGCCAGAT 2160  
 Qy 720 AlaGluProSerSerValLeuAlaPheHrParGluLeuCySaAspThrPheArgLysIle 739  
 Db 2161 GCAAGGCTAGTCTGTGCTGCTTCTGTGAGGCTGATCTGTGACACATTCGGAAAGTC 2220  
 Qy 740 ValAspSerLysTyPheG1yArgG1yI1eMetI1eAlaI1eLeuValAsnThrLeuSer 759  
 Db 2221 GTATATGACAAATCTTTGGCGCGGGAATCATGATCCGATCCGTGCAATACACTCAGC 2280  
 Qy 760 MetGlyI1eGluTyH1sGluGlnProGluGluLeuThrAsnAlaLeuGluI1eSerAsn 779  
 Db 2281 ATGGGCATCGAGTACCAAGACAGCCGAGAGGCTCACCAAGCCCTGGGAATCAGCAAC 2340  
 Qy 780 I1eValPheHrSerLeuPheAlaLeuGluMetLeuLysLeuValIYrg1yPro 799  
 Db 2341 ATGCTCTTACACAGCTCTTGCCTTGGAGATGCTGTGAAACTGTGTCTTACGGTCC 2400  
 Qy 800 PheG1yTyI1eLysAsnProTyAsnI1ePheAspG1yValI1eValI1eSerVal 819  
 Db 2401 TTTGGCTACATTAAGAACTCTTCAACAATCTTTGATGTGTCTGTCATCAGTGTG 2460  
 Qy 820 TrpGluI1eValG1yGlnGlnG1yG1yLeuSerValLeuArgThrPheArgLeuMet 839  
 Db 2461 TGGAGATTTGTGGCCAGGAGGAGTGTGCTGTGTGCTGCGGACCTTCCGCTGATG 2520  
 Qy 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859  
 Db 2521 CGGGTGTGGAAGCTGTGGCTTCTGTCCGGCCCTGCGAGCCGACGCTGTGTGCTCATG 2580  
 Qy 860 LysThrMetAspAsnValAlaThrPheCyMetLeuLeuMetLeuPheI1ePheI1ePhe 879  
 Db 2581 AAGACATGACAAAGTGGCCACTTTCGATGCTCTCTCATGCTGTTCATCTTCTC 2640  
 Qy 880 SerI1eLeuG1yMetHisLeuPheG1yCyS1ySAspPheAlaSerGluArgAspG1yAspThr 899  
 Db 2641 AGCATCTCGGCGCATGCTCTTGTGTGCAAGTTCGATCTGAACGGGATGGGAGACAG 2700  
 Qy 900 LeuProAspArgLysAsnAspSerLeuLeuTrpAlaI1eValI1eValI1ePheGlnI1e 919  
 Db 2701 TTTCGAGACCGGAAGATTTGACTCCCTGTCTGTGGGCAATGTCATGTCTTTCAGAT 2760

Qy 920 LeuThrGluGluAspThrPheLysValLeuTyAsnG1yMetAlaSerThrSerSerTrp 939  
 Db 2761 CTAGCTCAGGAACATGGAATTAAGTCTCTTACAAAGGCAAGCTCTTCAATGCTTTGG 2820  
 Qy 940 AlaAlaLeuTyPheI1eAlaLeuMetThrPheG1yAsnTyValLeuPheAsnLeuLeu 959  
 Db 2821 GCTGCTCTTACTTCAATCGCCCTCATGACTTTTGGCAACATGTGCTCTTTTACCTGCTG 2880  
 Qy 960 ValAlaI1eLeuValG1uG1yPheGlnAlaG1uGluI1eSerLysArgGluAspAlaSer 979  
 Db 2881 GTGGCATCTTGTGGAAGATTCAGGAGAG----- 2913  
 Qy 980 G1yGlnLeuSerCyS11eGlnLeuProValAspSerGlnG1yG1yAspAlaAsnLysSer 999  
 Db 2914 -----GGAATGCAACCAAGTCT 2931  
 Qy 1000 GluSerGluProAspPhePheSerProSerLeuAspG1yAspG1yAspArgLysLysCyS 1019  
 Db 2932 GAGTCAGAGCTCATTTCTTTGGCCCAAGTGTGATGTGTATGGGACAGAAAGAGCGC 2991  
 Qy 1020 LeuAlaLeuValSerLeuG1yGluH1sProGluLeuArgLysSerLeuLeuProLeu 1039  
 Db 2992 TTGGCCCTGTGTGCTTGGGAGAACAGCGGAACACTAGAAAGACTTTTGGCACCCTC 3051  
 Qy 1040 I1eI1eHisThrAlaAlaThrProMetSerLeuProLysSerThrSerHrGluG1y 1059  
 Db 3052 ATCATCATTCGGCTCGACACCAATGTCAACCCCAAGAGCTCCAGACAGAGTGTGGG 3111  
 Qy 1060 GluAlaLeuG1yProAlaSerArgTrHrSerSerSerG1ySerAlaGluProG1yAla 1079  
 Db 3112 GAAGCACTGGGCTCTGGCTTCAAGTACAGTACAGATGTGTCTCCCTGAGCTTGAAGCT 3171  
 Qy 1080 Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098  
 Db 3172 GCCACATGATGAATGAATGTCCGCAAGTGCAGGAGCTCCCGACAGTCCCTGGAGT 3231  
 Qy 1099 AlaAlaSerSerTrpHrSerArgArgSerSerArgAsnSerLeuG1yAlaAlaProSer 1118  
 Db 3232 GCGCAAGCAGCTGACACAGACAGGCGCTCCAGAGAAAGCTTGAGCGCGGCCCGCAGC 3291  
 Qy 1119 LeuLysArgArgSerProSerG1yG1uArgArgSerLeuLeuSerG1yGluGlnGlu 1138  
 Db 3292 CTAAAGGAGAGAGCCGAGAGGAGAGGAGTCCCTGTGTGTGAGAGGCGCAGAG 3351  
 Qy 1139 SerGlnAspGluGluSerSerG1uGluArgAlaSerProAlaG1ySerAspHis 1158  
 Db 3352 AGTCAGAGTGAAGAGAAATTCAGAAAGAGACCGGGCCAGCCACAGCAGCAGTGCAT 3411  
 Qy 1159 ArgHisArgG1ySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178  
 Db 3412 CGCCACAGGGGTTCTTGGAACTGAGGCCCAAGAGTCTTTTACCTGTGACACTCTG 3471  
 Qy 1179 GlnValProGluLysHisArgThrAlaSerG1yArgG1ySerAlaSerGluH1sGlnAsp 1198  
 Db 3472 CAGGTGCGGAGGCTGACCCGACAGCGAGCGCGGAGCTCTGTCTGTGACACCAAGAC 3531  
 Qy 1199 CyAsnG1yLysSerAlaSerG1yArgLeuAlaArgAlaLeuArgProAspAspProPro 1218  
 Db 3532 TGTATATGCAAGTCCGTTTCAAGGGCTTGTGGCCGACCTTGAGAGCTATGACCCCAA 3591  
 Qy 1219 LeuAspG1yAspAspAlaAspAspGluG1yAsnLeuSerLysG1yGluArgValArgAla 1238  
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 Qy 1239 TrpI1eArgAlaArgLeuProAlaCyS1yLysLeuGluArgAspSerTrpSerAlaTyI1e 1258  
 Db 3652 TGGGTCAAGTCCCGGCTTCTGCTGTGTGCGGAGAGGAAATCTGTGGCTTATTC 3711  
 Qy 1259 PheProProGlnSerArgPheArgLeuLeuCyHisArgI1eI1eThrHisLysMetPhe 1278  
 Db 3712 TTTCCTCTCAGTCAAGTTCGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3771



QY	1279	AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro	1298
Dp	3772	GACCATGGGCTCCGTCATCATCTCTTCAACTGTATTCACCACTGGCTATGTAGAGCGCCC	3831
QY	1299	LyxIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr	1318
Dp	3832	AAAAATGACCCCAAGCGCTGACGGCAATCTCTTGACCCCTTCACATCATCTTCAACG	3891
QY	1319	AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGlu	1338
Dp	3892	GCACTCTTTCTAGCTGAAATGACATGAAAGTGTGGCACTGGCGCTGTGGGGAG	3951
QY	1339	GlnAlaTyrLeuArgSerSerTyrAsnValLeuAspGlyLeuLeuValIleSerVal	1358
Dp	3952	CAGCCCTAACCTGGCAGACAGCTGGAAATGTCTGGACGGCTTGCTGGCTCATCTCGCTC	4011
QY	1359	IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg	1378
Dp	4012	ATGCACATCCCTGGCTCCATGATGCTCTCCGACAGCGCACCAAGATCTTGGATCTGAGG	4071
QY	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
Dp	4072	GTGCTCGCGCTGCTGGCGAACCTCGTCCACTCAGGGGCATCAACCGGGCCAGAGACTG	4131
QY	1399	LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle	1418
Dp	4132	AAGCTGGGTAGAGACTGTGATGTCATCTCCAAACCATTTGGCAACATTTGTGTGATTT	4191
QY	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438
Dp	4192	TGCTGGCTCTTCATCATATTTTGGAAATTCGCGGTGACGCTCTTCAAGGGAAAGTTC	4251
QY	1439	PheValCysGlnGlyGluAspTyrArgAsnIleThrAsnLysSerAspCysAlaGluAla	1458
Dp	4252	TTTCGGTCTCAGGGAGGAGACACAGAAKATCACTAACAAATCCGACTGGCTGAGGCC	4311
QY	1459	SerTyrArgTyrValArgHisLysTyrAsnDheAspAsnLeuGlyGlnAlaLeuMetSer	1478
Dp	4312	AGTACCGATGGGTCCGGCACAGTAACTTTGACAACTGGGCGCAGGCTGTGATGTC	4371
QY	1479	LeuPheValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAla	1498
Dp	4372	CTGTTTGGCTGGCCTCCAGAGATGGTGGTTGACATCACTATGATGAGGCTGGATGCT	4431
QY	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTyrMetLeuTyrPheIle	1518
Dp	4432	GTGGGTGGATTCAGACAGCCCATCATGAACACAAACCTTGGATGCTCTACTTCACTC	4491
QY	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu	1538
Dp	4492	TCTTCTCTCTCATGATGGCCCTTCTTGTCTGAAACATGTTTGGGGGTGTGTGTGGAG	4551
QY	1539	AsnPheHisLysCysArgGlnHisGlnGluGluGluGluAlaArgArgArgGlnGluLys	1558
Dp	4552	AACTTCCCTAAGTGCACACACACAGAGAGAGAGGCGAGCGCGCTGAGAGAGAG	4611
QY	1559	ArgLeuArgArgLeuGluLysLysArgArg-----LysAlaGln	1571
Dp	4612	CGACTCCAGAGCTGCAAAAAAGAGAGAGTAAAGAGAGACAGATGGCCGAAAGCCCG	4671
QY	1572	CysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLysLeuCysThr	1592
Dp	4672	TGCAAGCCCTACTGACTGACTGAGATTCGGGCTCTTGTGCCACCACTGTGTATCC	4731
QY	1592	SerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThiMetAla	1611
Dp	4732	AGCCACTACCTGGACTCTTCACTGCTGTGTCACTGGGCTGAAACGTGTACATATGGCC	4792
QY	1612	MetGlnHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIle	1631
Dp	4792	ATGGAACTTACCAACAGCCCATCTTGAACAGAGGCTCTGAAGATTTGCATTTCACTC	4851
QY	1632	PheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArg	1651

Db	4852	TTTAAACGCTCAACCTTGTCTTGGAGTCAAGTTTCAAACCTTGTGGCCTTGGCCCTTCCGCCCT	4911
Qy	1652	PhePheGlnsPaRgTTPaAngInLeuAspLeuAlaIleValLeuSerIleMetGly	1671
Db	4912	TTCTTCCAGAGACAGGTGGAAACCAAGCTGGACTGTGGCTTGTCTGTCCATCATGGCC	4971
Qy	1672	ILeThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArg	1691
Db	4972	ATCAACCTGAGAGGAGATTGAGGTCAACTGTGTGGTCCCATCAACCCCAACATCATCCGT	5031
Qy	1692	ILeMetArgValIleuArgIleAlaArgValLeuIleLeuLeuLeuMetAlaValGlyMet	1711
Db	5032	ATCATYAGGGGTGCTCCGCATGTGCTCGAGTTCGTGAAGCTGTGGAGATGGCTGTGGGCATG	5091
Qy	1712	ArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeu	1731
Db	5092	CGGGCATTGCTGCACACAGGTGATGACAGCCCTGGCCCAAGATGGGGAAACGTGGGACTTCTC	5151
Qy	1732	PheMetLeuLeuPhePheIlePheAlaIleLeuGlyValGluLeuPheGlyAspLeuGlu	1751
Db	5152	TTCAATGTTATGTGTTTTCATCTTTGCACTTGTGCAGCTGTGGCTGAGAGCTCTTGGAGACCTGGAG	5211
Qy	1752	CysAspGluThrHisProCysGluGlyLeuGluValArgHisAlaIlePheArgAsnPheGly	1771
Db	5212	TGTATATAGACACACCTCTGTGAGGGGTGTGGGTGTGGATGCACCTTTAGGAACCTTGGT	5271
Qy	1772	MetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTPaAngIylIleMetLys	1791
Db	5272	ATGGCCCTTTGCAACCCCTTCCAGAGTCCACATGTGTACAACTGGATGTGATATAGAG	5331
Qy	1792	AspThrLeuArgAspCysAspGlnGluSerThrCysTyArgAsnThrValIleSerProIle	1811
Db	5332	GACACCCCTCCGGGAGCTGTGACCAAGAGTCCACCTGCTACAACTGTCACTCCCTATC	5391
Qy	1812	TyrPheValSerPheValLeuThrAlaGluPheValLeuValAsnValValIleAlaVal	1831
Db	5392	TACTTTGTGTCCTTCGTGCTGACGGCCAGTTGTGTGTCGTCAACGTGGTCATAGCTGTG	5451
Qy	1832	LeuMetLysHisLeuGluGluLysSerAsnLysGluAlaLysGluGluAlaGluLeuGluAla	1851
Db	5452	CTGATGAAGCACTCGAAGAAAGCAACAAGGCCAAGAGAGGCCGAGACTCGAAGGCC	5511
Qy	1852	GluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerPro	1871
Db	5512	GAGCTGGAGGTGAGATGAGAAGACCTCAGCCCGCAGCCCACTCCCGCTGGCAGGCCCC	5571
Qy	1872	PheLeuThrProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeu	1891
Db	5572	TTCTCTCGGCCCGGGGTGAGGGGTGCACACGATCACTACAGCCTTAAGCCTGGGGCTCCA	5631
Qy	1892	HisProAlaIleHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGln	1911
Db	5632	CACACCACTGCCCAATTGGAGACAGCCTCGGGCTTCTCCCTTAGACACCCACAGATGGTA	5691
Qy	1912	ProHisProThrGluLeuPro-----GlyProAspLeuLeuThrValArgLysSer	1928
Db	5692	CCCCACCCCGAGGAGTGCAGTCCCCCTAGACCAAGCTGCTGAGACTGTGAGAGAACTCT	5751
Qy	1929	GlyValSerAlaGlnHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr	1948
Db	5752	GGTGTCAAGCCGAGACACTCTGTGCCCAATGACGTACATGTGCCCAATGGGAGACT	5811
Qy	1949	AlaGluGlyProLeuGluGlyHisArgGlyTTPGlyLeuProLysAlaGlnSerGlySerVal	1968
Db	5812	GCTAGAGATCCCTTAGAGACACAGGGGCTGGGGGCTCCCCAAAGCCAGTCAAGCTTCATC	5871
Qy	1969	LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAla	1988
Db	5872	TTGTTCGGTTCATCTCCAAACAGACAGACCAAGCTGATCTCAAGCTTCCCAAGAATGTG	5931
Qy	1989	ProHisLeuLeuGlnProHisSerAlaProThrTTPGlyThrIleProLysLeuProPro	2008
	::::	::::	::::

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Db      5932 CACTATTCCTCCAGCTCAATGGGGCTCCCACTGGGGGGCCCATCCCTAAACTAACCCCA 5991
Qy      ProGlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaAlaIleArgThrAsp 2028
Db      5992 CCGGGCGGCTCCCTCGCTGCTCAGAGGCTCTCAGGGGGCCAGGAGCATTAAGACTGAC 6051
Qy      SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuAlaGluValSerGlyPro 2048
Db      6052 TCCCTGATGTGACGGGCTGGGATGGCCGGGAGACCTGTGTTCAGAGGAGAGTGGGGCCC 6111
Qy      SerProLeuAlaArgAlaTyrSerPheThrGlyGlnSerSerThrGlnAlaGlnGln 2068
Db      6112 TCCGCTCTGACCCGCTCTCTATCTTCTGGGGGGGCTGACATCCAGCTCAGACAG 6171
Qy      HisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGly 2088
Db      6172 CGTTCCGGGATCCAGACGAAAGTGTCCAGACATCCGGCTGGCCAGGCCCTTGGCCAGGC 6231
Qy      ProGluProAsnThrGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThr 2108
Db      6232 CTGGAACTCCAGCTGGGCCAAGAACCTCCAGAGCCAGAAAGCAGCTTAGAGCTGACACG 6291
Qy      GluIleuSerThrLysSerGlyAspLeuLeuProProGlyGlyGlnGluProProSer 2128
Db      6292 GAGCTGAGCTGGATTTAGAGACCTCTCTT---CCAGACGCCAGGAAAGAACCTCTGTTCC 6348
Qy      ProArgAspLeuLysCysTyrSerValGlnAlaGlnSerCysGlnArgArgProThr 2148
Db      6349 CCACGGGACCTGAAAGAGTGTCAAGTCAAGTCAAGACCCAGAGCTCCAGGCGGAGGCTGGG 6408
Qy      SerTrpLeuAspGlnGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySer 2168
Db      6409 TTCTGCTGATAGTAAACGGGAGACACTCCATCTCTGCTGACGCTGTGACAGGCGCTCC 6468
Qy      GluProHisLeuGlyLysThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGly 2188
Db      6469 CAACCCCGCTATGTCCAGGCCCTCAAGCCTCGGGGGCCAACTCTTGGGGGCTCTGGG 6528
Qy      SerArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGln 2208
Db      6529 AGCGGGCTTAAGAAAATACTAGCCCAACCCAGTACTTCTAAGACCCCGGAGAGGACAG 6588
Qy      GlyProArgThrProProSerProGlyLysCysLeuArgArgAlaProSerSerAsp 2228
Db      6589 GGCTCTGGGCCCCCATGCAATCTGTGTCTGCTCTCAAGAGAGGGGGCCGCGCAATGAC 6648
Qy      SerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLys 2248
Db      6649 TCTTAAGATCTCTGGTCTCCAGGCCCTTGACAGACAGGCTGCTCACTCCCTCCAAAG 6708
Qy      LysAspValLeuSerSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db      6709 AAAGACAGCTGATCTCTCTGTGTTTGTCTTCTTAACCCAAACAGACATGAGACCCC 6762

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## RESULT 13

ADSI6295 standard; DNA; 6942 BP.

ADSI6295;

02-DEC-2004 (first entry)

Rat voltage-dependent T type alpha 1G subunit calcium channel DNA.

Voltage-dependent ion channel; drug candidate;

aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;

anticonvulsant; antiarrhythmic; rat; alpha 1G subunit; ds.

Rattus norvegicus.

US2004175761-A1.

09-SEP-2004.

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XX      01-MAR-2003; 2003US-00377139.
PF      01-MAR-2003; 2003US-00377139.
PR      01-MAR-2003; 2003US-00377139.
XX      (MACK/) MACKINNON R.
XX      (MACK/) MACKINNON A L.
PA      (JIAN/) JIANG Y.
PA      (RUTA/) RUTA V.
PI      Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;
XX      WPI: 2004-642122/62.
DR      REFSEQ; NM_031601.
XX      Screening drug candidates that target voltage dependent ion channel
PT      protein, involves contacting screening protein with chemical compound,
PT      which is drug candidate and determining whether chemical compound binds
PT      to screening protein.
XX      Disclosure; SEQ ID NO 7; 61pp; English.
PS      The invention relates to the composition of matter suitable for use in
CC      identifying chemical compounds that bind to voltage-dependent ion channel
CC      proteins. The composition comprises a screening protein that consists of
CC      an ion channel voltage sensor domain of the ion channel protein
CC      immobilised on a solid support. The invention is useful for identifying
CC      chemical compounds (drug candidate) that bind to voltage-dependent ion
CC      channel proteins. The drug candidate of the invention is utilised for
CC      treating a condition mediated by aberrant electrical activity that
CC      initiates uptake or release of neurotransmitters and contraction of
CC      muscles. The drug candidate of the invention is also utilised for
CC      treating epilepsy and arrhythmia. The present sequence is a voltage-
CC      dependent calcium channel DNA.
SQ      Sequence 6942 BP; 1383 A; 2126 C; 1961 G; 1472 T; 0 U; 0 Other;

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## Alignment Scores:

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Pred. No.: 0 Length: 6942
Score: 10945.00 Matches: 2107
Percent Similarity: 93.9% Conservative: 34
Best Local Similarity: 92.4% Mismatches: 101
Query Match: 91.94% Indels: 36
DB: 13 Gaps: 6

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US-09-611-257A-37 (1-2266) x ADSI6295 (1-6942)

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Qy      1 MetAspGluGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20
Db      114 ATGACGAGGAGGAGGATGAGGCGGGCCGAGGAGTGGGACAGCCCCCTAGCTTCACG 173
Qy      21 ArgLeuAsnAspLeuSerGlyAlaGlyLysArgProGlyProGlySerAlaGluLysAsp 40
Db      174 CAGCTCAACGACCTGTCTCGGGGCGGGGGCGCGCAGGGGCTGGGGTGAACGAAAGAGAC 233
Qy      41 ProGlySerAlaAspSerGlyAlaGluGlyLeuProTyrProAlaLeuAlaProValAl 60
Db      234 CCGGGCAGCGCGGACTCCGAGGCGGAGGGCTCCGACCCCGGCGCTAGGCCGGTGT 293
Qy      61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
Db      294 TTCTTCTACTTGGCCAGGACAGCCGCGCGGAGCTGGTGTCTCCGACGGTCTGTAAAC 353
Qy      81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db      354 CCGTGGTTTCAAGGAGGACATATAGCTGTGATCTTCTCAACTGTGTGACTCTGGGATAG 413
Qy      101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db      414 TTCAGGCGGTGTGGGACATTTGCTGTGACTCCAGGCGGTGCGGATCTGACAGGCTTC 473
Qy      121 AspAspPheIlePheAlaPhePheAlaValAlaGluMetValLysMetValAlaLeuGly 140

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Db 474 GATGACTTCATCTTTCCTTCTTTCCTGTGGAAATGATGTGTAAGATGNGGCGCTTGAGC 533  
QY 141 ILePheGlyLylValysCyStyTleuGlyAspThrTTPAsnArgLeuAspPhePheIleVal 160  
Db 534 ATCTTGGGAGAAAGTAACTGAGAGACACTTGAAACCGGCTTACCTTTTCATCTGTC 593  
QY 161 ILeAlGlyMetLeuGlyIuTySerSerLeuAspLeuGlyAsnValSerPheSerAlaValArg 180  
Db 594 ATTGCAGGAGATGCTGAGATTCCTGACACCTGCACAACTGACTCTTCGAGAGCAG 653  
QY 181 ThrValArgValIleuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 654 ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGATGCGCATTC 713  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValIleuLeuLeuCysPhePhe 220  
Db 714 GTCACATTAATGCTGACACCTTGCTTAATGCTGGGACAGTCTGTGCTGTCTTC 773  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuThrAlaGlyLeuLeuArgAsnArg 240  
Db 774 GTCTTTTTCATCTTGGCATGTGGCGGTCCAGCTGTGGGAGAGACTGCTTCGCAACCG 833  
QY 241 CysPheLeuProGlyLuanPheSerLeuProLeuSerValAspLeuGlyArgTyTyrgln 260  
Db 834 TGCTTCTCCCGAGAACTTCAGCTCCCTGAGCGTGGACCTGGAGCTTATTACAG 893  
QY 261 ThrGluAsnGlyLuanAspGlySerProPheIleCysSerGlnProArgGlyLuanGlyMetArg 280  
Db 894 ACAGAAATGAGAGACAGAGCCCTTCATCTGCTTCAGCTCGGAGATGCGAATGCAAGAA 953  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu 300  
Db 954 TCTTCGAGAGATGTGCCACACTGCTGGGGAGAGGGGTGTGTGCCACCTGCACTG 1013  
QY 301 AspTyGlyLuanIleTyAsnSerSerSerAsnThrThrCysValAsnThrAsnGlnTyTy 320  
Db 1014 GACTATGAGACCTATAACAGTTCCACCAACACCACTGTGTCAACCTGAAACAGTACTAT 1073  
QY 321 ThrAsnCysSerIleAlaGlyLuanIleAsnProPheGlyValIleAsnPheAsnIle 340  
Db 1074 ACCAACTGCTGTGGCGGAGCAACCCCTTCAAGGGCGCCATCACTTGTGCAACATT 1133  
QY 341 GlyTyAlaIleAlaIlePheGlnValIleThrLeuGlyGlyTyTyValAspIleMet 360  
Db 1134 GGTATAGCTCGATTCGCATCTTCAGGTATCATCACTGAGGGCTGGGTGCACATCATG 1193  
QY 361 TyrPheValMetAspAlaHisSerPheTyAsnPheIleTyPheIleLeuLeuIleIle 380  
Db 1194 TACTTGTAATGAGCGCTCACTCTTCTACAACTTCATCATCTTCTTCATCATCTC 1253  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGly 400  
Db 1254 GTGGGTCTCTTCTTCATGATCAACCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTG 1313  
QY 401 ThrTyGlyLuanArgLuanSerGlnLeuMetArgGlyGlnArgValArgPheLeuSerAsnAla 420  
Db 1314 ACCAAACAGGGAGAGATCACTGATGATGCGGAGACAGCGTACGATTCCTGTCCATGCT 1373  
QY 421 SerThrLeuAlaSerPheSerGlyProGlySerCysTyGlyGlyLuanLeuLeuTyTyLeu 440  
Db 1374 AGCACCCTGGCAAGCTTCTCTGAGCCAGGCACTGTATGAGAGCTACTCAAGTACATG 1433  
QY 441 ValTyTyIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460  
Db 1434 GTGTACATCTTCGAAAGAGCCGAAAGGCTGGCCAGGTCCTGTGGGTATATAGCGGTG 1493  
QY 461 ArgValAlaGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGlnThrGlnProSerSer 480  
Db 1494 CGGGCTGGGTGCTGCAGACCCAGTGGCCCGTAAGTGGGAGAGACCCAGCCCAATGGC 1553  
QY 481 SerCysSerArgSerIleSarArgLeuSerValHisIleLeuValHisHisHisHisHis 500  
Db 1554 AGGTGACATCTGCTCACACGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1613

QY 501 His 520  
Db 1614 CACCATACCACTTACCACTTGGGTAAATGGAGCTCAAGATTCCTCCGGGAGCCAGCAG 1673  
QY 521 ILeGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540  
Db 1674 ATCCAGAGACAGGAGATGCCAATGGTCTCGCGGCTCATGTATCACACCACTCTACACC 1733  
QY 541 AlaLeuSerGlyAlaProProGlyGlyValAlaGlySerValHisSerPheTyHisAlaAsp 560  
Db 1734 ACTCCCTCGGGGGCCCTCCAGGGGTGCGAGTGTACACAGCTTCTTACCATCTGAC 1793  
QY 561 CysHisLeuGlyLuanProValArgCysGlnAlaProProProArgSerProSerGlyLuan 580  
Db 1794 TGCACCTTGAGCCAGCTGCTGTCAGAGACCCCTCCCAATGTCCCATCGAGGACATCT 1853  
QY 581 GlyArgThrValGlySerGlyLysValTyProThrValHisThrSerProProProGly 600  
Db 1854 GGTAGGACTGTGGTAAATGGGAGGTGTACCCCATGTGATACAGCCCTTCACACAGAG 1913  
QY 601 ThrLeuLysGlyLuanAlaLeuValGlyValAlaAlaSerSerGlyProProThrThrThr 620  
Db 1914 ATACTGAAGATTAAGCACTACTGAGGTGGCCCAAGCCCTGGGAGCCCTCAACC 1973  
QY 621 SerLeuAsnIleProProGlyProTySerSerMetHisLysLeuLeuGlyLuanGlnSer 640  
Db 1974 ACCTTCACATCCCACTGAGGCTTCAGCTTCATGACACAGCTCTGAGAGACAGAGT 2033  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLuanAlaAspSerGly 660  
Db 2034 ACGGAGCGCTGCATATGCTCCGCAAAATCTCCAGCCCTTGCTCCAGGAGACAGTGA 2093  
QY 661 AlaCysGlyProAspSerCysProTyTyCysAlaAlaArgAlaGlyValGlyLuanLeu 680  
Db 2094 GCCTCGGGCCGAGAGTGTCTCTTCACTGTGCTCGGAGAGAGAGAGAGAGAGAGAGT 2153  
QY 681 AlaAspArgGlyLuanProAspSerAspSerGlyAlaValTyGlyLuanPheThrGlnAspAla 700  
Db 2154 GCTGACATGTATCTGATCTGATCAAGACAGAGCTGTGTATGATTCACACAGAGAGCT 2213  
QY 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719  
Db 2214 CAGCAAGTGAAGCTCCGGGATCCCAAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGT 2273  
QY 720 AlaGlyProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPheArgLysIle 739  
Db 2274 GCAGAGCCTAATCTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2333  
QY 740 ValAspSerLysTyPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759  
Db 2334 GTAGATGACAAATCTTGTGGCGGGGAATCATGATCGCATCTGTGTATACATCACTGAC 2393  
QY 760 MetGlyIleGlyTyHisGlyLuanProGlyLuanLeuThrAsnAlaLeuGlyLuanIleSerAsn 779  
Db 2394 ATGGGATCGAATACAGAGAGAGCCGAGAGCTCACCAAGCCCTGGAATTCAGCAAC 2453  
QY 780 ILeValPheThrSerLeuPheAlaLeuGlyLuanLeuLeuValTyTyTyPro 799  
Db 2454 ATCGTCTTCACAGGCTCTTCCTGCTGTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTG 2513  
QY 800 PheGlyTyTyIleLysAsnProTyAsnIlePheAspGlyValIleValValIleSerVal 819  
Db 2514 TTTGGCTACATTAAGATTCCTCAACAATCTTGTATGTGTGTGTGTGTGTGTGTGTGTGTG 2573  
QY 820 TrpGlyIleValGlyGlnGlnGlyGlyLysLeuSerValLeuArgThrPheArgLeuMet 839  
Db 2574 TCGAGATTTGTGGCCAGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2633  
QY 840 ArgValAlaLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859  
Db 2634 CGGTGCTGAGAACTG 2693

QY 860 LysThrMetAspIleValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe 879  
| | | | |  
DB 2694 AAGACCATGACAACTGGCCACCTTCGTCATGCTCTCATGCTGTCATCTTC 2753  
| | | | |  
QY 880 SerIleLeuValMetHisleuPheGlyCysIlePheAlaSerGluAspAspGlyAspThr 899  
| | | | |  
DB 2754 AGCATCTCGGCGCATGCAATCTCTTTGTTGGCAAGTCCCATCTGAACGGGATGGGAGACG 2813  
| | | | |  
QY 900 LeuProAspArgIleAsnIlePheAspSerLeuLeuTrpAlaIleValIlePheGlnIle 919  
| | | | |  
DB 2814 TTGGCAGACCGGAAGATTTCGACTCCCTGCTGGGCACTGGTCACTGCTTTCAGATT 2873  
| | | | |  
QY 920 LeuThrGlnGluAspTrpAsnIleValLeuIleTrpAsnGlyMetAlaSerThrSerSerTrp 939  
| | | | |  
DB 2874 CTGACTCAGAGAACTGGAATAAAGTCTCTACAAACGCGCATGGCTCCACATCTCTGG 2933  
| | | | |  
QY 940 AlaAlaIleuValPheIleAlaIleuMetThrPheGlyAsnIleValIlePheAsnIleu 959  
| | | | |  
DB 2934 GCTGCTCTTAACTTCATCGCTTCATGACTTTTGGCAACTATGCTCTTAACTTCCTG 2993  
| | | | |  
QY 960 ValAlaIleuValIleGluGlyPheGlnAlaGluGluIleSerIleAspGluAspAlaSer 979  
| | | | |  
DB 2994 GTGGCCATTCTTGTGGAAAGATTCCAGGCAAG----- 3026  
| | | | |  
QY 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnIleSer 999  
| | | | |  
DB 3027 -----GGAGATGCCCAACCAAGTCT 3044  
| | | | |  
QY 1000 GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgIleCys 1019  
| | | | |  
DB 3045 GAGTCAGAGCTGATTTCTTTTCCGCAAGTGTGATGTGATGGAGACAGAAAGAGCCG 3104  
| | | | |  
QY 1020 LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgIleSerLeuLeuProLeu 1039  
| | | | |  
DB 3105 TTGGCCCTGTGGCTTTGGAGAAACCGCGAATTAAGAAAGACCTTTTGGCCACCTCTC 3164  
| | | | |  
QY 1040 IleIleHisThrAlaAlaThrProMetSerLeuProIleSerThrSerThrGlyLeuGly 1059  
| | | | |  
DB 3165 ATCATTCATACGGCTGGCAGACCAATGTCACACCCCAAGACTCCAGACAGGTGTGGG 3224  
| | | | |  
QY 1060 GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla 1079  
| | | | |  
DB 3225 GAACCACTGGGCTGTGCTCTGACGTACAGTACAGTGGGTCCGCTGAGACCTGAGACT 3284  
| | | | |  
QY 1080 Ala---HisGluMetIleSerProProSerAlaArgSerProHisSerProTrpSer 1098  
| | | | |  
DB 3285 GCCCAACATGAGATGAATATCCGCCAAGTCCCGCAAGTCCCGCAAGTCCCTGGAGT 3344  
| | | | |  
QY 1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118  
| | | | |  
DB 3345 GCGGCAAGCACTGGACAGCAGCGCTCCAGCAGAAACAGCTGGGCGGCGCCCGCAGC 3404  
| | | | |  
QY 1119 LeuIleAspArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlu 1138  
| | | | |  
DB 3405 CTTAAAGCGGAGAGACCCGAGCGGAGCGAGGTCTCTGCTGTGGAGAGGCGCCAGGAG 3464  
| | | | |  
QY 1139 SerGlnAspGluGlnGluSerSerGlnGluGlnAlaSerProAlaGlySerAspHis 1158  
| | | | |  
DB 3465 AGTCAGATGAGAGAGAAAGTTTCAGAGAGAGACCGGGCCAGCCACGACGAGTGAACAT 3524  
| | | | |  
QY 1159 ArgHisArgGlySerLeuGluArgGluAlaIleSerSerPheAspLeuProAspThrLeu 1178  
| | | | |  
DB 3525 CGCCACAGGGGCTCTCTGGAACGTGAGGCGCAAGAGTCTCTTGGACTGCTCGACACTCTG 3584  
| | | | |  
QY 1179 GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp 1198  
| | | | |  
DB 3585 CAGGTGCGGAGGCTGACCGACAGCCAGCGCGAGCTCTGCTCGACACCAACAGAC 3644  
| | | | |  
QY 1199 CysAsnGlyIleSerSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro 1218  
| | | | |  
DB 3645 TGTATATGCAAGTCCGCTTCAAGGGGTTTGGCCCGCACCTGAGAGACGTGATGACCCCA 3704  
| | | | |  
QY 1219 LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerIleGlyArgValArgAla 1238  
| | | | |

DB 3705 CTGGATGGGATATATACATATGAGGAAATCTGACAAAGGAGAACCATACAGC 3764  
| | | | |  
QY 1239 TrpIleArgAlaArgLeuProAlaCysTrpLeuGluArgAspSerTrpSerAlaTrpIle 1258  
| | | | |  
DB 3765 TGGGTCAAGATCCCGGCTTCCTGCTGTGCGGAGACGAGATTCCTGTGCGGCTTATATC 3824  
| | | | |  
QY 1259 PheProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisIleCysMetPhe 1278  
| | | | |  
DB 3825 TTTCCTCTCAGCAAGGTTTGTCTCTGTGTACCGGATCATCCACCAAGATGTTT 3884  
| | | | |  
QY 1279 AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro 1298  
| | | | |  
DB 3885 GACCATATGATCTCTCTCATCATCTTCTCAACTGTATACCATTCCTATGAGCGCCGCC 3944  
| | | | |  
QY 1299 LysIleAspProHisSerAlaGluArgIlePheLeuThrIleuSerAsnTrpIlePheThr 1318  
| | | | |  
DB 3945 AAATTTGACCCCAAGCGGTGAGCCATCTCTCAACCTCTCCAACTACATCTTCACG 4004  
| | | | |  
QY 1319 AlaValPheLeuAlaGluMetThrValIleValAlaIleGluIleTrpCysPheGlyGlu 1338  
| | | | |  
DB 4005 GCAGTCTTTCTACCTGAATAAGACAGTGAAGTGTGACATGAGCTGTGTGTGGGAG 4064  
| | | | |  
QY 1339 GlnAlaTrpLeuArgSerSerTrpAsnValIleuAspGlyLeuLeuValIleuIleSerVal 1358  
| | | | |  
DB 4065 CAGGCTTACTCTGCGCAGACGACTGGAATGTCTGACGCGCTGTGTGCTCATCTCGTCTC 4124  
| | | | |  
QY 1359 IleAspIleLeuValSerMetValSerAspSerGlyThrIleIleLeuGlyMetLeuArg 1378  
| | | | |  
DB 4125 ATGACATCTCTGTCTTCATGATGCTCCGACAGCGGACCAAGATCTTGGCATGTGAGG 4184  
| | | | |  
QY 1379 ValLeuArgLeuLeuArgThrIleuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398  
| | | | |  
DB 4185 GTGCTGGCTGTGCTGGAGACCTGCGTCACTGAGGTCTACGCGGCGCGGAGGAGCTG 4244  
| | | | |  
QY 1399 LysLeuValValGluThrIleuMetSerSerLeuIleProIleGlyAsnIleValIle 1418  
| | | | |  
DB 4245 AAGCTGATGATGAGACTTGATGTCAATCTCTCAACCCATTGGCAACATTTGTGTCATT 4304  
| | | | |  
QY 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheIleGlyIlePhe 1438  
| | | | |  
DB 4305 TGTGTGCTCTTCTTCATCATTTTGGAAATCTCGGGGTGACGCTTCAAGGGAAGTTC 4364  
| | | | |  
QY 1439 PheValCysGlnGlyIleuAspThrArgAsnIleThrAsnIleSerAspCysAlaGluAla 1458  
| | | | |  
DB 4365 TTGCTGTGTCAGGGTGAGACACAGGAAATCATCTAAACAACTCCGACTCGCTGAGGCC 4424  
| | | | |  
QY 1459 SerTrpArgTrpValArgHisIleArgTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478  
| | | | |  
DB 4425 AGCTACCGATGGGTCCGGCAAGATACACTTGGACAACTGGGCGAGGCTGTGATGTC 4484  
| | | | |  
QY 1479 LeuPheValIleuAlaSerIleAspGlyTrpValAspIleMetTrpAspGlyLeuAspAla 1498  
| | | | |  
DB 4485 CTGTTTGTGCTGGCTCCAAAGATGTTGGTGTGACATGATGATGAGCTGGAGTCT 4544  
| | | | |  
QY 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTrpPheIle 1518  
| | | | |  
DB 4545 GTGGGTGTGATCAGCGCCCATCATGAAACAAACCCCTGATGCTGTACTATC 4604  
| | | | |  
QY 1519 SerPheLeuLeuIleValAlaPhePheValIleuAsnMetPheValGlyValAlaIleGlu 1538  
| | | | |  
DB 4605 TCTCTCTCTCATCGGGCTCTCTTGTCTGTGAACATGTTTGTGGCGCTGTGTGGAG 4664  
| | | | |  
QY 1539 AsnPheHisIleCysArgGlnHisGlnGluGluGluAlaArgArgGluGluIle 1558  
| | | | |  
DB 4665 AACTTCATTAAGTGCACAGACACAGAGAGAGAGGCGGCGGTGAGAGAGAG 4724  
| | | | |  
QY 1559 ArgLeuArgArgLeuGluIleValIleValArgArg-----LysAlaGln 1571  
| | | | |  
DB 4725 CGACTACGAGGCTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4784  
| | | | |  
QY 1572 CysIleProGlyTrpTrpSerArgTrpSerArgPheArgLeuLeuValHisIleLeuCysThr 1591  
| | | | |

Db 4785 TGCAAGCCCTACTACTGTGACTGAGATTCCGGCTCTTGTCACCACTGTGTACC 4844  
QY 1592 SerHisTylLeuAspLeuPheH1eThrGlyValI1eGlyLeuAsnValI1ThrMetAla 1611  
Db 4845 AGCGACTACTCGGACCTCTTCATCACTGTGTCATCGGGCTGAACTGTGTCATATGACC 4904  
QY 1612 MetGlnH1eTyrGlnGlnProGlnI1LeuAspGluAlaLeuYsI1eCysAsnTyrIle 1631  
Db 4905 ATGGAACTTACAGACAGACCCCGATCCTGAGAGAGGCTTGAAAGATCTGCATTTCATC 4964  
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QY 2029 SerLeuAspValGlnGlyLeuGlyYSerArgLeuAspLeuLeuAlaGlyValSerGlyPro 2048  
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QY 2089 ProGlnProAsnTrpGlyYsGlyProProGlnThrArgSerSerLeuGlnLeuAspThr 2108  
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QY 2169 GlnProHisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGly 2188  
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QY 2189 SerArgProYsLeuYsLeuSerProProSerI1eThrI1eAspProProGlnSerGln 2208  
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QY 2229 SerYsAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProYs 2248  
Db 6762 TCTAAGAACTCTCGGTCTCCAGCCCTTGAACAACAAGGCTGCTCAACCTTCCCAAG 6821  
QY 2249 YsAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266  
Db 6822 AAAGACAGCTAGTCTCTGTGTTGTCTGTGACCAACAGACATGAGACCC 6875

RESULT 14  
AAK83486  
ID AAK83486 standard; cDNA; 6795 BP.  
XX  
AC AAK83486;  
AC  
DT 07-DEC-1999 (first entry)  
XX



Dh 1321 GTGTACATCTCCGAAAGACAGCCGAAAGGCTGGCCAGGTCCTCTAAGGCTATAGGCGTG 1380  
Qy |||||  
Dh 461 ArgValAGlyLeuLeuSerSerProAlaPLeuLeuGlyGlyGlnGluThrGlnProSerSer 480  
Qy |||||  
Dh 1381 CGGGCTGGGCTGTCTCAGACAGCCCAAGTGGCCCTGATGGGCGAGAGCCCAAGCCCACTGGCC 1440  
Qy 481 SerCysSerArgSerSerIAsrArgLeuSerValHisHisLeuValHisHisHisHisHis 500  
Qy |||||  
Dh 1441 AGGTGACACTGGCTCAACCGGTCTGTCTGTCTCAACACTGGTCCACCACTCACTCAAC 1500  
Qy 501 HisHisHisHisIleThrHisLeuGlyLeuGlyLeuGlyLeuValAlaProAlaAspProGlu 520  
Qy |||||  
Dh 1501 CACCATCAACCACTACCACTGGGTAATGGAGCGCTCAGAGTTCCCGGGCCAGCCAGAG 1560  
Qy 521 ILeGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540  
Qy |||||  
Dh 1561 ATCCAGAGACAGGATATCCAAATGGGTCTCGCCGGCTATGCTACACACCCTCTTACACCC 1620  
Qy 541 AlaLeuSerGlyValaProProGlyGlyAlaGluSerValHisSerPheThrHisAlaAsp 560  
Qy |||||  
Dh 1621 ACTCCCTCTGGGGGCGCTCCGAGGGGTGGGAGTCTGTACACAGCTTCTACCACTGCTGAC 1680  
Qy 561 CysHisLeuGluProValaArgCysGlnAlaProProProArgSerProSerGluAlaSer 580  
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Qy 601 ThrLeuIleGlyLeuValaLeuValaGluValaAlaAspSerGlyProProThrLeuThr 620  
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Qy 621 SerLeuAsnIleProProGlyProIleProIleSerMetHisIleLeuGluThrGlnSer 640  
Dh 1861 AGCTTCAACATCCCACTGGGCGCTTCAAGCTCATCAACAGCTCTGAGAGACAGAGT 1920  
Qy 641 ThrGlyValaCysGlnSerCysIleHisSerProCysLeuValaAspSerGly 660  
Dh 1921 ACGGAGCGCTGCATGCTCTGCAAAATCTCCAGCCCTTGTCCCAAGGAGCACTGTGA 1980  
Qy 661 AlaCysGlyProAspSerCysProIleCysAlaArgAlaGlyValaGlyGluValaGluLeu 680  
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Qy 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719  
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Qy 720 AlaGluProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPheArgGlySile 739  
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Qy 780 ILeValPheThrSerLeuPheAlaLeuGluMetLeuLeuLeuValIleArgIlePro 799  
Dh 2341 ATGCTCTTACCGAGCTCTTCCCTTGGAGATCTGCTGAATCGCTTGTCTACGCTGCC 2400  
Qy 800 PheGlyIleIleValAsnProIleAsnIlePheAspGlyValaIleValaIleSerVal 819  
Dh 2401 TTGGGCTACATTAAGATCCCTCAACATCTTGTATGTGTCTATGTGGTCACTGATGTGG 2460

Qy 820 TrpGluIleValAGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839  
Dh 2461 TGGAGATTTGGGGCAGACAGGAGGTGGCTGTGTGCTGCCGACCTTCGCTGATG 2520  
Qy 840 ArgValaLeuValaLeuValaArgPheLeuProAlaLeuGlnArgGlnLeuValaLeuMet 859  
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Dh 2581 AAGACCATGAGCAAGGTGGCCACTTGTGCATGCTCTCACTGTCTTCACTTCACTTC 2640  
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Qy 900 LeuProAspArgLeuAsnPheAspSerLeuLeuThrAlaIleValaIlePheGlnIle 919  
Dh 2701 TTGCCAGACCGGAAGAAATTCGATCCCTGCTGGGCGCATGTCTCATGCTTTCAGATT 2760  
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Dh 2821 GCTGCTCTTACTTATATGCTTGCCTCATGACTTTGGCAACTAATGTCTCTTTAACCCTGCTG 2880  
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Dh 2881 GTGGCCATCTTGTGGAAGATTCAGGACAGAG----- 2913  
Qy 980 GlyGlnLeuSerCysIleGlnLeuProValaAspSerGlnGlyValaAspAlaAsnLysSer 999  
Dh 2914 -----GAGATGCCCAAGTCT 2931  
Qy 1000 GluSerGluProAspPhePheSerProSerLeuAspGlyAspArgLysLysCys 1019  
Dh 2932 GAGTCAGAGCTGATTTCTTTTCCGCCAGTGTGATGTGATGGGACAGAAAGAACGCC 2991  
Qy 1020 LeuAlaLeuValaSerLeuGlyGluHisIleProGluLeuArgLysSerLeuLeuProLeu 1039  
Dh 2992 TTGGCCCTGTGCTTGGGAGAACCGGGAATCAAGAAAGGCTTTTGGCAACCCCTC 3051  
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Dh 3052 ATCATTCATACGGCTGCGACACCAATGTCAACCCCAAGAGCTCCAGCAGAGTGTGGG 3111  
Qy 1060 GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla 1079  
Dh 3112 GAAACATGGGCTCTGGCTCTGACGTACAGTACAGTGGGTCCGCTAGCTGGAGCT 3171  
Qy 1080 Ala--HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098  
Dh 3172 GCCCAACATGATGAATGAATGTCGCGCAAGTCCCGCAGCTCCCGCAGAGTCCCTGAGT 3231  
Qy 1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118  
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Qy 1139 SerGlnAspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHis 1158  
Dh 3352 AGTCAGGATGAGAGGAATTAATTCAGAAAGAGACCGGCGCAAGCCAGAGGAGTACCAT 3411  
Qy 1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178  
Dh 3412 CCGCACAGGGGTCTCTTGGAAAGTGAAGGCAAGAGATTCCTTTGACCTGCTGACACTGTG 3471



Qy	1179	GlnValProGlyLeuHilbArgThrAlaSerGlyValArgGlySerAlaSerGlyLuhIsglnAsp	1198
Db	3472	CAGGTGCGGGGCTGCACCCGCAAGCCAGCGCGCGGAGCTCTGCTTGTGACCAAGAC	3531
Qy	1199	CysHsnGlyIlyssSerAlaSerGlyValArgLeuAlaArgAlaLeuArgProAspAspProPro	1218
Db	3532	TGTATGGCAAGTCGGCTTCAGGGCGTTTGCCCGCACCTCGAGAGACTATATGACCCCCA	3591
Qy	1219	LeuAspGlyAspAspAlaAspAspGlyUGlyValAsnLeuSerIlysglyValArgAlaArgAla	1238
Db	3592	CTGATGGGGATGTATGACAAATGATGAGGAAATCTGAGCAAAAGGGAACCATATCAAGACC	3651
Qy	1239	TrpIleArgAlaArgLeuProAlaCysTrpTyrLeuGlnArgAspSerTrpSerAlaTyrIle	1258
Db	3652	TGGGTACAGATCCCGGCTTCCTGCTGTTCGCGAAGAGGAGATCTCTGTGTGGCTCTATATC	3711
Qy	1259	PheProProGlnSerArgPheArgLeuLeuCysHilbArgIleIleThrHilbIlyMetPhe	1278
Db	3712	TTTCCCTCCAGTCAGAGGTTTCGCTCTGTGTACCGAGATCATCACCAAGATGTTT	3771
Qy	1279	AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro	1298
Db	3772	GACCATGTGTCTCTGTATATCTTCTCTCAACTGTATACCAATCGCTATGAGCGGCC	3831
Qy	1299	LysIleAspProHilbSerAlaGluArgIlePheLeuThrIleuSerAsnTyrIlePheThr	1318
Db	3832	AAATATGACCCCAAGCGCTGAGGGCATCTTCTCGACCCCTCCCACTCATCTTCACG	3891
Qy	1319	AlaValPheLeuAlaGluMetThrValIlybValAlaLeuGlyTTPCybPheGlyGlu	1338
Db	3892	GCAGCTTTCTAGCTGGAATACAGTGAAGGTGTGTGCGCATGGCTGTGTGGGAG	3951
Qy	1339	GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal	1358
Db	3952	CAGCGCTACCTGCGCAGCAGCATGTGATGCTGTGACCGCTTGCTGTGTCTATCTCGTC	4011
Qy	1359	IleAspIleLeuValSerMetValSerAspSerGlyThrIlyIleuGlyMetLeuArg	1378
Db	4012	ATGCATCTCTGTCTCCATGGTCTCCGACAGCGGCACAAAGATCTTGGCATCTGAGG	4071
Qy	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
Db	4072	GGCTGCGCGCTGCGGACCCCTGGTCCACTCAGGATCATCACCGGCGCCAGAGACTG	4131
Qy	1399	LysLeuValValGluThrLeuMetSerSerLeuIlyProIleGlyAsnIleValValIle	1418
Db	4132	AAGCTGTGTGTAGACATCTGTATGTCACTCTCAAAACCATTTGGCACATTTGTGTCTAT	4191
Qy	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheIlysglyIlyPhe	1438
Db	4192	TGCTGTGGCTTCTTCATCATATTTTGGATTCCTCGGGGTGCAGCTCTTCAAGGGAAGTTC	4251
Qy	1439	PheValCysGlnGlyGlyLeuAspThrArgAsnIleThrAsnIlySerAspCysAlaGlyAla	1458
Db	4252	TTTCGTGTGTACGGGTGAGAGACCCAGGAACATCATTAACAATCGATGCGCTGAGGCC	4311
Qy	1459	SerTyrArgTrpValArgHilbIlybTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478
Db	4312	AGCTACCGATGGGTCCGGCAACAATGCACTTTGCAAACTGTGGCGAGGCTCTATGTCC	4371
Qy	1479	LeuPheValLeuAlaSerIlyAspGlyTTPValAspIleMetTyrAspGlyLeuAspAla	1498
Db	4372	CTGTTTGTGTGCTGCCCTCCAAAGGATGGTTGGGTTGATCATGTATGATGAGGCTGGATGCT	4431
Qy	1499	ValGlyValAspGlnGlnProIleMetAsnHilbAsnProTrpMetLeuLeuTyrPheIle	1518
Db	4432	GGGGGTGTGATCAGACAGCCATCATGAAACCAACCCCTGAGTGTCTCATACTTATTC	4491
Qy	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGlu	1538
Db	4492	TCTTCTCTCTCATCTGTGCTTCTTTGTGCTGTAACATGTTTGTGTGGGTGTGTGGAG	4551
Qy	1539	AsnPheHilbIlyCysArgGlnHilbGlnGlyUGlyGlnAlaArgArgArgGlnGlyIly	1558

Db	4552	AACTTCATTAAGTCGACACGACACGAGAGAGAGAGAGCGGCGGTGAGGAAG	4611
Qy	1559	ArgLeuArgArgLeuGluIuIySlySArgArg-----	1568
Db	4612	CGACTACGGAGGCTCGGAGAAAAGAGAGAACTTAATGTTGGACGATGTAATTGCTTCC	4671
Qy	1569	-----LysAlaGlnCylAspProTyrTyrSerAspTyrSer	1580
Db	4672	GGCAGCTCAGCCAGCGCTGCGTCGACAGCCCAAGTGCACAGCCCTACTACTCTGACTACTCG	4731
Qy	1581	ArgPheArgLeuLeuValIhIshIleuCySthSerHisTyrIleuAspLeuPheIleThr	1600
Db	4732	AGATTTCGGGCTCCTTGTCACACCTGTGTGACAGCCACTACTCGAACCCTTCACTACT	4791
Qy	1601	GlyValIleGlyLeuAsnValIleThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1620
Db	4792	GGTTCATTCGGGCTCGAAGCGTGTCACTCAATGCGCATGGAACATTACACGAGCCCAAGATC	4851
Qy	1621	LeuAspGluAlaLeuIuIySleCyAsnTyrIlePheThrValIlePheValLeuGluSer	1640
Db	4852	CTGACAGAGGCTCGAAGATCTGCACAAATTACATCTTACCCGTCACTTTCGCTTGAATCA	4911
Qy	1641	ValPheIuIySleuValAlaPheGlyPheArgArgPheGlnAspArgTyrPasnGlnLeu	1660
Db	4912	GTATTTCAAACTTGCGGCTTGGCTTCCGCGTTCTTCACGACAGGTGGAACTGACCTG	4971
Qy	1661	AspLeuAlaIleValIleLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1680
Db	4972	GACCTGGCTATGTGTGCTTCTGTCCATCATATGGGCATCACTGAGAGGAAATTGAGGTCAAT	5031
Qy	1681	AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuAlaGlyIleAlaArg	1700
Db	5032	CTGTGCGTGGCCCATCAACCCACCATCATCTCGTATCATGTAGGGGTGCTCCGCAATTGCTCGA	5091
Qy	1701	ValLeuIuIySleuLeuIuIySmetAlaValAlaGlyMetArgAlaLeuLeuAspThrValMetGln	1720
Db	5092	GTTCGTGAAGCTGTGAAGATGGCTGTGGGACATGGGACACTGCTGCACACAGTATCATGAG	5151
Qy	1721	AlaLeuProGlnValIleGlyAsnLeuGlyIleuLeuPheMetLeuLeuPhePheIlePheAla	1740
Db	5152	GCCCTGCCCAAGGTGGGGAACCTGGGACTTCTCTTCATGTTATGTTTTCATCTTTGCA	5211
Qy	1741	AlaLeuGlyValIleGluLeuPheGlyAspLeuGluIuIyCysAspGluIuIySproCySgluGly	1760
Db	5212	GCTGTGGGCGTGGAGCTCTTTGGAGACTGGAGTGTATGAGACACACCTTGTGAGAGGGC	5271
Qy	1761	LeuGlyArgHisAlaIleThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1780
Db	5272	TTCGGGTGGGACATGCGACCTTTAGGAACTTGTGTGCTTTTCGACCTTTCGAGTCC	5331
Qy	1781	SerThrArgIuIyAspAsnTyrPasnGlyIleMetIuIyAspThrLeuAlaGlyAspCyAspGluIu	1800
Db	5332	TCCACTGGTGTGCAACTGGATGTGATTATGAGAGACCTCTCCGGAGCTGTGACACAGAG	5391
Qy	1801	SerThrCyStryrAsnThrValIleSerProIleTyrPheValSerPheValIleuThrAla	1820
Db	5392	TCCACTGCTCAACACATCTCATCTCCCTATCTACTTGTGTGCTTCTGCTGCTGACGGCC	5451
Qy	1821	GlnPheValIleuValAsnValValIleAlaValLeuMetIySHisIleuGluGluSerAsn	1840
Db	5452	CAGTTTGTGCTGTCAACGTGTATATGCTGTGATGAAAGCACCTGTGAGAAAGAAC	5511
Qy	1841	LysGluAlaIuIySgluGluIuIyAlaGluLeuGluIuIyGluIuIySleuGluIuIySThrLeu	1860
Db	5512	AAAGAGGCCAAGAGAGAGGCCGACCTGAGGCCAGCTGAGAGCTGTGATAAACGCTC	5571
Qy	1861	SerProGlnProHisSerProLeuGlyIleSerProPheLeuThrProGlyValIleGluIyPro	1880
Db	5572	AGCCGCGAGCCCACTCCCGCTGGGAGGCCCTTCTTCCTGCGCCGGGGGTGAGAGGTGTC	5631
Qy	1881	AspSerProAspSerProIuIySProGlyValAlaLeuHisProAlaAlaHisAlaArgSerAla	1900
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Db      5632 AACAGTACTGACGACCCCTTAAGCTGGGGCTCCACACACCACTGCCACATTGGAGCAGCC 5691
QY      1901 SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuPro----- 1918
Db      5692 TCGGGCTTCTCCCTTGAAGACCCCAAGATGTACCCACCACCCGAGGAGGACAGTCCCC 5751
QY      1919 ---GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937
Db      5752 CTAAGACACAGACTGCTGACTGTGAGGAAGTCTGCTGTACCGCGACGCACTCTCTGCC 5811
QY      1938 AsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGluHisArgGly 1957
Db      5812 AATGACAGCTACATGTCGCAATGGGAGCATGCTGAGAGATCCCTTAGACACACAGGGGC 5871
QY      1958 TrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAsp 1977
Db      5872 TGGGGGCTCCCAAAACCCAGTACGCTCATTTGCTTCGTTACCTCCCAACACAGACAGC 5931
QY      1978 ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAla 1997
Db      5932 ACCAGCTGCATCTTAAGCTTCCCAAGATGTGCACTATCTGTCTCAGCTCTCATGGGGCT 5991
QY      1998 ProThrTyrGlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArg 2017
Db      5992 CCCACCTGGGGCCCATCCCTTAATACCCCACTGACCGCTCCCTCTGCTGCTCAGAGG 6051
QY      2018 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2037
Db      6052 CTTCTAGGGCGCAGCAGCATATAGACTGCTCCCTGATGTGACAGGGCTGGGTATAC 6111
QY      2038 ArgGluAspLeuLeuAlaGlnSerGlyProSerProProLeuAlaArgAlaTyrSer 2057
Db      6112 CGGGAAAGACTGTTGTCAAGAGTGAGTGGGCTCTCTGCTCTGACCCGCTCTCATCC 6171
QY      2058 PheTyrGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSer 2077
Db      6172 TTCTGGGGCGGGTGCAGCATCCAGTGACAGCAGTCCGCTCCGACCAAGTCTCC 6231
QY      2078 LysHisMetThrProProAlaProCysProGlyProGluProAsnThrGlyLysGlyPro 2097
Db      6232 AACACATATCCGCTGCAGGCCCTTGTCCCAAGCTGTGAACCCAGCTGGGCCAAGAACCT 6291
QY      2098 ProGluThrArgSerSerLeuGlnLeuAspThrGluLeuSerTyrIleSerGlyAspLeu 2117
Db      6292 CCAGAGACCAAGACGACTTAAAGCTGACACGAGACTGAGCTGATTCAGAGACGCTC 6351
QY      2118 LeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysCysTyrSer 2137
Db      6352 CTT---CCCGACGACGAGAAAGAACCCCTGTCTCCACGCGGACCTGAAGAAGTCTACAGT 6408
QY      2138 ValGluAlaGlnSerCysGlnArgArgProThrSerThrLeuAspGluGlnArgArgHis 2157
Db      6409 GTAGAGACCCAGAGCTGACAGCCGACGCTGGGTTCTGGCTAATATAACAGCGGAACAC 6468
QY      2158 SerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSer 2177
Db      6469 TCCATTGCTCTCAGCTGTCTGACACGCGCTCCCAACCCCGCTTAATGTCACACCCCTCA 6528
QY      2178 AsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLeuSerPro 2197
Db      6529 AGCCTCGGGGGCCCAACTCTTGGGGGCTCTGGGAGCGGCTTAAGAAAAAACTCAGCCCA 6588
QY      2198 ProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSerProGly 2217
Db      6589 CCAAGATCTCTTAAGACCCCGGAGAGCCAGGGCTCTGGGCCCATGCAATCTCTGGT 6648
QY      2218 IleCysLeuArgArgAlaProSerSerAspSerIleAspProLeuAlaSerGlyPro 2237
Db      6649 GTTCTGCTCAGAGAGAGGGCGCGGCAAGTACTTAAGATCTCTCGCTCTCAGCCCC 6708
QY      2238 ProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeu 2257
Db      6709 CTTGACAGACAGGGCTGCTCACCCTCCCAAAAGAACACGCTGAGTCTCTGGTTTG 6768

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QY      2258 SerSerAspProAlaAspLeuAspPro 2266
Db      6769 TCTTCTGACCCCAACAGACATGAGACCC 6795

```

## RESULT 15

```

ID AAX83487
ID AAX83487 standard; cDNA; 6816 BP.
XX
XX

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AC AAX83487;
XX
XX

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```

DT 07-DEC-1999 (first entry)
XX
XX

```

```

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCav11c) cDNA.
XX
XX

```

```

KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; db.
XX
XX

```

```

OS Rattus sp.
XX
XX

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PN W0929847-A1.
XX
XX

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PD 17-JUN-1999.
XX
XX

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PF 30-OCT-1998; 98WO-US023161.
XX
XX

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```

PR 05-DEC-1997; 97US-00985809.
XX
XX

```

```

PA (LOYO ) UNIV LOYOLA CHICAGO.
XX
XX

```

```

PI Perez-Reyes E, Cribbs LL;
XX
XX

```

```

DR WPI: 1999-394972/33.
XX
XX

```

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DR P-PSDB; AAY14592.
XX
XX

```

```

PT New T-type voltage-gated calcium channels.
XX
XX

```

```

PS Disclosure; Page 85-94; 138pp; English.
XX
XX

```

CC This sequence represents the coding region for a rat T-type voltage-gated calcium (Ca) channel alpha-1-G designated rCav1.1c. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The CC large alpha subunits form a pore in the membrane that is selective for a CC given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical CC segments (81-86). T-type Ca channels are activated at a lower voltage CC than L- or N-type channels. Characteristics of T-type channels include CC short current time, slow activation kinetics near threshold, fast CC inactivation kinetics and slow tail current. The sequences AAX83481- CC X83492 represent novel T-type voltage-gated Ca channel genes from humans CC and rats. Each of the novel Ca-channels contains a putative IVS4 region CC comprising the amino acid sequence AAY14598. Cells expressing the T-type CC voltage-gated calcium channel proteins can be used to screen for drugs CC which affect calcium channels. Methods are also disclosed for treating a CC disease or disorder associated with a deficiency in a native T-type CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc CC XX

Sequence 6816 BP; 1373 A; 2058 C; 1932 G; 1453 T; 0 U; 0 Other;

## Alignment Scores:

```

Prid. No.: 0 Length: 6816
Score: 10925.00 Matches: 2106
Percent Similarity: 93.16% Conservative: 33
Best Local Similarity: 91.72% Mismatches: 103
Query Match: 91.78% Indels: 54
DB: 2 Gaps: 6

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```

US-09-611-257A-37 (1-2266) x AAX83487 (1-6816)

```

```

QY      1 MetAspGluGluGluAspGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db      1 ATGAGACGAGAGAGATGAGACGGGCGCGGAGAGTGGGACAGCCCGTGTTCACG 60

```



Db	2221	GTAGATGACCAATATCTTTGGCCGGGAAATCATATGCCATCTCGTTCATATACCTAGC	2280
Oy	760	MetGylIleGluYrhiSgluGlnProGluGluLeuThrAsnAlaGluIleSerAsn	779
Db	2281	ATGGGCATCGAGTACAGAGACGCGGAGGCTCACAAACGCCCTGGAAATCAGCAAC	2340
Oy	780	IleValPheThrSerLeuPheAlaGluIleMetLeuLeuLysLeuValTyrGlyPro	799
Db	2341	ATCGCTTCACACAGCTCTTCGCTTGGAGATGCTGTGAAACGTCTGTCTACAGCTCC	2400
Oy	800	PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal	819
Db	2401	TTGGCTACATTAAGAAATCCCTACACATCTTTATGCTGTCATTTGGTATCATCAGTGTG	2460
Oy	820	TyrGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMet	839
Db	2461	TGGGAGATTTGGGCGACGAGGAGGTGGCTGTGCGGTGCTGGGAGCTTCGCTCATG	2520
Oy	840	ArgValLeuLysLeuValArgPheLeuProAlaGluGlnArgGlnLeuValValLeuMet	859
Db	2521	CGGGGTGGAAGCTGTGTGCGCTTCCTCGCGCCCTGCAGCCCGACGCTGTGTGCTCATG	2580
Oy	860	LysThrMetAspAsnValAlaThrPheCysMetLeuMetLeuPheIlePheIlePhe	879
Db	2581	AAGACCATGAGCAACAGTGGCCACTTCGACAGTCTCCTCAGCTGTTCATCTTATCTTC	2640
Oy	880	SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr	899
Db	2641	AGCATCCCTGGGCAATCATCTCTTGGTGTGCAAGTTCGATGTGAACGGAGGGGACAGC	2700
Oy	900	LeuProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIle	919
Db	2701	TTGCACAGCCGGAAGAAATTTGCACTCCCTGCTGGGCAATCGTCACTGTCTTCAATTT	2760
Oy	920	LeuThrGlnGluAspTyrAsnLysValLeuLysTyrAsnGlyMetAlaSerThrSerSerTyr	939
Db	2761	CTGACTCAGGAGAGCTGGAAATTAAGTCTCTTACAAACGGCAGTGGCTCCACATCGTCTTG	2820
Oy	940	AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu	959
Db	2821	GCTGCTCTTACTTCATCGCCCTCATGACTTTTGGCACTATGTGCTCTTTAACTGTCTG	2880
Oy	960	ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer	979
Db	2881	GTGGGCATTTCTTGGAGAGAAATTCACAGCAAG-----	2913
Oy	980	GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer	999
Db	2914	-----GAGAGATGCCACCAAGCT	2931
Oy	1000	GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLeuCys	1019
Db	2932	GAGTCAGAGCTCGATTTCTTTTCCGCCAGTGTGATGTATGGGGACAGAAATAACGCC	2991
Oy	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuLeu	1039
Db	2992	TTGGCCCTGTGTGCTTTGGAGAAACACGCGAAACTACGAAGAAGACCTTTTCCACCCCTC	3051
Oy	1040	IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly	1059
Db	3052	ATCATCCCATACGGGCTGCACACCAATGTCAACACCCCAAGACTCTCAGACAGTGTGGGG	3111
Oy	1060	GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyVala	1079
Db	3112	GAGCACTGGGCTCTGGCTCTTGACGTACCAAGTACAGTGTGGGTCCGCTGACCTGAGACT	3171
Oy	1080	Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTyrSer	1098
Db	3172	GCCACCACTGAGATGAATATGTCCGCAAGTCCCGCAAGCTCCCGCAACAGTCCCTGGAGT	3231
Oy	1099	AlaAlaSerSerTyrThrSerArgArgSerSerArgAsnSerLeuGlyValArgAlaProSer	1118
Db	3232	GCGGCAACACACTGAGACCAAGAGGCTCTCAGCAGGAACACTGTGGGCGGGCCCGACG	3291

Qy	1119	LeuIyAaRgArSerProSerGIyGIuAaRgArSerLeuLeuSerGIyGIuGIyGIuGIu	1138
Dp	3292	CTAAAGCGAGGAGGCCCGACCGGGGAGCGGAGAGCTCTGCTGTCTGGAGGGCCAGAG	3351
Qy	1139	SerCIuAaPgluGIuGIuSerSerGIuGIuGIuAaRgAlaSerProAlaGIySerAaPHis	1158
Dp	3352	AGTCAGATAGAGAGAAATTCAAGAGAGGACCGGCCAGCCACGACGGCAGTGAACAT	3411
Qy	1159	ArgHIaRgAlSerLeuGIuAaRgGIuAlaLySerSerPheAaPLeuProAaPThrLeu	1178
Dp	3412	CGCACAGGGGTTCTCTGGAACTGAGGCCAAGATTCCTTTGACCTGACCTGACACTCG	3471
Qy	1179	GIuVAIProGIyLeuHIaAaRgThraIaSerGIyAaRgAlaSerIaSerGIuHIaGIuAaP	1198
Dp	3472	CAGGTGCGGGGCGTCGACCCGACAGCCAGCGGGCGGAGCTTGTGCTTGACCAAGAC	3531
Qy	1199	CyAaAaGIyLySerAlaSerGIyAaRgLeuAlaAaRgAlaLeuAaRgProAaPProPro	1218
Dp	3532	TGTATATGGCAAGTCGCTTCAGGGCGTTTGGCCCGACCTTGAGGACTATGACCCCCA	3591
Qy	1219	LeuAaPglYaAaPpaIaAaPaaPgluGIyAaAaAaSerIySGIyGIuAaRgValaAaRgAla	1238
Dp	3592	CTGATATGGGATGATGACAAATGATGAGGAAATCTGAGCAAGGGAAACCAAGAACGC	3651
Qy	1239	TryIleAaRgAlaAaRgLeuProAlaCyAaTyLeuGIuAaRgAaPSerTPaAaIaTyIle	1258
Dp	3652	TGGATCGAATCCCGGCTCTGCTGCTGTGCCAGAGGAGATTCCTGTGTGCGCTATATC	3711
Qy	1259	PheAaPProGIuAaRgAaRgPheAaRgLeuLeuCyAaHIaRgIleIleThraIyAaMetPhe	1278
Dp	3712	TTTCTCTCTCAAGTCAAAGTTCGTCTGCTGTGTACACCGGATATATACCCCAAGATGTT	3771
Qy	1279	AaPHisAaIyAaLeuValIleIlePheLeuAaAaCyIleThraIleAaMetGIuAaRgPro	1298
Dp	3772	GACCATGGGTCTGTCATCATCTTCTCAACTGTATCCATCGCTTAAGAGCGCCCC	3831
Qy	1299	LySleIaAaPProHISaAaIaGIuAaRgIlePheLeuThraLeuSerAaAaTyIlePheThr	1318
Dp	3832	AAATTTGACCCCCACAGCGCTGAGCGCATCTTCCTGACCTTCACATCATCTTCACG	3891
Qy	1319	AlaValaPheLeuAlaGIuAaMetThraIyAaValaAlaLeuGIyTPCySPheGIyGIu	1338
Dp	3892	GCACTCTTTCTTCAAGTGAATGACGTGAAGGTGTGGACCTGGGCTGTGTGGGGAG	3951
Qy	1339	GIuAlaTyIleAaRgAaSerSerTPaAaValLeuAaPglYleuLeuValleuIleSerVal	1358
Dp	3952	CAGGCCATACCTCGGCACACACTGGAATGTCTGGAGCGCTTGGTGGTCAATCTCGTC	4011
Qy	1359	IleAaPglleuValaSerMetValaSerAaPSerGIyThraIyIleLeuGIyMetLeuAaRg	1378
Dp	4012	ATCAGCAATCTGTGCTTCATGAGTCTCGAAGCGGACCAAGATTCCTTGGCATGTGAGG	4071
Qy	1379	ValleuAaRgLeuAaAaRgThraLeuAaRgProLeuAaRgValIleSerAaRgAlaGIuGIyLeu	1398
Dp	4072	GTCGTGCGGCTGCTGCGGACCTGTGCTCACTAGGGTCAATCAGCGGGCCAGGAGCTG	4131
Qy	1399	LySleuValaGIuThraLeuMetSerSerLeuLyAaPProIleGIyAaAaIleValIle	1418
Dp	4132	AAGCTGTGTGAAGACTGTGATGTCACTCCCTCAAAACCAATTTGGCAACATTTGTGTAT	4191
Qy	1419	CyAaCyAaIaPhePheIleIlePheGIyIleLeuGIyValGIuLeuPheLySGIyLyPhe	1438
Dp	4192	TGCTGTCTCTTCATCATTTTGGAAATTCGGGGTGAAGCTTCYCAAAAGGAAGTTC	4251
Qy	1439	PheValaCySGIuGIyGIuAaPThraAaAaIleThraAaLySerAaPcyAaIaGIuAla	1458
Dp	4252	TTTCTGTGTCAAGGTGAGACACAGGAACATCACTAAATTCGACTGTGCGTGAAGCC	4311
Qy	1459	SeTyIaRgTrValaAaRgHisLyTyIyAaAaPheAaPLeuGIyAlaIleAaMetSer	1478
Dp	4312	AGTACCGATGTGGTCCGCGCAAGTACAACTTTGACAACTGGGGCCAGGCTGTGATGTCC	4371

1479 LeuPheValIleuAlaSerIyVaSPGlyTyrValAspIleMetTyrAspGlyLeuAspAla 1498  
1499 ValGlyValIleProGlnIleProIleMetAspHisAsnProIlePheLeuLeuTyrPheIle 1518  
4432 GTGGGTGTGGATCGACAGCCCATCATGACCAACCCCTGGATGCTGCTTACTTATC 4491  
1519 SerPheLeuLeuIleValAlaPhePheValIleuAsnMetPheValGlyValIleValGlu 1538  
4492 TCCTTCTCTCCATCGTGGCTTCTTTGTCTGAACATGTTGTGGCGTGGTGTGGAG 4551  
1539 AsnPheHisIyVaSPGlyValGlnIleGlnGluGluGluValAlaGAGAGAGGluGlu 1558  
4552 AACTTCATTAAGTGCACACAGCACAGAGAGAGAGAGAGGCGAGCGCGTGAAGAG 4611  
1559 ArgLeuAspArgIleLeuGlyValIyVaSPGlyArg----- 1568  
4612 CGACTACGAGAGCTGGAGAAAAGAGAGAGTAAAGAGAACAGATGGCCGATCTAATG 4671  
1569 -----LysAlaGlnCysIys 1573  
4672 TTGACACATGTAATTGCTCCGAGCTCAGCCAGCCGCTGGTCAAGAACCCAGTGCAG 4731  
1574 ProTyrTyrSerAspTyrSerArgPheArgIleuLeuValHisIleuCySerHis 1593  
4732 CCCTACTCTGACTACTCGAGATTCGGGCTCTTCCACCACTGTGTACAGGCAC 4791  
1594 TyrIleuAspLeuPheIleThrGlyValIleGlyLeuAsnValValIleThrAlaMetGlu 1613  
4792 TACCTGACCTCTTCATCATCGTGTGCATCGGGCTGAACGTTGTACATATGGCAAGAA 4851  
1614 HisTyrGlnGlnProGlnIleLeuAspGlyValIleuIyValIeCyAsnTyrIlePheThr 1633  
4852 CATTAACACAGACCCCGAGATCTCGAGAGAGGCTCTGAAGATCTCAATTACATCTTAAC 4911  
1634 ValIlePheValIleuGlySerValPheIyValIleValIlePheArgIlePhePhe 1653  
4912 GTCATCTTTGCTTTGAGTCAAGTTTCAAACTTGGGCTTGGCTCCGCGTTCTTC 4971  
1654 GluAspArgTyrPheAsnGlnLeuAspLeuAlaIleValIleuLeuSerIleMetGlyIleThr 1673  
4972 CAGACACAGGTGAACCAAGTGAACCTGATGCTTGTGCATCATGGGCAATCA 5031  
1674 LeuGluGlnIleGlyValIleAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet 1693  
5032 CTGAGAGAGATTTGAGTCAATCTGTGCTGCCATCAACCCCATCATCTGATCATG 5091  
1694 ArgValIleuArgIleAlaArgValIleuIyValIleuIyMetAlaValIyMetArgAla 1713  
5092 AGGGTCTCCGATTTGCTCGAGTTCTGAAGCTGTGAAGATGGCTGTGGCATCGGGCA 5151  
1714 LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet 1733  
5152 CTGCTGCACACAGGTGAATGACAGCCCTGCCAGAGGTGGGAACTTGTCTTCTCATG 5211  
1734 LeuLeuPhePheIlePheAlaAlaLeuGlyValIleuPheGlyAspLeuGlyCyAsp 1753  
5212 TTATTTGTTTTCATCTTTGACGCTCGGCGGTGAGCTTTTGGAGACCTGAGAGTGTAT 5271  
1754 GluThrHisProCySPGlyGlyLeuGlyValArgHisAlaThrPheArgAsnPheGlyMetAla 1773  
5272 GAGACACACCTTGTGAGGGCTTGGGTGGCATGCCATTTAGAACTTTGTATGGCC 5331  
1774 PheLeuThrIleuPheArgValIleSerThrGlyAspAsnTyrPheGlyIleMetIyAspThr 1793  
5332 TTTCTGACCCCTCTTCCGAGTCTCCACTGTGACCACTGAATGTATTAAGAGAACCC 5391  
1794 LeuArgAspCyAspGlnIleSerThrCySerIyAsnThrValIleSerProIleTyrPhe 1813  
5392 CTCGGGACGTGACCAAGAGTCCACTGTCAACACATGTATCTCCCTATCTACTTT 5451  
1814 ValSerPheValIleuThrAlaGlnPheValIleuValAsnValValIleAlaValIleuMet 1833  
5452 GTGTCTTGTGCTGACGCGCCAGTTTGTGCTGTCAAGTGTCACTGCTGCTGAGT 5511  
1834 IySHIleuGluGluIleSerAsnIyGlyValIyGluGluAlaGluLeuValIleGluLeu 1853  
5512 AAGCACTCGAAGAAAGCAAAAGAGGCCAAAGAGAGAGAGGCGGAGCTCGAGGCTG 5571  
1854 GluLeuGluIleMetIyPheThrIleuSerProGlnProHisSerProLeuGlySerProPheLeu 1873  
5572 GAGCTGAGATGAAGACGCTCAGCCCGAGCCGACCTCCCGGTGGAGAGCCCTTCTTC 5631  
1874 TyrProGlyValIleGluIyProAspSerProAspSerProIyAspProGlyValIleuHisPro 1893  
5632 TGCCCGGGGTGAGAGGTGTCAACATGACAGGCTTAAGCTGGGTCCACACACAC 5691  
1894 AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHis 1913  
5692 ACTGCCACATTTGAGACAGCTCGGCTTCTCCTTGAGACACCCACGATGTACCCAC 5751  
1914 ProThrGluLeuPro-----GlyProAspLeuLeuThrValArgIySerGlyVal 1930  
5752 CCGAGAGGTGTCAGTCCCTTACAGACAGACCTGTGATGTGAGAACTGTGTGTC 5811  
1931 SerArgThrHisSerLeuProAsnAspSerTyrMetCySerHisIySerThrAlaGlu 1950  
5812 AGCGGAGAGCACTCTGCCCATAAGACCTTACATGTCCGCAATGGAGACATGCTGAG 5871  
1951 GlyProLeuGlyHisIleArgIyTyrGlyLeuProIyValIleGlnSerGlySerValIleSer 1970  
5872 AGATCCCTAAGACACAGGGCTGGGGCTGCCAAAGCCAGTCAAGCTCATCTGTTC 5931  
1971 ValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProIyAspAlaProHis 1990  
5932 GTTCACCTCCCAACAGACACACAGCTGCATCTTCAAGTTCACAAAGTGTGACTAT 5991  
1991 LeuLeuGlnProHisSerAlaProThrTyrGlyIleProIyLeuProProProGly 2010  
5992 CTGCTCAAGCTTATGAGGGCTCCACCTGGGGGCCCATCCCTTAACATCCCACTGGC 6051  
6052 CGCTCCCTCTGGGTCAAGAGCTCTTCAAGCGCAGGCAAAATAAGACATGATCTCTGC 6111  
2011 ArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeu 2030  
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6112 GATGTGACGGGCTCGGTGACCGGGAAGACTGTGTCAAGAGTGAAGTGGCCCTCTGC 6171  
2051 ProLeuAlaArgAlaTyrSerPheThrGlyGlnSerSerThrGlnAlaGlnHisSer 2070  
6172 CTTCTGACCGGCTCTATCTTCTGGGGCGGTCCAGCATCCAGTGCAGACGCTTCC 6231  
2071 ArgSerHisSerIyHisIleSerHisMetThrProProAlaProCySPGlyProGlu 2090  
6232 GGCATCCAGAGCAAAAGCTCCAGACATCGGCTGCCACCCCTTCCAGGCTGGAA 6291  
2091 ProAsnTyrGlyIySPGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeu 2110  
6292 CCCAGCTGGCCAAAGACCTCCAGAGACCAAGAGCGCTTAAGCTGAGACACGAGACTG 6351  
2111 SerTyrIleSerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArg 2130  
6352 AGCTGGAATTCAGAGACCTCTT---CCAGACACCGAGAAAGAACCCCTGTTCCACGG 6408  
2131 AspLeuIyIySPGlyTyrSerValGluAlaGlnSerCySPGlnArgArgProThrSerTyr 2150  
6409 GACTTGAAGAACTCTACAGTGAAGACCAAGAGCTGACAGGCGCAGGCTGGGTCTGG 6468  
2151 LeuAspGluGlnArgArgHisSerIleAlaValIleSerCyIleuAspSerGlySerGlnPro 2170  
6469 CTATATGAACAGCGGAGACACTCATTTGCTGTGACGCTGTGACAGCGGCTCCCAACC 6528  
2171 HisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArg 2190



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 18, 2005, 18:10:57 ; Search time 714.688 Seconds  
(without alignments)  
5188.000 Million cell updates/sec

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Perfect score: 11904  
Sequence: 1 MBEEDGAGAESGQPRSF.....PKKDVLSGLSSDPADLDP 2266

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues  
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : Issued Patents NA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11877.5	99.8	6822	3	US-09-426-998-3 Sequence 3, Appl1
2	11877.5	99.8	7741	3	US-09-426-998-4 Sequence 4, Appl1
3	11241	94.4	7405	4	US-09-949-016-3859 Sequence 3859, Ap
4	6315.5	53.1	3993	4	US-09-398-522-51 Sequence 51, Appl
5	6214.5	52.1	7898	3	US-08-984-709A-49 Sequence 49, Appl
6	5492.5	46.1	6816	3	US-09-404-650-1 Sequence 1, Appl1
7	5492.5	46.1	6816	4	US-09-935-541-1 Sequence 1, Appl1
8	5484	46.1	6855	4	US-09-404-650-3 Sequence 3, Appl1
9	5484	46.1	6855	3	US-09-935-541-3 Sequence 3, Appl1
10	5418.5	45.5	6503	4	US-09-404-650-12 Sequence 12, Appl
11	5418.5	45.5	6503	4	US-09-935-541-12 Sequence 12, Appl
12	2237	18.8	70308	4	US-09-949-016-15601 Sequence 13601, A

13	1971.5	16.6	1669	3	US-08-984-709A-51 Sequence 51, Appl
14	1786.5	15.0	7376	3	US-09-268-163-3 Sequence 3, Appl1
15	1784.5	15.0	7362	1	US-08-455-543A-7 Sequence 7, Appl1
16	1784.5	15.0	7362	2	US-08-193-078B-7 Sequence 7, Appl1
17	1784.5	15.0	7362	2	US-08-223-305C-7 Sequence 7, Appl1
18	1784.5	15.0	7362	2	US-08-149-097D-7 Sequence 7, Appl1
19	1784.5	15.0	7362	3	US-08-949-386-7 Sequence 7, Appl1
20	1784.5	15.0	7362	3	US-08-450-562-7 Sequence 7, Appl1
21	1784.5	15.0	7362	3	US-08-984-709A-7 Sequence 7, Appl1
22	1784.5	15.0	7362	3	US-08-450-272-7 Sequence 7, Appl1
23	1784.5	15.0	7362	4	US-08-450-273-7 Sequence 7, Appl1
24	1784.5	15.0	7266	3	US-08-713-118-1 Sequence 1, Appl1
25	1784.5	15.0	7266	3	US-09-452-007-1 Sequence 5, Appl1
26	1782.5	15.0	7364	3	US-09-268-163-5 Sequence 8, Appl1
27	1778	14.9	7175	1	US-08-455-543A-8 Sequence 8, Appl1
28	1778	14.9	7175	2	US-08-193-078B-8 Sequence 8, Appl1
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33	1778	14.9	7175	3	US-08-984-709A-8 Sequence 8, Appl1
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37	1728.5	14.5	7011	3	US-09-268-163-7 Sequence 9, Appl1
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39	1711.5	14.4	5975	1	US-08-314-083B-1 Sequence 1, Appl1
40	1711.5	14.4	5975	1	US-08-435-675B-1 Sequence 1, Appl1
41	1711.5	14.4	5975	3	US-08-884-599-1 Sequence 3, Appl1
42	1701.5	14.3	5975	1	US-08-336-257A-3 Sequence 3, Appl1
43	1691	14.2	6114	4	US-09-495-714C-3 Sequence 5, Appl1
44	1690	14.2	6114	4	US-09-495-714C-5 Sequence 25, Appl1
45	1690	14.2	7089	3	US-08-949-386-25

ALIGNMENTS

RESULT 1  
US-09-426-998-3 ; Sequence 3, Application US/09426998  
; Patent No. 6358706  
; GENERAL INFORMATION:  
; APPLICANT: DUBIN, ADRIENNE E.  
; APPLICANT: PIATTI, DAYASHREE  
; APPLICANT: ZHU, JESSICA Y  
; APPLICANT: ERLANDER, MARK G  
; APPLICANT: GALINDO, JOSE E  
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM  
; FILE REFERENCE: ORT-1057  
; CURRENT APPLICATION NUMBER: US/09/426,998  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PATENTIN VER. 2.0  
; SEQ ID NO 3  
; LENGTH: 6822  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-426-998-3  
  
Alignment Scores:  
Pred. No.: 0  
Score: 11877.50  
Percent Similarity: 99.65%  
Best local Similarity: 99.60%  
Query Match: 99.78%  
DB: 3  
Caps: 1  
  
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Db 1 ATGACGACGAGACGACGATGACGCCGCCGAGGAGTGGGACACGCCGCCGAGCTTCATG 60



QY	21	ArgLeuAsnAspLeuSerGlyValAGlyGlyValArgProGlyProGlySerAlaGlyValAsp	40
Db	61	CGGCTCAACGACCTGTCCGGGGGCGGGGGGCGGGCGGGGCTACGAGAAAAGAC	120
QY	41	ProGlySerAlaAspSerGlyAlaGlyGlyLeuProTyrProAlaLeuAlaProValVal	60
Db	121	CCGGGACGGCGGACTCCGAGGCGGAGGGGCTGCCGTAACCGGGGCTGGCCCGGTGTT	180
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
Db	181	TYCTCTCACTTGAGCGACGAGACAGCGCCCGCGGAGCTGGTGTCTCCGACGGTCTGTAC	240
QY	81	ProTyrPheGlyValArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
Db	241	CCCTGGTTTGAGCCGATACGATGGATGGTATCTTCTCACTCGGTAACCTCGGGCATG	300
QY	101	PheArgProCysGlyAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
Db	301	TTCCGGCCCATCGAGAGCATCGCTGTGACTCCGAGGGCTCGGATCTTGACAGGCTTT	360
QY	121	AspAspPheIlePheAlaPhePheAlaValGlyMetValValIysMetValAlaLeuGly	140
Db	361	GATGACTTCATCTTTCCTTCCTTCCTTCCTGAGATGGTGGAAGATGGTGCTTGGGC	420
QY	141	IlePheGlyIlySlyCysTyrLeuGlyValAspThrTyrAsnArgLeuAspPheIleVal	160
Db	421	ATCTTTGGGAAAAGTGTACTCTGGAGACACTTGGAAACGGCTTGACTTTTCAATGCTC	480
QY	161	IleAlaGlyMetLeuGlyTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
Db	481	ATCGCAGGAGATGCTGGAGTACTCGCTGGACCTCGACGAAACGTCACTTCTCAGCTGACG	540
QY	181	ThrValAlaGlyValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
Db	541	ACAGTCCGTGGCTCGACCGCTCAAGGACATTAAACGGAGTGGCCAGCATGCGATCTT	600
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
Db	601	GTCACGTTGCTGCTGATACGCTGCGCCACGTGGGGCAACGTCTGCTGCTTCCTTC	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlyMetThrAlaGlyIleLeuLeuArgAsnArg	240
Db	661	GCTCTCTTCATCTTCCGCGATGTCGGCGCTCAAGCTGTGGGAGGGCTGTCTCGGAACCGA	720
QY	241	CysPheLeuProGlyAsnAspPheSerLeuProLeuSerValAspLeuGlyValTyrGln	260
Db	721	TGCTTCTTACCTCGAAGATTTCAGCGCTCCCGTGAAGCGTGAACCTGGAGCGCTTATTACAG	780
QY	261	ThrGlyAsnGlyAspGlySerProPheIleCysSerGlnProArgGlyAsnGlyMetArg	280
Db	781	ACAGGAACGAGAGTGAAGAGCCCTTCATCTGCTCCACGCAACCGAGAAAGGATCCGG	840
QY	281	SerCysAspSerValProThrLeuArgIleAspGlyGlyGlyIlyProProCysGlyLeu	300
Db	841	TCCTGCAAGAACGTGCCACCGCTGCGGGGACGGGGGCGGTGGCCACTTGGGGTCTG	900
QY	301	AspTyrGlyAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrPasnGlnTyrTyr	320
Db	901	GACTATGAGGCTTACACACAGCTCCAGCAACACCTGTGTCACTGGAAACCACTATCAC	960
QY	321	ThrAsnCysSerAlaGlyGlyIleAsnProPheIysGlyValIleAsnPheAspAsnIle	340
Db	961	ACCAACTCTCAAGCGGGGAGACACACCCCTTCAAGGGCGCCATCACTTGAACAACATT	1020
QY	341	GlyTyrAlaTyrPleAlaIlePheGlnAlaIleThrLeuGlnGlyIlyTyrValAspIleMet	360
Db	1021	GCGTATGCGCTGGATGCGCATCTTCCAGGTATCAACGCTGAGAGGGCTGGGTGCATCATG	1080
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
Db	1081	TACTTTTGATGGAGTCACTATCTCTTCAACAATTCACTTCACTTCACTCTCTCATCATC	1140

OY	381	ValGlySerPhePheMetIle	LeuLeuCy	LeuValValIle	IleAlaThrGlnPhe	SerGlu	400
Db	1141	GTGGGCTCTTCTTCAATGATCAACCTGTGCTGTGTGTATGGCCACGGAGTTCACAG					1200
OY	401	ThrIleGlnArgGluSerGlnLeuMetC	ArgGluGlnArgVal	ArgPheLeuSer	AsnAla		420
Db	1201	ACCAAGACGGGGAAAGCCACAGCTGAAGCGGAGACAGTGTGGGTTCTTGTCACAGCC					1260
OY	421	SerThrLeuAlaSerPheSerGluProGlySerCy	TyrGluGluLeuLeu	ysrTyrLeu			440
Db	1261	AGACCCCTGGCTAGTCTCTCTGAGCCCGGAGCTGTATGAGGAGCTGCTCAAGTACCTG					1320
OY	441	ValTyrTlleLeuArglysalaa	laaArglaGleuAlaGlnVal	SerArgAla	aglyVal		460
Db	1321	GTGTAACATCTCTGTAAAGGACGCCCCAGGCTGGCTCAAGTCTCTCGGACACAGGTGG					1380
OY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer					480
Db	1381	CGGGTGTGGCTGCTCAAGACCCACGACCCCTCGGGGGCCAGAGACCCAGCCACACAC					1440
OY	481	SerCySerSerArgSerHisArgArgLeuSerValHis	IleLeuValHisIleHisIleHis				500
Db	1441	AGCGTCTGTGGCTCCACGCCGCCCTATCCGTCCACACACTGGTGACACACACACACAC					1500
OY	501	HisIleHisIle	sTyrHisLeuGlyIle	anglyThrLeuArgAlaProArgAla	SerProGlu		520
Db	1501	CATCACCAACCACTACCACTGGGCAATGGGACGCTCAGGAGCCGCCCGGCGACGCCGAG					1560
OY	521	IleGlnAspArgAspAla	aaanglySerArgArgLeuMetLeuProProProSerThrPro				540
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OY	541	AlaLeuSerAlaValaProProGlyGlyAlaGluSerValHis	SerPheTyrHisAla	aa			560
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OY	561	CysHisLeuGluProValaArgCy	sglnAlaProProProArgSerProSerGluAlaSer				580
Db	1681	TGCCACTTAAGACACAGTCCGCTCCAGGGCGCCCCCTCCAGAGTCCCATCTGAGGATCC					1740
OY	581	GlyArgThrValGlySerGlyly	ysValTyrProThrValHis	ThrSerProProProGlu			600
Db	1741	GGCAGGACTGTGGCGACGGGAAAGGTATCCACCGTGACACACAGCCTTCACCGGAG					1800
OY	601	ThrLeuylsglysalalaleuValaGluVala	laaIleSerSerGlyProProThrLeuThr				620
Db	1801	ACGCTGAAGAGAAAGGACATAGTAGAGTGGCTGCCAGCTCTGGCCCCCAACCTCACAC					1860
OY	621	SerLeuAsnIleProProGlyProTyr	SerSerMetHisIle	ysLeuLeuGluThrGlnSer			640
Db	1861	AGCTTCAACATCCACCCGGGCTCTACAGCTCATGACACAAAGCTGTGAGAGACACAGACT					1920
OY	641	ThrGlyAlaCy	egInserSerCyly	sIleSerSerProCy	bleuylsalaa	aaSerGly	660
Db	1921	ACAGGTCCCTGCCAACAACCTTTCCAAGATCTCCAGCCTTGTGAAACACAGCACTGGA					1980
OY	661	AlaCy	sgIlyProaa	aaSerCyProTyrCy	saIlaArgAlaGlyAla	aglyGluValGluLeu	680
Db	1981	GCTGTGTGTCAAGACAGCTCCCTTACTGTGGCCCGGGCCGGGACAGGAGGTGGAGCTC					2040
OY	681	AlaAspArgGluMetProa	aaSerSerAspSerGluAlaVal	TyrGluThr	ThrGlnAspAla		700
Db	2041	GCGACCGTGAAATGCTGACTCAGACAGGAGGAGGAGTTATGAGTTACACACAGATGACC					2100
OY	701	GlnHisSerAspLeuArgAspProHis	erArgArgGlnArgSerLeuGlyProa	aaAla			720
Db	2101	CAGACACGCACTCCCGGACCCCCACAGCCGGCGGCAACGGAGCTGGGGCCACAGTGA					2160
OY	721	GluProSerSerValleuAlaPhe	TTPArgLeuIleCy	aa	spThrPheArgly	ylIleVal	740
Db	2161	GAGCCCAAGCTGTGTGCTGGCTTCTGGAGCTATGTGTGACACTTCCGAAAGATTGG					2220
OY	741	AspSerly	sTyrPheGlyArgGlyIleMetIle	AlaIleLeuVala	aa	ThrLeuSerMet	760

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Qy 801 G1YTYr11e1ySaSnPro1YrA5n11ePheA5pG1YVal11eVal11eSerVal1Trp 820
Db 2401 GGCCTACATCAAGATCCCTACAAATCTTGCATGGTGTCAATGTGTCAATCAGAGTGG 2460
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Qy 861 ThMeCAsPaSnVal1a1aThrPheCyMeLeuLeuMeLeuPhe11ePhe11ePheSer 880
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Qy 1001 SerG1uProA5pPhePheSerProSer1eLeuA5pG1YArqP1a1a5n1YSerG1u 1020
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QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPhe 1540  
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QY 1574 ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCySerHis 1593  
DB 4741 CCTTACTACTCCGACTACTCCGCTCCGGCTCTGTCACACCTTGTCACACGACCAC 4800  
QY 1594 TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu 1613  
DB 4801 TACCTGACCTCTTCATCACAGGTGTCACTGGGTCAAGTGTGTCAACAGGCAATGAG 4860  
QY 1614 HisTyrGlnGlnProGlnIleLeuAspGlnAlaLeuGlyIleCyAsnTyrIlePheThr 1633  
DB 4861 CACTACACAGAGCCCAAGATTCTGATGAGGCTCTGAAGATCTGCAACTGCACATCTTCACT 4920  
QY 1634 ValIlePheValIleGlnSerValPheGlyLeuValAlaPheGlyPheArgPhePhe 1653  
DB 4921 GTCATCTTTGTCTTGGAGTCAAGTTTCAAACTTGCGCTTGGTTCGCTGCTTC 4980  
QY 1654 GlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr 1673  
DB 4981 CAGGACAGGTGGAAACAGCTGACCTGGCCATTTGCTGTCACATCGGCAACAG 5040  
QY 1674 LeuGlnGlnIleGlnValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet 1693  
DB 5041 CTGGAGGAATCGAGGTCAACGCTCGCTGCCATCAACCCCACTCATCTCGCATCAG 5100  
QY 1694 ArgValLeuArgIleAlaArgValLeuGlyLeuLeuGlyMetAlaValGlyMetArgAla 1713  
DB 5101 AGGGTCTGCGCATTCGCCGAGTGTGAAGCTGTGAAGATGGCTGTGGCATGCGGGCG 5160  
QY 1714 LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet 1733  
DB 5161 CTGCTGACACGGGTGATGACGGCCCTGGCCCAAGTGGGAACCTGGGACTTCTTTCAG 5220  
QY 1734 LeuLeuPhePheIlePheAlaAlaLeuGlyValGlnLeuPheGlyAspLeuGlnCyAsp 1753  
DB 5221 TTGTTTCTTTTCACTTTTGAGCTCTGGGCTGGAACTCTTTGGAAACCTGGAGTGTGAC 5280  
QY 1754 GlnThrHisProCysGlnGlnGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla 1773  
DB 5281 GAGACACACCCCTGTAGGGGCTGGGCGCTGATGCCACCTTTCGGAACCTTTGGCATGGCC 5340  
QY 1774 PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetGlyAspThr 1793  
DB 5341 TTCTTAACCTCTTCGAGCTCCACAGGTGACAAATGGATGGCAATMGAAAGGACCC 5400  
QY 1794 LeuArgAspCyAspGlnGlnSerThrCysTyrAsnThrValIleSerProIleTyrPhe 1813  
DB 5401 CTCGGGACCTGTACAGAGAGTCCACTGTATACAACAGGTACTCTCGCTATCTACTTT 5460  
QY 1814 ValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet 1833  
DB 5461 GTGTCTCTGTGCTGACGGGCCAGTTCTGTGCTAGTCAACGTGTGATGCCGTGTGATG 5520

QY 1834 LysHisLeuGlnGlnSerAsnGlyValAlaGlnGlnGlnGlnGlnGlnGlnGlnGln 1853  
DB 5521 AAGCACCTGGAGAGAGCAACAAGAGGCCCAAGAGAGAGGCCAGTGAAGGCTGAGCTG 5580  
QY 1854 GlnLeuGlnMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu 1873  
DB 5581 GAGCTGAGATGAAGACCTTCAGCCCCCAGGCCCTCCAGCTGGGAGGCCCTTCTCTC 5640  
QY 1874 TrpProGlyValGlnGlyProAspSerProAspSerProLysProGlyValAlaLeuHisPro 1893  
DB 5641 TGGCTGGGGTCTGAGAGGCCCAAGCCCAAGCCCAAGCTGGGGCTCTTGACACCA 5700  
QY 1894 AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGlnHisProThrMetGlnProHis 1913  
DB 5701 GGGGCCACGCGAGATCAGCTCCCACTTTTCCCTGGAGCAACCCACGATGAGGCCAC 5760  
QY 1914 ProThrGlnLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThr 1933  
DB 5761 CCCACGAGCTGCCAGACACAGACTTACTGACTGTGGGAGTCTGGGGTCAGCCGAACG 5820  
QY 1934 HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGlnGlyProLeu 1953  
DB 5821 CACTCTGCCCCAATGACAGCTACATGTGTGCGCATGGAGCATGCCCCAGGGGCTCCG 5880  
QY 1954 GlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSer 1973  
DB 5881 GGACACAGGGGCTGGGGGCTCCCAAGCTCAGTGAAGCTCGTCTTGTCCGTTCACTCC 5940  
QY 1974 GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAlaProHisLeuLeuGln 1993  
DB 5941 CAGCAGCAGATACAGACTACATCTGCAAGCTTCCCAAGATGCACTCATCTGCTCAG 6000  
QY 1994 ProHisSerAlaProThrTrpGlyThrIleProLysLeuProProProGlyValArgSerPro 2013  
DB 6001 CCCCAAGGCCCAACTGGGGCAACATCCCAACATGCCCCACAGAGAGCTTCCCT 6060  
QY 2014 LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln 2033  
DB 6061 TTGGCTCAGAGGCCACTCAGGGCCAGGCAAGCAATGAAGACTGCTCTGGACGTTGAG 6120  
QY 2034 GlyLeuGlySerArgGlnAspLeuLeuAlaGlnValSerGlyProSerProProLeuAla 2053  
DB 6121 GGTCTGGGACGCGGGAAGACTGCTGGCAGAGTGAAGTGGGCTCCCGGCTGGGC 6180  
QY 2054 ArgAlaTyrSerPheTrpGlnGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis 2073  
DB 6181 CGGGCTTACTTTCTGGGGCCAGTCAAGTACCAAGGACAGACACTCCGGCAGCCAC 6240  
QY 2074 SerLysIleSerLysHisMetThrProProAlaProCysProGlyProGlnProAsnTrp 2093  
DB 6241 AGCAAGATCTCAACACATGACCCCGCAGGCCCTTGCACAGGCCCAAGACCAACTGG 6300  
QY 2094 GlyLysGlyProProGlnThrArgSerSerLeuGlnLeuAspThrGlnLeuSerTrpIle 2113  
DB 6301 GGCAAGGGCCCTCCAGAGACCAAGAGACTTGAAGTTGACACAGACTGAGCTGCAAT 6360  
QY 2114 SerGlyAspLeuLeuProProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2133  
DB 6361 TGAAGAGACTTCTTCCCTGGGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6420  
QY 2134 LysCysTyrSerValGlnAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGln 2153  
DB 6421 AAGTGTACAGGCTGAGAGGCCCAAGAGCTGCCAGGCCCGGCTGAGTGTGATGAG 6480  
QY 2154 GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly 2173  
DB 6481 CAGAGAGACACTATGCGCCGTGAGCTGCTGGACAGGGGCTCCCAACCCCACTGGGC 6540  
QY 2174 ThrAspProSerAsnLeuGlnGlnGlnProLeuGlnGlnGlnGlnGlnGlnGlnGlnGln 2193  
DB 6541 ACAGACCCCTTAACTTGGGGGCCAGGCTCTTGGGGGGCCCGGGAAGCCCAAGAA 6600  
QY 2194 LysLeuSerProProSerIleThrIleAspProProGlnSerGlnGlyProArgThrPro 2213

Db 6601 AACTCGACCCGCTGATATACCATGACCCCGCCAGAGCCAAAGTCTCGACCCCG 6660  
Qy 2214 ProSerProGlyIleCyLeuArgArgAlaProSerSerAspSerIlyAspProLeu 2213  
Db 6661 CCCAGCCCTGGTATCTGCTCCGAGAGAGGCTCTCGACGACTCCAGAGATCCCTTG 6720  
Qy 2234 AlaSerIlyProProAspSerMetAlaAlaSerProSerProIlyAspValLeuSer 2253  
Db 6721 GCCTCTGGCCCCCTGACAGCATGGCTGCTCGCCCTCCCAAGAAAGATGTGTAGT 6780  
Qy 2254 LeuSerIlyLeuSerSerAspProAlaAspLeuAspPro 2266  
Db 6781 CTCTCGGTTTATCTCTGACCCAGACGACTGAGCCCC 6819

RESULT 2  
US-09-426-998-4  
Sequence 4, Application US/09426998  
Patent No. 6358706  
GENERAL INFORMATION:  
APPLICANT: DUBIN, ADRIENNE E.  
APPLICANT: PYATI, JAYASHREE  
APPLICANT: ZHU, JESSICA Y  
APPLICANT: BRIANDER, MARK G  
APPLICANT: GALINDO, JOSE E  
TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAI G T-TYPE CALCIUM  
FILE REFERENCE: ORT-1057  
CURRENT APPLICATION NUMBER: US/09/426,998  
CURRENT FILING DATE: 1999-10-26  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PATENTIN VER. 2.0  
SEQ ID NO 4  
LENGTH: 7741  
TYPE: DNA  
ORGANISM: HOMO SAPIENS  
US-09-426-998-4

Alignment Scores:  
Pred. No.: 0 Length: 7741  
Score: 11877.50 Matches: 2264  
Percent Similarity: 99.65% Conservative: 1  
Best Local Similarity: 99.60% Mismatches: 1  
Query Match: 99.78% Indels: 7  
DB: 3 Gaps: 1  
US-09-611-257a-37 (1-2266) x US-09-426-998-4 (1-7741)

Qy 1 MetAspGluGluGluAspGlyAlaGluGluSerGlyGlnProArgSerPheMet 20  
Db 523 ATGACGAGGAGGAGATGAGCGGCGCGAGAGGTGCGGAGACCCCGAGCTTCATG 582  
Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40  
Db 583 CGGCTCAACGACCTGTGCGGGGCGCGGGGCGGGGCGGGGCTGCGAGAAAGGAC 642  
Qy 41 ProGlySerAlaAspSerGlyAlaGluGlyLeuProIlyProAlaLeuAlaProValVal 60  
Db 643 CCGGAGACGGGACTCCGAGGCGGAGGGGCTGCGTACCCGGGCTGGCCCGGTGTT 702  
Qy 61 PhePheIlyLeuSerGlnAspSerArgProArgSerIlyPheLeuArgThrValCysAsn 80  
Db 703 TTCTTCTTACTTGAAGCAGACAGCGCGCGAGCTGTCTCCGACCGTCTGTAAAC 762  
Qy 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnValThrLeuGlyMet 100  
Db 763 CCGTGTTTGAAGCGATAGATGTTGGTCACTCTTCACTGCTGATACCTTGAGATG 822  
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
Db 823 TTCCGGCATGCGAGGACATGCGCTGTGATCCCAAGCGCTGCCGATCTCTCAAGCCCTTT 882  
Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140

Db 883 GATGACTTCACTCTTGGCTTTCTTGGCCGTGAGATGTGTGAAATGTGGCTTGGGG 942  
Qy 141 IlePheGlyLysLysCysIlyLeuGlyIleAspThrTrpAsnArgLeuAspPheIleVal 160  
Db 943 ATCTTTGGGAAAAGTTTACCTGGAGACACTTGGAAACCGGCTTCACTTTTCATGTC 1002  
Qy 161 IleAlaGlyMetLeuGluIlyTrpSerIleAspLeuGlnAsnValSerPheSerAlaValArg 180  
Db 1003 ATGCGAGGAGTGTGGAGTACTGCTGACCTGCAAGACCTCAAGCTTCTCAAGTCAAG 1062  
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 1063 ACAGTCGTGTGCTGAGACCGCTCAAGGCGATTACCGGCTGCCAGATGCCATCTT 1122  
Qy 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhe 220  
Db 1123 GTCAAGTGTGCTGGATAGCTGCGCATGCTGGGCAAGCTCTGCTGCTCTTCTTC 1182  
Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240  
Db 1183 GTCTTCTTCACTTTCGGCATGTCGGGCTCCAGCTGTGGCAGGCTGCTTGGAAACGA 1242  
Qy 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgIlyTrpGln 260  
Db 1243 TGCTTCTTACTTGAATTTCAAGCTTCCCTTGAAGCTGAGCTTGAGCCCTTACAG 1302  
Qy 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
Db 1303 ACAGAGAACGAGATAGAGACCCCTTCATCTGCTCCAGCACGCGAGAACGCGATCGG 1362  
Qy 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyLysProCysGlyLeu 300  
Db 1363 TCCTGCAGAACGTCGCCACAGCTGCGGGGAGCGGGGCGGGTCCACCTTGGGCTG 1422  
Qy 301 AspTrpGluAlaTrpAsnSerSerSerSerThrCysValAsnTrpAsnGlnIlyTrp 320  
Db 1423 GACTATGAGCTTACACACACTCCAGACACACACCTGTGTCACTGACAGACTACTAC 1482  
Qy 321 ThrAsnCysSerAlaGlyGluIleAsnProPheIleAsnIleAsnPheAspAsnIle 340  
Db 1483 ACCAAGCTGCTCAAGGGGAGGACCAACCCCTTCAAGGGCGCATCACTTGAACAATT 1542  
Qy 341 GlyTrpAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360  
Db 1543 GGCTATGCTGATGCGCATCTTCCAGTCACTCAAGTGAAGGCGCTGGAGCATCATG 1602  
Qy 361 TyrPheValMetAspAlaHisSerPheTrpAsnPheIleTrpPheIleLeuLeuIle 380  
Db 1603 TACTTGTGATGATGCTCAATCTCTTACAAATTTCACTTCACTTCACTTCACTATC 1662  
Qy 381 ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu 400  
Db 1663 GTGGGCTCTTCTTCAATGATCAACCTGTGCTGTGTGTATGGACAGGATCTCTGAG 1722  
Qy 401 ThrIlyGlnArgIleSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
Db 1723 ACCAAGCAGCGGAGAAAGCCAGCTGATGCGGAGCAGAGTGTGGCTTCTGTCMAAGCC 1782  
Qy 421 SerThrLeuAlaSerPheSerGluProGlySerCysTrpGlyGluGluLeuLysTrpLeu 440  
Db 1783 AGCACCTGTGCTAGCTTCTGAGCCCGGAGCTGCTATAGAGAGCTGCTCAATACTCTG 1842  
Qy 441 ValIlyTrpLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVal 460  
Db 1843 GTGTACATCTTCTTGAAGAGAGCCGAGGCTGAGGCTCTCTGCGGAGAGAGTGTG 1902  
Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluTrpGlnProSerSer 480  
Db 1903 CCGGTTGGGCTGCTCAGACACCCAGACCCCTCGGGGGCAGAGAACCCAGCCAGAGC 1962  
Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisIleHisIle 500

Dd	1963	AGCTGCTCGCTCCCAACCGCCGCTATCGTCCACCAACCTGGTGCACACCAACCAAC	2022
Qy	501	HisHisHisHisTyrHisHisLeuGlyHisnGlyThiLeuArgAlaProArgAlaSerProGlu	520
Dd	2023	CATCAACCAACCACTACCACTGGGCAATGGACGGCTCAGGGCCCCCGGGCCAGCCGGAG	2082
Qy	521	IllegInaBPATgAspAlaasnGlySerArgArgLeuMetLeuProProProSerThiPro	540
Dd	2083	ATCCAGGACAGAGGATGCGCAATGGGGTCCCGCAGGGCTCATGCTGCACCAACCTTCAGCCT	2142
Qy	541	AlaLeuSerGlyAlaProProGlyVGlyValaGluSerValHisSerPheTyrHisAlaAsp	560
Dd	2143	GCCCTCTCGGGGGCCCCCTGGTGGGCGCAGAGTCTGTGCACAGCTTCTACATGCCGAC	2202
Qy	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
Dd	2203	TGCCACTTAGAGCCAGTCCGGCTGCCAGCGCCCCCTCCAGTCCCATCTGAAGCATCC	2262
Qy	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu	600
Dd	2263	GGCAGGAGCTGTGGGACGCGGGAGGTGTATCCACCGGCACACAGCCCTCCACCGGAG	2322
Qy	601	ThiLeuLysGlyLysAlaLeuValGlnValAlaIleSerSerGlyProProThrLeuThr	620
Dd	2323	ACGCTGAAGGAGAAAGCACTAGTAAAGGTGGCTGCAAGCTGTGGACCCCAACCTCAAC	2382
Qy	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThiGlnSer	640
Dd	2383	AGCTCAACATCCCAACCCGGGCCCTTACAGCTTCATGCACAAAGCTGTGGACACAGAT	2442
Qy	641	ThiGlyAlaCysGlnSerSerCysLysValLeSerSerProCysLeuLysAlaAspSerGly	660
Dd	2443	ACAGGTGCTCTCCAAAGCTCTTGGACAGATCTCCAGCCCTCTTGAAGAAGCAGACGTGGA	2502
Qy	661	AlaCysGlyProProAspSerCysProThrCysAlaIleArgAlaGlyValGlnValGluLeu	680
Dd	2503	GCGTGTGGTCCAGAGAGCTGCCCCCTACTGTGCCGGGGCCGGGGAGAGTGAAGCTC	2562
Qy	681	AlaAspArgGluMetProAspSerAspSerGlnAlaValTyrGluPheThiGlnAspAla	700
Dd	2563	GCCGACCGTGAATGCTGACTCAGACAGCGAGGAGATTATGATTCACACAGATGCC	2622
Qy	701	GlnHisSerAspLeuArgAspProHisSerArgArgLeuSerLeuGlyProAspAla	720
Dd	2623	CAGCACACGCACTCCGGGACCCCCACAGCGCGGGCAACGGAACCTGGGCCCAAGTGA	2682
Qy	721	GluProSerSerValLeuAlaPheThrArgGluIleCysAspThrPheArgLysIleVal	740
Dd	2683	GAGCCCACTCTGTGCTGGCCCTTCGAGGGCTTAATGTGTGACACCTTCGAAATATGTG	2742
Qy	741	AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThiLeuSerMet	760
Dd	2743	GACAGCAAGTACTTTGGCCCGGGGAATCATATCCCACTCGGTCAACACACTCAGCATG	2802
Qy	761	GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle	780
Dd	2803	GGCATTCGAATCCACAGACAGCCGAGGAGCTTACCAACGCCCTTGAATCAGCAATC	2862
Qy	781	ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe	800
Dd	2863	GTCCTTCAACACACCTCTTGGCCCTGGAGATGCTGTGAAGCGCTGTGTATAGTCCCTTT	2922
Qy	801	GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyrPro	820
Dd	2923	GGCTACATCAAGATCCCTTACACATCTTCCATGTGTCACTTTGGTGCATAGCGTGTGG	2982
Qy	821	GluIleValGlyGlnGlnGlyGlyValLeuSerValLeuArgThrPheArgLeuMetArg	840
Dd	2983	GAGATCGGGGCGACGAGGGGGGGCGGCTGTCCGGTGGTGGCGACCTTCGCTGATGGT	3042
Qy	841	ValLeuLysLysLeuValArgPheLeuProAlaLeuGlnIleArgGlnLeuValValLeuMetLys	860
Dd	3043	GTGCTGAAGCTGTGTGCTGCTTCGTCGGCGGTGCAGCGCGAGCTGTGTGTCTCATGAG	3102

QY	861	THrMTCAspAsnValAlaThrPheCysMeLeuLeuMeLeuPheIlePheSer	880
Db	3103	ACCATGACAAACGTGGCCACCTTCTGCATGCGCTTAATCTCTCAATCTTCAC	3162
QY	881	ILeLeuGIyMeHisIleuPheGIyCysLysPheAlaSerGIuAArgAspGIyAspThrLeu	900
Db	3163	ATCTGGGCATGCATCTCTTCCGGCTGCAGATTGGCTCTGCAGCGGGATGGGGACACCTGG	3222
QY	901	ProAspArgLysAnPheAspSerLeuLeuThrPalaIleValIThrValPheGIuIleLeu	920
Db	3223	CCAGACCGGAAGAATTTGACTCTCTGCTCGGGCCATGTCATCTCTTCAGATCCCG	3282
QY	921	ThrGIuGIuAspThrAsnLysValIleuLysAsnGIyMeAlaSerThrSerSerThrPala	940
Db	3283	ACCCAGAGAGCATCGAACAAAGTCTCTACATAGTAATGGCTTCCACGTCTGCTGGGG	3342
QY	941	AlaLeuTyRPhelIleAlaLeuMetThrPheGIyAsnTyRValIleuPheAnLeuLeuVal	960
Db	3343	GCCCTTAATTTCATTGGCCCTCATGACTTCGGCAATACGTGCTCTTCATTATTCGTGTC	3402
QY	961	AlaIleLeuValGIuGIyPheGIuAlaGIuGIuIleSerLysArgLysAspAlaSerGIy	980
Db	3403	GCCATTCTGGTGGAGGGCTTCCAGGGGAGAAATAGCAAAACGGGAATGCGATGGA	3462
QY	981	GIuLeuSerCysIleGIuLeuProValAspSerGIuGIyGIyAspAlaAsnLysSerGIu	1000
Db	3463	CAGTTAAGCTGATTTCAGCTGCTGCTGCATCTCCAGGGGGAGATGCCAACAAAGTCCGA	3522
QY	1001	SerGIuProAspPhePheSerProSerLeuAspGIyAspGIyAspArgLysCysLeu	1020
Db	3523	TCAAGAGCCCAATTTCTTCTCACCCACCGTAGAGTGATGGGACAGGAAGAAGTCTTGG	3582
QY	1021	AlaLeuValSerLeuGIyGIuHisProGIuLeuArgLysSerLeuLeuProProLeuIle	1040
Db	3583	GCTTGTATGTCCTTGGAGAGCACCCGGAGCTCGGAAAGCTGCTGCGCTCTCATC	3642
QY	1041	IleHisThrAlaIleThrProMetSerLeuProLysSerThrSerThrGIyLeuGIu	1060
Db	3643	ATCCACACGGCCCCCACCCCATGTCGTGCCCAAGACACCGACCGGGCTCGGGCGAG	3702
QY	1061	AlaLeuGIyProAlaSerArgArgThrSerSerSerGIySerIleAluProGIyAlaIle	1080
Db	3703	GCGGTGGAGCCCTGCTGTCGCCGCCACACAGACAGCGGGTGGCAAGCTTGGAGCGGCC	3762
QY	1081	HisGIuMetLysSerProProSerAlaArgSerSerProHisSerProThrSerAlaIle	1100
Db	3763	CAGAGATGAAGTCCACCGCCAGCGCCGAGCTTCCGCACAGCCCTCGAGCGCTGCA	3822
QY	1101	SerSerThrPheSerArgArgSerSerArgAsnSerLeuGIyArgAlaProSerLeuLys	1120
Db	3823	AGCAGCTGAGCACAGACGGCTCTCACCCGGAACAAGCTTCGGCGTGACCCAGCTGAAG	3882
QY	1121	ArgArgSerProSerGIyGIuArgArgSerLeuLeuSerGIyGIuGIyGIuGIuSerGIu	1140
Db	3883	CGAGAGAACCCCAAGTGGAGAGCGCGCTCTTGTTCGGAGAGAGCCACAGAGAGCCAG	3942
QY	1141	AspGIuGIuGIuSerSerGIuGIuArgAlaSerProAlaGIySerAspHisArgHis	1160
Db	3943	GATGAAGAAGAGAGCTCAGAAAGAGAGCGGACCGCTCGGGCGAGTACCATCCCCAC	4002
QY	1161	ArgGIySerLeuGIuArgGIuAlaLysSerSerPheAspLeuProAspThrLeuGIuVal	1180
Db	4003	AGGGAGTCCCTGGAGCGGAGGCGCAAGAGTCTCTTGAACCTGCAACACATCGACGGTG	4062
QY	1181	ProGIyLeuHisArgThrAlaSerGIyArgGIySerAlaSerGIyHisGIuAspCysAsn	1200
Db	4063	CGAGGCTGCATGCACCTGCCAATGGCCAGGGGTCTGCTTCGAGCACAGAGCTGCAAT	4122
QY	1201	GIyLysSerAlaSerGIyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
Db	4123	GGCAGAGTCGCTTCAGGCGCGCTGGGCCCTTGCCTGCGCTGTAGTATACCCCCACATGAGAT	4182

QY	1221	GIyAaPaBaPaLaAaPaBaPGLUGLyAaLnLeuSeRySGLyGUAyGValAaGAlaITPLe	1240
Db	4183	GGGAGATGACGGCGATGACGAAGGGCAACTTGAGCAAAAGGGGAACGGTCCGGCGCTGATC	4242
QY	1241	ArpAlaAaGLeuProAlaCyEThLeuGluAaPaSeRTpSeRaLaTyRLeAaPhPro	1260
Db	4243	CGAGCCGACATCCCTGGCTGGCTGGAGGAAAGCTCTGTAAGGCTTACATCTTCCCT	4302
QY	1261	ProGlnSeRaTPheArGLeuLeuCyHisAaRgLeLeIeThRAlaLyAmeTPheAsPHis	1280
Db	4303	CCTCAAGTCAGAGTTCCGGCTCTGATGACCGGATCATCAACCAAGATGTTGACAC	4362
QY	1281	ValValLeuValLeIeAaPheLeuAaNCyAlLeThRLeAlaAmeGUAaTProLyAlle	1300
Db	4363	GTGGCTCTTGATCATCATCTCTTAACTGATCAATCCATCGCATGAGCGCCCAAAATT	4422
QY	1301	AaPProHIsSeRaLaGUAaRgLeAaPheLeuThreUsSeRaNTyLeAaThAlaVal	1320
Db	4423	GAACCCCAACACGGCTGAAGACATCTTCCGACCCTTCAAATACATTTACCGCAATC	4482
QY	1321	PheLeuAlaGLeuMeThValLyAaValAlaLeuGlyTyTPCySpheGlyGluGlnAla	1340
Db	4483	TTTCCGCTGAATATACATGAAGTGGTGACATGGCTGGTGTTCGGGACAGACGGCG	4542
QY	1341	TyRLeuAaRgSeSeRTpAaNVaLLeuAaPGLyLeuLeuValLeuLeSeRaValLeaSP	1360
Db	4543	TACCTGCGGACAGATTTGGAACGTGCTGACGGGCTGTTGGTGCATCTCCGTATGCAC	4602
QY	1361	ILeLeuValSeRmeValSeRaPSeRcLyThRySILeLuGlyMeLeuAaRgValLeu	1380
Db	4603	ATTCTGGTGCATATGCTCTTGACACGGGACCAAGATCTCGGAGATCTAAGGAGTGCTG	4662
QY	1381	ArgLeuLeuAaRGTThLeuAaRgProLeuAaRgValLeSeRaGAlaGlnGlyLeuLySLeu	1400
Db	4663	CGCGCTGCTGGGACCCCTGCGCCGCTGACGGGTGAATCACCGGCGGACGGGCTGAAGCTG	4722
QY	1401	ValValGluThrLeuMeSeSeRLeuLySProlleGlyAaNLLeValValLeCyCyS	1420
Db	4723	GTGGTGAGAGACGTATGCTCATCTGAACCAATCGGCAACATTTGATGATCTGCTGT	4782
QY	1421	AlaPhePheLeIeLePheGlyTILEuGlyValGlnLeuPheLySGLyAaPhePheVal	1440
Db	4783	GCCTTCTTCATCATTTTGGCATCTTGGGAGTGGAGCTTTCAAAGGGAATTTTCGTG	4842
QY	1441	CysGlnGlyGUAaPThRaAaNLLeThRaNLySSeRaPcYAlaGAlaASeTyR	1460
Db	4843	TGCCAGGGGAGAGATACCAAGAACTCACCAATAAATGGAGTGGCCGAGGCCAGTTAC	4902
QY	1461	ArgTyRValAaRgHIsLyTyRaNPheAaPaNLLeuGlyGlnAlaLeuMeSeRLeuPhe	1480
Db	4903	CGGTGGGTCCGGCAACAATCACTTTGACAACCTTGGCCAGGCGCTGATGCTCCCTGTTCC	4962
QY	1481	ValLeuAlaSeRlyAaPGLyTyTPValaNLleMeTyRaPpGLyLeuAaPaLaValGly	1500
Db	4963	GTTTTGGCTCCAAAGATGTTGGTGGTGAACATCATGTCAGTGGCTGAGTGGCTGGGC	5022
QY	1501	ValAaPGLInGlnProILeMeRaNLIsaNPcOTpMeLeuLeuTyRPhelIeSeRPh	1520
Db	5023	GTGGACCAAGCCCATCATGAACCAACACCCCTGGATGCTGCTACTTCATCTCGTTC	5082
QY	1521	LeuLeuLLeValAlaAaPheValLeuAaNLpheValGlyValValValGluAaNPhe	1540
Db	5083	CTGCTCATATTTGGCTTCTTGTCTTGAACATGTTTGTGGGTGTGTGTGTGGAGAACTTC	5142
QY	1541	HisLyvCyvAaRgGlnHisGlnGluGluGluGluAlaAaRgAaRgTGLUGLInLyAaRgLeu	1560
Db	5143	CACAAAGTGCAGGACACACAGAGAGAAAGAGAGGCGCGCGGAGAGAGAAAGGCGCTTA	5202
QY	1561	ArgAaRgLeuGlnLyvLyAaRgAaRg-----LyAaGlnCyLyS	1573
Db	5203	CGAAAGCTGGAGAAAAGAAAGAAAGTAAGAGAAACAGATGGCTGAAGCCCAAGTGCADA	5266
QY	1574	ProTyTySeRaPtySeRaRgPheArGLeuLeuValNLHisLeuCyThSeRHis	1593

Db	5263	CTTACTACTCCGACTCTCCCGCTCCGCTCTCCGCTCCACCACTTGTGCACCAAGCAC	5322
QY	1594	TYRLEUASPHEUPHEIIEHNGIYVALIEGIYLEUANVALVALTHRMETALAMECGLU	1613
Db	5223	TACTGGACCTCTTCATCACAGGTCATCGGGCTGAACGGTGCACCATGGCCATGAG	5382
QY	1614	HISYRGLINGINPROGINIIIELEUASGLUNALAEUYSIIECYASANTYRIIEPHETHR	1633
Db	5383	CACATACAGACGCCCGAGATTCTGGAGTAGGCTTGAAGATCTGCACATCATCTTCACT	5442
QY	1634	VALIEPHEVALIEUGUSERVALIPIHEIYIEUVALIALPHEGIYPIHEARGYPHEPHE	1653
Db	5443	GTCACTCTTGTCTTGGAGTCAAGTTTCAACTTGTGGCCCTTGGTTTCCGCGSCTTCTC	5502
QY	1654	GLNAPARTGTTPAENGINLEUASPHEUALALIEVALLEUUSERIIEMETGIYIETHR	1673
Db	5503	CAGACAGGTGGACCAAGCTGCAGCTGCAGCTTGTGCTGCTGCATCATGGGCATACG	5562
QY	1674	LEUGLUGLUIEGIUVALASNAIASERIEUPROILEASPROMRIIEIIEARGIIMET	1693
Db	5563	CTGAGAGAAATCGAGGTCAACGCTCGCTGCCATCAACCCACATCATCCGATCATG	5622
QY	1694	ARGVALLEUARGIIEALAEYVALIEUYSLEUENUSMETALAVAGIYMETARGIILA	1713
Db	5623	AGGGTGCTGGCATTTGGCCCGAGTCTGTAGCTGTGAAGATGCTGTGGCATGGGGCG	5682
QY	1714	LEUENUSPETHRVALMETGINALAEUPROGINVALGIYASNLEUGIYLEUENUPHEMET	1733
Db	5683	CTGCTGCAGACAGGTGATGACAGGCCCTCGCCACAGGTGGGAACTGGGACTTCTTCATG	5742
QY	1734	LEULEUPHEPHEIIEPHEALALAEUGIYVALIGULEUPHEGIYASPLEUGIUCYASAP	1753
Db	5743	TTGTGTTTTTCATCTTTGACGCTCTGGCGCTGAGCTCTTTGGAGACTTGGAGCTGTGAC	5802
QY	1754	GLUHPHISAPCYSGIUGIYLEUGIYARHISALATHRPHEARGASNPHEGIYMETALA	1773
Db	5803	GAGACACACCCCTGTGAGGCGCTGAGCGCTGATGCACITTCGAACTTTGGCATGGCC	5862
QY	1774	PHLEUTHRLEUPHEARGVALSERTHGIVASPAANTRPANCIYIIMETLYSAPETHR	1793
Db	5863	TTCTTAACCTCTTCCAGTCTCCACAGTGCACAAATTGGATGGATTATGAAGACAC	5922
QY	1794	LEUARGAPCYASAPGINLUSERTHRCYSYRYSANTHRVALIIESEPROIIEYRPHET	1813
Db	5923	CTCGGGAGCTGTGACAGAGATCCACCTGCTACAAACGGTCACTCCCATCTACTT	5982
QY	1814	VALSERPHEVALIEUTHRALAGINPHEVALIEUVALASNVALVALIIEALVALIEUMET	1833
Db	5983	GTGTCTTCTGTGCTGACGCGCCAGTCTGCTAGTCAACGTGTGATGCCGTGCTATG	6042
QY	1834	LYSHISLEUGIUGIUSERASNLISGLUNALAYSGIUGIUALIGIUEUGIUALAGIULEU	1853
Db	6043	AAGCACTCGAGAGAGAGACAAGAAGGCCAAGGAGAGGCCGAGCTAGAGAGCTGAC	6102
QY	1854	GLUUEUGIUMETLYETHRLEUSERPROGINPROHISERPROLEUGIYSERPROPHLEU	1873
Db	6103	GAGCTGAGATGAAGACCTCTCAGCCCCACAGCCCACTCGCCACTGGGAGGCCCTTCTC	6162
QY	1874	THRPROGIYVALIGIUGIYPROASPSETPROASPSETPOLYASPROGIYALAEUHIAPRO	1893
Db	6163	TGGCTGTGGGTGAGAGGCCCGACAGCCCCACAGCCCAAGCCCTGGGGCTCTGCACCA	6222
QY	1894	ALAALAHSAIARYSERIASERHISPHESERLEUGIUNHISPROTHMETGINPROHIS	1913
Db	6223	GCGGCCACCGAGATCAAGCTCTCCACTTTTCCCTGAGACACCCACGATCGAAGCCAC	6282
QY	1914	PROTHRGIUEUPROGIYPROASPHEUETHRVALARGIYSESGIYVALISERHGTHT	1933
Db	6283	CCCAAGGAGCTGCACGACACTTACTGCTGTGCGAAGTCTGGGGTCAAGCCGAACG	6342
QY	1934	HISSERIEUPROANASPSETHYMETCYARHISGLIIESETHRALAGIUGIYPROLEU	1953

Db 6343 CACTCTGCGCAATGACAGCTACATGTGTGGCATGGAGACATGCGGAGGCGCCCTG 6402  
QY 1954 GYHIAARGIGLYTPGLYEUPOLYGAAGINSERGLYSERVALHEUSER 1973  
Db 6403 GGACACAGGGGGCTGGGGGGCTCCCAAGGCTCACTGAGGCTCCCTGTCCTGCTCACTCC 6462  
QY 1974 GINPRALASPHRISERTYRILEUGINLEUPROLYSAPALPROHISLEUGIN 1993  
Db 6463 CAGCCGACAGATTCAGACTACATCTGCACTTCCCAAGATGACACTCATCTGCTCCAG 6522  
QY 1994 PROHISERIALPROTHRTIPGLYTHRIEPROLYSEUPROBPROGLYARGSERPRO 2013  
Db 6523 CCCCACAGGCGCCCAACTGCGGAGCAACATCCCAATGCGCCCAACAGGAGCGCTCCCT 6582  
QY 2014 LEUALGIMARGPROLEUARGAGINAAIAAIIAARGTHRASPERLEUASPVALGIN 2033  
Db 6583 TTGGCTCAGAGGCGCTCAGGCGCCGAGGACGAGATAGAGCTGACCTTGGACGTTGAG 6642  
QY 2034 GLYLEUGLYSERARGIUSAPLEUAEUALAGLUALSERGLYPROSERPROFOLAEUALA 2053  
Db 6643 GGTCTGGGCGAGCGGGAAGACCTGCTGGCAGAGTAGTAGGCGCTCCCGCCCTGGCC 6702  
QY 2054 ARGALATYSERPHETIPGLYINSERSETHGINALAGINHIISERARGSERHIS 2073  
Db 6703 CGGGCCCTACTCTTCTGGGGGCGAGTCAAGTACCCAGGACAGCAGCACTCCGCGACGAC 6762  
QY 2074 SETLYELLISERTYSHISWETHRPROFROLAPROCYEPROGLYPROGLUPROANTTP 2093  
Db 6763 AGCAAAATCTCCAGACATGAGACCCCGGACGCTTGGCCCAAGGCCCAAGAACCACTGG 6822  
QY 2094 GLYLEUGLYPROPROGLUPTHARGSERSETHLEUGIUEUASPETHRGILEUSERTPILE 2113  
Db 6823 GCGAAGGCGCTCCAGAGACCAAGACAGCTTGAAGTGGACACGAGCTGAGCTGATT 6882  
QY 2114 SERGLYASPLEUENUPROPROGLYGLYINGIUGLUPROBROSERPROARGAPLEULYS 2133  
Db 6883 TCAGAGAGACCTCTGCGCCCTGGCGGCGAGAGAGAGGCCCATCCCAAGGAGCTGAGAG 6942  
QY 2134 LYSCEYTYRISERVALGILUALGINSECYSGILNARGARGPROTHRSETRPLEUASPGLU 2153  
Db 6943 AATGTCTACGCGCTGAGAGGCGCCAGACCTGCGAGCGCGGCTACGCTGCTGATGAG 7002  
QY 2154 GINARGRGHISERTILEALVALSERCYSEUASPSEGLYSERGINPROHISLEUGLY 2173  
Db 7003 CAGAGAGACACTTATCGCGCTGACGCTGGAACGCGGCTCCCAACCCACCTGGGC 7062  
QY 2174 THRASPPOSERANLEUGIYGLYINPROLEUGLYGLYPROGLYSEARGPROLYS 2193  
Db 7063 ACAGACCCCTTAACCTTGGGGGCGCAGGCTCTTGGGGGGCGCGGAGCGGCCCAAGAAA 7122  
QY 2194 LYSLEUSERPROBROSERILETHRIIEAPPROPROGLUINGLYPROAGTHTRPRO 2213  
Db 7123 AAACCTAGCCCGCTGATACACCATAGACCCCGGAGGCCAAGCTCTCGACCCCG 7182  
QY 2214 PROSERPROGLYILECYSEUARGARGALAPROSERSEZASPERLYSAPPROLEU 2233  
Db 7183 CCGAGCGCTGATCTGCGCTCCGGAAGAGGCTCCGTCCAGCAGCACTCCAAAGATTCCTTG 7242  
QY 2234 ALASERGLYPROBROSPSERMETALALASERPROSERPROLYSAPVALLEUSER 2253  
Db 7243 GCCTCTGGCGCCCTTACAGCATGCTGCTCGCTCCCAAGAAAGATGTGTAAGT 7302  
QY 2254 LEUSERGLYLEUSERSERAPPROALAAPLEUASP 2266  
Db 7303 CTCTCGGTTATCTCTGACCCAGACGACCTGACCC 7341

RESULT 3  
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; Sequence 3859, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 3859  
; LENGTH: 7405  
; TYPE: DNA  
; ORGANISM: Human  
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Pred. No.: 0 Length: 7405  
Score: 11241.00 Matches: 2162  
Percent Similarity: 95.12% Conservative: 1  
Best Local Similarity: 95.07% Mismatches: 1  
Query Match: 94.43% Indels: 110  
Gaps: 4  
  
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QY 21 Argleuaspseuaseuerglyalaglilyargprogliproglyseralagluyasap 40  
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QY 41 Progliseralaaspserglualaglilyleuprotyrproalaleualaprovalval 60  
Db 493 CCGGCGAGCGCGGACTCCAGGCGGAGGGGCTGCTACCGCGCTGCGCCGGTGTT 552  
QY 61 Phepetyrleuserglunaspserargproargsertrpcysleuargthryalcyasap 80  
Db 553 TTCTTCTACTTGAACAGGACAGCGCGCGCGAGCTGCTGCTCCGACGCTGTAAAC 612  
QY 81 Pro---TrrpghgluargllesemetleuallileuleuasnCyvalthrlengly 99  
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QY 100 Metpheargprocyeglunaspillealacysaspserglunargcysarglleuagluala 119  
Db 673 ATGTTCCGGCCATGAGAGACATGCGCTGTGATCTCCAGCGCTGCGGATCTGCAAGGC 732  
QY 120 Pheaspaspheillephealphehealavallguetvalvallymetvalaleu 139  
Db 733 TTTGATGACTTATCTTTCCTTTCCTTTCGCGGAGATGGGTAAAGTGTGCTTG 792  
QY 140 GYIIEPHEGLYLYSECYSEYTRLEUGIYASPTTRTPASNARGLEUASPHEHEIIE 159  
Db 793 GGCATCTTGGAAAAAGTTTACCTGGAGACACTTGAACCGGCTTCACTTTTCATC 852  
QY 160 Valillealaglmetleuglutyserleuaspseuasnvalaserpheseralaval 179  
Db 853 GTCATCGAGGGAATGCTGAAGTATCGCTGACCTCGAGAACGTAGCTTCACTGTC 912  
QY 180 Argthryalargvalleuargproleuargalalleasnargvalprosermetargille 199  
Db 913 AGGACAGTCCGTGTGCTGACCGCTCAGGGGCATTAAACCGGCTCCAGCATGCGCATC 972  
QY 200 Leuvalthrlleuleuasnspthrlleuprometleuglyasnvalleuleuencysphe 219  
Db 973 CTGTGACGCTTGTCTGTGATACGCTGCGCCATGCTGGGCAAGTCTGCTGCTGCTTC 1032  
QY 220 Phevalphepheillephegllylevalglyvalginleutrpallaglyleuleuargasn 239



D	1033	TTCTCTTTCTTCATCTTCGCGATCTCGGCTCCAGCTGTGGGAGGGGCTTCGGAAC	1092
Q	240	ArgCysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyr	259
D	1093	CGATGCTTCCTACCTGAGAAATTTCAAGCTCCCTCGAGCGGTGACCTGGAGCGCTATTAC	1152
Q	260	GlnThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMet	279
D	1153	CAGCAGAGAAACGAGATGAGAGCCCTTCATCTGCTCCAGCCACCGAGAAAGGAGATG	1212
Q	280	ArgSerCysArgSerValProThrLeuArgGluAspGluGlyGlyProProCysGly	299
D	1213	CGGCTTCGAGAAACGATGCCACCTGGCGGGAACGGAGGCGGTGCCACTTGGCGGT	1272
Q	300	LeuAspTyrGluAlaTyrAsnSerSerSerAsnThrCysValAsnTyrAsnGlnTyr	319
D	1273	CTGGACATATAGGCGCTTCACAAGCTCCAGAACACACACTGTGTCACTGGAACTGATAC	1332
Q	320	TyrThrAsnCysSerAlaGlyGluHisAsnProPheIleGlyAlaIleAsnPheAspAsn	339
D	1333	TACACCAACTGCTCAGCGGGGAGACACACCTTCAAAGGCGCCATCACTTGGACAC	1392
Q	340	IleGlyTyrAlaTyrPileAlaIlePheGlnValIleThrLeuGluGlyTyrPvalAspIle	359
D	1393	ATTGGCTATGCTGTGATCGCATCTTCAGGTCATCAGCTGAGAGGCTGGGTGACATC	1452
Q	360	MetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle	379
D	1453	ATGACTCTTGTGATGATGCTCATTTCTTCACAATTCTCATCTTCACTCTCTCATC	1512
Q	380	IleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSer	399
D	1513	ATCTGGGCTCTCTTCATGATCAACCTGTGCTGGTGGATGGACAGCACTTCTCA	1572
Q	400	GluThrTyrGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsn	419
D	1573	GAGCCAGACGCGGGAAGCAGCTGATGCGGAGCAGCGTGGCGGTTCTTCCAAC	1632
Q	420	AlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuTyr	439
D	1633	GCCAGCACCTCGGCTAGCTTCTTGAGCCCGGACGCTGCTATGAGAGCTGCTCAATAC	1692
Q	440	LeuValTyrIleLeuArgValAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGly	459
D	1693	CTGCTGATACATCTTCGTAAAGCAGCCGCGAGCTGAGTCTCGGGGACGAGGT	1752
Q	460	ValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSer	479
D	1753	GTGGGGGTGGGCTGCTCAGCAGCCAGCACCTCGGGGGCCAGAGAACCCAGCCAGC	1812
Q	480	SerSerCysSerArgSerHisArgArgLeuSerValHisIleAsnValHisIleHis	499
D	1813	AGCAGCTGCTTCTGCTCCACCGCGCTTATCTCTCCACCACTGGTGGACACACACAC	1872
Q	500	HisHisIleHisIleGlyTyrHisIleGluIleAsnGlyThrLeuArgAlaProArgAlaSerPro	519
D	1873	CACCATCAGCACCACTACCACTGGGCAATGGAGCGCTCAGGGCCCCCGGGGACGCGG	1932
Q	520	GluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThr	539
D	1933	GAGATCCAGGACAGGATGCGCAATGGGTCCCGCGGCTCATGCTGCCACCTTCAGC	1992
Q	540	ProAlaLeuSerGlyAlaProProGluValAlaGluSerValHisSerPheTyrHisAla	559
D	1993	CTTGCCCTCTCGGGGCCCCCTGTGTGGCGCAGAGTGTGTGCACAGTTTACATGCC	2052
Q	560	AspCysHisIleGluProValArgCysGlnAlaProProProArgSerProSerGluAla	579
D	2053	GATGCGCACCTTAGAGCAGTCCGCTGCAGAGCGCCCTCCAGATGCCCATCTGAGGCA	2112
Q	580	SerGlyArgThrValGlySerGlyValTyrProThrValHisThrSerProProPro	599
D	2113	TCGGCAGAGCTGTGGGACGGGGAAGTGTATCCACCGTGCACACAGCCCTCCAGCC	2172
Q	600	GluThrLeuIleGlyGlyValAlaLeuValAlaAlaSerSerGlyProProThrLeu	619
D	2173	GAGACCTGAAAGAGAGGACATGATGAGGTGGCCAGGCTTGGGCCCCCAACCTTC	2232
Q	620	ThrSerLeuAsnIleProProGluProTyrSerSerMetHisIleValLeuGluThrGln	639
D	2233	ACCAAGCTCAACATCCACCCGGGCTTACAGTCTCATATGACAAAGTCTTGAGAACAG	2292
Q	640	SerThrGlyAlaCysGlnSerSerCysIleSerSerProCysLeuIleAspSer	659
D	2293	AGTACAGGTGCTCGCAAGAGCTTTCAGAGATCTCCAGCCCTTGTGAAGACAGACGT	2352
Q	660	GlyValCysGlyProAspSerCysProTyrCysAlaArgAlaGlyValGlyValGlu	679
D	2353	GGAGCTGTGTGTCAACAGCTGCCCCCTCTGTGGCCGGGCGGAGGAGGGAGGAG	2412
Q	680	LeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAsp	699
D	2413	CTGCCGACCGTGAATGCTGACTGACAGACGAGGACAGTTTATAGTTCAACAGAT	2472
Q	700	AlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAsp	719
D	2473	GCCACGACAGCAGCACTCCGGGACCCCAACAGCCGCGGGAACGAGCTGGGCCAGAT	2532
Q	720	AlaGluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgIle	739
D	2533	GCAAGGCCAGCTGTGCTGCGCTTCTGGAGGCTATGTGACACCTTCCAAAGATT	2592
Q	740	ValAspSerTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer	759
D	2593	GTGAGCAGCAAGATCTTGGCGGGAATATATATGCACTTGATCAACACATCAGC	2652
Q	760	MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn	779
D	2653	ATGGGATCGAATACACAGCAGCGCCGAGACTTACCAAGCCCTTGAATACAGAAC	2712
Q	780	IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuIleLeuValTyrGlyPro	799
D	2713	ATCGTCTTACACAGCTCTTGGCCCTGGAGATCTGTAAGCTGCTGTGTATGTGCC	2772
Q	800	PheGlyTyrIleIleAsnProTyrAsnIlePheAspGlyValIleValIleSerVal	819
D	2773	TTTGGCTAACATCAAGATCTTCAACATCTTGATGTGTCAATGTGTGATCAGCGTG	2832
Q	820	TyrGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet	839
D	2833	TGGAGATCTGGGCGACAGGGGGGGCGGCTGTGGGTGCGGACCTTCGGCTGATG	2892
Q	840	ArgValLeuIleLeuValArgPheLeuProAlaLeuGlnArgGluLeuValIleMet	859
D	2893	CGTGTGTAAGCTGGGGGCTTCTCGCGGCGCTCAGCGGAGCTGGGTGATCATG	2952
Q	860	LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe	879
D	2953	AAAGACATGGAACAAGTGGCACTTCTGATCTCTTAATGTCTTCACTTCACTTCTC	3012
Q	880	SerIleLeuGlyMetHisIleLeuPheGlyCysIlePheAlaSerGluArgAspGlyAspThr	899
D	3013	AGCATCTGGGATGATCTCTTCGGCTGCAATTTTCCCTTGAAGCGGATGGGACACC	3072
Q	900	LeuProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIle	919
D	3073	CTGCGACAGCCGGAAGATTTTGACTCTTGTCTGTGGGCATCGTCACTGCTTCAATC	3132
Q	920	LeuThrGlnGluAspTyrPheAsnLysValLeuTyrHisGlyMetIleAspThrSerSerTyr	939
D	3133	CTGACCCAGAGAGATCGGAACAAAGTCTTCTTAACATGTATGCTTCCACGTCGTCTG	3192
Q	940	AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu	959
D	3193	GCGGCTTTATTTCAATGCTTCATGACTTGGCACTACGTGCTTCAATTTGCTG	3252

Oy	960	ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer	979
Db	3253	GTCCGCAATTCCTGGTGAAGGCGCTTCAGCGCGAG-----	3285
Oy	990	GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSer	999
Db	3286	-----GGAGATGCCAACAAGTCC	3303
Oy	1000	GluSerGluProAspPhePheSerProSerLeuAspGlyAspArgLysAlaCys	1019
Db	3304	GAATCAGAGCCCGAATTTCTTCTCAACCCAGCTGGATGTGTATGGGGACAGGAAGAATGCG	3353
Oy	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeu	1039
Db	3364	TTGGCTTGTGTGCTCCCTGGGAGAGACCCGGAGCTGCGGAAGACCTGCTCCCTCTC	3423
Oy	1040	IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly	1059
Db	3424	ATCATCCACAGCGCCGACACCCATGTGCTGGCCCAAGACACACAGCAGGCGCTGGGC	3483
Oy	1060	GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla	1079
Db	3484	GAGGGCGTGGGCGCTGGCGTGGCGGACACAGACAGACGGGGTGGACAGACTGGGGCG	3543
Oy	1080	AlaHisGluMetLysSerProProSerAlaArgSerSerProHisSerProTyrSerAla	1099
Db	3544	GCCCAACGAGATGAAGTCAACCCGCCCGCCCGCAGCTTCCGCACAGCCCTCGAAGCGCT	3603
Oy	1100	AlaSerSerTyrThrSerArgSerSerArgAsnSerLeuGlyArgAlaProSerLeu	1119
Db	3604	GCAAGCACTGGACCAAGAGGCGCTCCAGCCGGAAACAGCTTCGGCCGTGCACCAAGCTTG	3663
Oy	1120	LysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnLys	1139
Db	3664	AAGCGAGAGAGCCCAAGTGAAGAGCGCGGTCCCTGTTGTCCGGAAGAGGCCAGAGAGGC	3723
Oy	1140	GlnAspGluGluGlnLysSerSerGluGluGlnArgAlaSerProAlaGlySerAspHisArg	1159
Db	3724	CAGGATGAAGAGAGAGCTCAGAAAGAGAGGGCGCACCTTCGGCGAGTGAACATTCGC	3783
Oy	1160	HisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGln	1179
Db	3784	CACAGGGGGTCCCTCGAGCGGGAAGGCCAAGAGTTCTTTGACTTGCACAGACACTGCAG	3843
Oy	1180	ValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCys	1199
Db	3844	GTGCCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGCTGTGTTTGAGCACCAAGACTGC	3903
Oy	1200	AsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeu	1219
Db	3904	AATGGCAAGTGGGCTTCAAGGGCGCTGGCCCGGGCCCTGATGAAGACCCCCCACTG	3963
Oy	1220	AspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTyr	1239
Db	3964	GATGGGATGACGCCGATGACGAGGGCACTTGAGCAAGGGAGAACGGGTCCGGCGCTGG	4023
Oy	1240	IleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTyrSerAlaTyrIlePhe	1259
Db	4024	ATCCGAGCCGACATCCCTGCTGCTGCTGCAGAGCAAGACTCTCGTATGACTTATCATCTTC	4083
Oy	1260	ProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAsp	1279
Db	4084	CCTCTCTAGTCCAGGTTCCGGCTCTGTGTACCCGAGATCAACCAACAAATATTGGAC	4143
Oy	1280	HisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLys	1299
Db	4144	CACGTGATCTTGTATCATCTTCTTAACTGCATCAACATCGCCATGAGCGCCCCAA	4203
Oy	1300	IleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAla	1319
Db	4204	ATTGACCCCCACAGCGCTGAAGCATCTTCTTCGAGCCCTTCCAATATCATCTTCACCGCA	4263

QY	1320	ValPheLeuEua1aG1wMeThrrValIysValAlaLeuG1yTTPCySPheG1yG1uG1n	1339
Dp	4264	GTCCTTTTCGCTGCTGAAAAGACAGAGAGAGTGTGTGCATCTGGGCTGTGTCTTCGGGGAGACAG	4323
QY	1340	AlaTyrLeuLysRGSerSerTTPaSnValLeuASpG1YLeuLeuValLeu1LeSerVal1Le	1359
Dp	4324	GCGTACCTGGGAGACATTGGAAAGCTGTCTGGACGGGCTGTGGTGTCTCATCTCCGTATTC	4383
QY	1360	Asp1LeuValSerMeTVal1SerASPSeG1YThrrLys1LeLeuG1yMeLeuArgVal1	1379
Dp	4384	GACATTCCTGGGTGTCTATGATCTGTGAACAGCGGACCAAGATCTCGGGCATGTGAGGGGTG	4443
QY	1380	LeuArgLeuLeuArgThrrLeuArgProLeuArgVal1LeSerArg1aG1nG1yLeuLys	1399
Dp	4444	CTGGGCTGTGTGGGAGACCTTCGGCCGCTCAGGGGTATTCAGCGGGGAGGGGCTGTAAG	4503
QY	1400	LeuValValG1uThrrLeuMeTSeSerSerLeuLysPro1LeG1yAsn1LeVal1LeCys	1419
Dp	4504	CTGGTGGTGGAGACCTGATGTCTCTCATTAACCCATCCGGCAACATTGTATGTATCTGC	4563
QY	1420	CysAlaPhePhe1Le1LePheG1y1LeLeuG1yValG1nLeuPheLysG1yLysPhePhe	1439
Dp	4564	TGTGCTCTTTCATCATTTTGGGATCTTGGGGGTGAGCTTTCAAAGGAAGTTTTC	4623
QY	1440	ValCysG1nG1yG1uAspThrrArgAsn1LeThrrAsnLysSerAspCysAlaG1uAlaSer	1459
Dp	4624	GTCGGCCAGGGCGGAGATACAGAGACATCAACAATTAATCGACTGTGTCCGAGGCCAGT	4683
QY	1460	ThrrArgThrrAlaArgHisLysTyrAsnPheAspAsnLeuG1yG1nAlaLeuMeTSeLeu	1479
Dp	4684	TACCGGTGGGTCCGGACAGATGCACATTGTGACAACTTGGCCAGGGCTGTATGTCCCTG	4743
QY	1480	PheValLeuAlaSerLysAspG1yTrrPValAsp1LeMeTyrAspG1yLeuAspAlaVal1	1499
Dp	4744	TTGCTTTTGGCTCCAGAGATGTGTGGTGTGACATCATATGACATGGGCTGGATGTGCTG	4803
QY	1500	GlyValAspG1nG1nPro1LeMeTAsnHisAsnProTrrPMeLeuLeuTyrPhe1LeSer	1519
Dp	4804	GGCGTGGACGAGCCCATCATGAACCAACCCCTGGATGTGTCTGTATCTTCATCTCG	4863
QY	1520	PheLeuLeu1LeValAlaPhePheValLeuAsnMeT-PheValG1yVal1Val1G1uAsn	1539
Dp	4864	TTCTGCTCATGTGGGCTTCTTGTCTCTGAACATGTTTGTGGTGTGGTGTGGAGAAC	4923
QY	1540	PheHisLysCysArgG1nHisG1nG1uG1uG1uAlaArgArgArgG1uG1uLysArg	1559
Dp	4924	TTCCACAAAGTGTGGGACGACACACAGAGAAAGAGAGGCCCGCGCGCGAGAGAAAGCCG	4983
QY	1560	LeuArgArgLeuG1uLysLysArgArg-----LysAlaG1nCys	1572
Dp	4984	CTACGAAGACTGGAGAAAAGAGAGAGATGTAAGAGAAAGACATGTGCTGAAGCCCAATGC	5043
QY	1573	LysProTrrTyrSerAspTrrSerArgPheArgLeuLeuValHisHisLeuCySerThrSer	1592
Dp	5044	AAACCTTACATCTCCGACATCTACCTCCCGCTTCGCGCTCTCTGCACCACTTGTGCACAGC	5103
QY	1593	HisTrrLeuAspLeuPhe1LeThrrG1Val1LeG1yLeuAsnVal1ThrrMeTAlaMeT	1612
Dp	5104	CACATCTGGACCTCTTCATCACAGAGGTGATGTGGGCTGAACCTGTGTACACATGAGGCATG	5163
QY	1613	GluHisTrrG1nG1nProG1n1LeLeuAspG1uAlaLeuLys1LeCyAsnTrr1LePhe	1632
Dp	5164	GAGACATACAGAGAGCCCAAGATTCGTGATGAGGCTCTGAAGAATCTTGCACTCATCTTC	5223
QY	1633	ThrrVal1LePheValLeuG1uSerValPheLysLeuValAlaPheG1yPheArgArgPhe	1652
Dp	5224	ACTGTCACTCTTGTCTTGGAGGTCAATTTCAAACTTGTGGCTCTTGGTTTCCTCGGTTC	5283
QY	1653	PheG1nAspArgTrrTPaSnG1nLeuAspLeuAla1LeValLeuLeuSerTrr1LeMeTG1yLe	1672
Dp	5284	TTCCAGAGACGGTGGAAACCAAGCTGGACCTGGCAATGTGCTGTCTTCATCATAGGGCATC	5343
QY	1673	ThrrLeuG1uG1uLeG1uValaSnAlaSerLeuPro1LeAsnProThrr1Le1ArgG1Le	1692

Db 5344 ACCGTGAGGAAATCGAGTCAAGCTCGCTGCCATCAACCCACCACTCATCCGATC 5403  
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 1713 AlaLeuLeuLeuLeuValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPhe 1732  
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 Db 5824 ATGAAGACCTCGAGAGAGACCAAGAGGCGAAGAGGCGGAGCTGAGAGGCTGAG 5883  
 1853 LeuGlnLeuGlnLysLeuSerThrLeuSerProGlnProHisSerProLeuGlySerProPhe 1872  
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 1873 LeuTrpProGlyValGlnGlyProAspSerProAspSerProLysProGlyValAlaLeuHis 1892  
 Db 5944 CTCTGGCTGTGGGTGAGAGGCGCCGACAGCCCGACAGCCCAAGCCTTGGGGCTCTGCAC 6003  
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 Db 6004 CCAAGCGGCCACGGGAGATGAGCTCCCACTTTTCCCTGGAGACCCCAAGATGACAGCC 6063  
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 Db 6064 CACCCCAAGGAGCTGCGACGACCACTTGACTGTGCGAAGTCTGGGGGTACGCCGA 6123  
 1933 ThrHisSerLeuProAsnAspSerLysMetCysArgHisGlySerThrAlaGlnGlyPro 1952  
 Db 6124 ACGCACTCTCTGCCCAATGACACTAATGTGTGGCATGGAGACACTGCCGAGGGGCC 6183  
 1953 LeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHis 1972  
 Db 6184 CTGGGACACAGGGGCTGGGGGCTCCCAAAAGCTCAGTCAGGCTCGTCTTGTCTGCATC 6243  
 1973 SerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeu 1992  
 Db 6244 TCCAGGCGACAGATACCACTCATCTGACGTTCCCAAAAGATGACCTCATCTCTCTC 6303  
 1993 GlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProProGlyArgSer 2012  
 Db 6304 CAGCCCAACAGCGGCCCACTGGGGCACATCCCAAACTGCCCAACAGGACGCTCC 6363  
 2013 ProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspVal 2032  
 Db 6364 CTTTGGCTCAGAGGCACTCAGGCGGCGACGAATPAAGACTGACTCTTGAGACGTT 6423  
 2033 GlnGlyLeuGlySerHisArgGlnAspLeuLeuAlaGlnValSerGlyProSerProLeu 2052

Db 6424 CAGGCTGTGGGACCGCGGGAAGACTGTGCGAGAC----- 6459  
 2053 AlaArgAlaTrpSerPheTrpGlyGlnSerSerThrGlnAlaGlnHisSerArgSer 2072  
 Db 6459 ----- 6459  
 2073 HisSerLysIleSerLysHisMetThrProProAlaProCysSerProGlyProGlnProAsn 2092  
 Db 6459 ----- 6459  
 2093 TrpGlyLysGlyProProGlnThrArgSerSerLeuLeuAspThrGlnLeuSerTrp 2112  
 Db 6459 ----- 6459  
 2113 IleSerGlyAspLeuLeuProProGlyGlyGlnGlnGlnProProSerProAlaAspLeu 2132  
 Db 6460 -----GAGAGACCCCAACCCCAAGGACCTG 6486  
 2133 LysLysCysThrSerValGlnAlaGlnSerCysGlnArgArgProThrSerTrpLeuAsp 2152  
 Db 6487 AAGAGGTGCTACAGCGCTGAGAGGCCCAAGCTGCGAGCGCGCGGCGCACTGCTGGAT 6546  
 2153 GlnGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeu 2172  
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 Db 6607 GGCACAGACCCCTCTAACCTTGGGGGCGCAGCCCTTGGGGGCGCTGGAGCGCGCCAG 6666  
 2193 LysLysLeuSerProProSerIleThrIleAspProProGlnSerGlnGlyProArgThr 2212  
 Db 6667 AAAAACTCAGCGCGCTGATGATCACCATTAGACCCCGAGAGCCAAAGTCTCGGACC 6726  
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 2233 LeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeu 2252  
 Db 6787 TTGGCTCTGGCCCGCTGACAGACTGCTGCTCGCCCTCCCAAAAGATGTGCTG 6846  
 2253 SerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266  
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 6888  
 RESULT 4  
 US-09-398-522-51  
 : Sequence 51, Application US/09398522  
 : Patent No. 6783933  
 : GENERAL INFORMATION:  
 : APPLICANT: Issa, Jean-Pierre  
 : TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND  
 : TITLE OF INVENTION: METHODS OF USE THEREFOR  
 : FILE REFERENCE: JHU1590  
 : CURRENT APPLICATION NUMBER: US/09/398,522  
 : NUMBER OF SEQ ID NOS: 120  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 51  
 : LENGTH: 3993  
 : TYPE: DNA  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel  
 : FEATURE:  
 : NAME/KEY: CDS  
 : LOCATION: (373)...(3993)  
 : US-09-398-522-51  
 Alignment Scores:  
 Pred. No.: 0 Length: 3993  
 Score: 6315.50 Matches: 1207

Percent Similarity:	98.13%	Conservative:	0
Best Local Similarity:	98.13%	Mismatches:	23
Query Match:	53.05%	Indels:	0
DB:	4	Gaps:	1
US-09-611-257A-37 (1-2266) x US-09-398-522-51 (1-3993)			
QY	1	MetAspGluGluGluuAspGlyAlaGlyAlaGluGluSerGlyGluProArgSerPheMet	20
DB	373	ATGACAGAGAGAGAGATGAGCGGCGCCGAGAGATCGGAGACAGCCCGAGACTTTCATG	432
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluYAsp	40
DB	433	CGGCTCAACGACTGTCCGGGGGCGGGGGCGGGCGGGGGCGGGGTCAGAGAAAAGAGC	492
QY	41	ProGlySerAlaAspSerGlyAlaGlyGlyLeuProTyrProAlaLeuAlaProVal	60
DB	493	CCGGGAGCGCGGACTCCGAGGCGGAGGGGCTCCGTAACCCGGCGCTGGCCCGGTGGATT	552
QY	61	PhePheTyrLeuSerGluuAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
DB	553	TTCCTTACTTGAAGCAGAGAGACCGCCGCGAGCTGGTGCTCCGACCGATTGTAAAC	612
QY	81	ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
DB	613	CCCTGGTTGAGGCGAATCAGCAATGTTGTATCTCTTCAACTGCGTGAACCTGGGCATG	672
QY	101	PheArgProCysGluuAspIleAlaCysAspSerGluArgCysArgIleLeuGluAlaPhe	120
DB	673	TTCGGGCAATGAGGAGCATCGCTGTGACTCCAGGCGTGGCCGGAATCCTGCAAGGCTTT	732
QY	121	AspAspPheIlePheIlePhePheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	733	GATGACTTCAATCTTGTCTTTGCTTTGCCGTGAGATGGTGTGAAGATGGTGGCTTGGGC	792
QY	141	IlePheGlyLysIleCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal	160
DB	793	ATCTTTGGGAAAAGTTTAACTCGGAGACACTTGGAAACCGGCTTGACTTTTCAATGCTC	852
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGluAsnValSerPheSerAlaValArg	180
DB	853	ATCGCAGGAGATGCTGGAGTACTCGCTGAGCTCAGAACTCAGCTTCAAGCTGTACAG	912
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
DB	913	ACAGTCCGTGTGCGACCGCTCAGGCAATTAACGGGTGCCACAGCATGCCATCTT	972
QY	201	ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
DB	973	GTCACGTTGCTGCTGATACGCTGCCCATGCTGGGCAAGTCTGCTGCTGCTTCTTCTTC	1032
QY	221	ValPhePheIlePheGlyIleValGlyValGluLeuTyrAlaGlyLeuLeuArgAsnArg	240
DB	1033	GTCCTTCTTCACTTCGCGCATCGTCGGGCTCAGCTGTGGGCAAGGCTGCTTCCGAACCGA	1092
QY	241	CysPheLeuProGluuAsnPheSerLeuProLeuSerAlaAspLeuGluArgTyrTyrGln	260
DB	1093	TGCTTCTTACTTGAATTCAGCTCCCTCGTAGCGTGAACCTGGAGCGCTATATCCAG	1152
QY	261	ThrGluAsnGluuAspGluSerProPheIleCysSerGlnProArgGluuAsnGlyMetArg	280
DB	1153	ACAGAGAACAGAGATGAGAGCCCTTCACTGTCTCCAGCAGCAGCAGAAACGGCATGCGG	1212
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu	300
DB	1213	TCTCGCAGAGCGGCGCCACGCTGCGCGGGAGACGGGGCGGTGGCCCACTTCGCGTCTG	1272
QY	301	AspTyrGluuAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrPheAsnGlnTyrTyr	320
DB	1273	GACTATAGGCTTAACAACAGCTCCAGCAACCACTGTGTCAACTGGAAACGATGACTAC	1332
QY	321	ThrAsnCysSerAlaGlyGluuIleAsnProPheLeuGlyAlaIleAsnPheAspAsnIle	340

DB	1333	ACCAATGCTCAGCGGGGAGACAAACCTTCAAGGCGCCATCAACTTGAACAACATT	1392
QY	341	GlyTyrAlaTyrPheIleAlaIlePheGluValIleThrLeuGluGlyTyrProValAspIleMet	360
DB	1393	GGCTATGCTGATGCCATCTTCCAGGTCATACGCTGAGGGCTGGGTGCATCTATG	1452
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
DB	1453	TACTTTGGATGGATGCTCATTTCTTCAATTTCAATTTCACTTCACTTCTCTCATCATC	1512
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGluPheSerGlu	400
DB	1513	GTGGGCTCTTCTTCAATCACTGTGCTGGGTGGATGGCCACGACGTTCTCAAG	1572
QY	401	ThrLysGluuAspGluSerGluLeuMetArgGluGluAlaArgValArgPheLeuSerAsnAla	420
DB	1573	ACCAAGCAGGGGAAAGCCAGCTGATGGGAGACAGCTGTGCGATTCTGTGTCACGCC	1632
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGlyGluLeuLeuLysTyrLeu	440
DB	1633	AGCACCTGTGCTAGCTTCTGTAGCCCGGAGCTGTATGAGAGCTGTCAAGTACCTG	1692
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
DB	1693	GTGTACATCTTCTGTAGGCAAGCCCGCAGGCTGGCTCAGGTTCTTCGGGCAAGAGTGTG	1752
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGluGluuThrGluProSerSer	480
DB	1753	CGGGTGGGCTGTCAAGAGCCACACCTTCGGGGGCGAGAGAACCAACCCAGCAGCC	1812
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisIleHisHis	500
DB	1813	AGCTGTCTCGCTCCACCGCGGCTATCCGTCACCACTGTGTGACACACCAACACAC	1872
QY	501	HisHisHisHisTyrHisIleuGlyAsnGlyThrLeuAlaGluAlaProArgAlaSerProGlu	520
DB	1873	CATCAACCACTTCACTTCACTTGGCAATGAGAGCTCAGAGGCCCGGCGGCGGAG	1932
QY	521	IleGluAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro	540
DB	1933	ATCCAGAGAGAGAGATGCATATGATCCGCGGCTCATATGTCACCACTTCAGAGCTT	1992
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
DB	1993	GGCTTCTCGGGGCCCGCTGTGGCGGAGTGTGACAGCAAGCTTCAACATGCCGAC	2052
QY	561	CysHisIleuGluProValArgCysGluAlaProProArgSerProSerGluAlaSer	580
DB	2053	TGCCACTTAGACCAAGTCGCTGCCAGAGGCGCCCTCCAGGTTCCCATGTGAGGCATTC	2112
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu	600
DB	2113	GGAGGACTGTGGGAGCGGGAAGTGTATCCACCGTGACACACAGCCCTTCAACGGAG	2172
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
DB	2173	ACGCTGAAGAGAAAGCACTATAGAGGTGCTGCAGAGCTTGCGGCCCAACCTCAACC	2232
QY	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640
DB	2233	AGCTCAACATCCACCCCGGCTTACAGCTCCAGTGCAACAGCTCTGAGACACAGAT	2292
QY	641	ThrGlyAlaCysGluSerSerCysLysIleSerSerProCysLeuValAlaAspSerGly	660
DB	2293	ACAGGTGCTGCAAGCTCTTGCAAGATCTCAAGCCCTTGTAAGACAGACAGTGGCA	2352
QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680
DB	2353	GCTGTGTGCCAGACAGCTGCCCTACTGTGCTCCGGGCGGGGCGAGGAGGTGGAGCTC	2412
QY	681	AlaAspArgGluMetProAspSerAspSerArgAlaValTyrGluPheThrGluAspAla	700
DB	2413	GCCGACCGTGAATGCTGACTCAGACAGCGAGGAGTTATGATTCACACAGGATGCC	2472

QY 701 GlnHisSerAspLeuArgProHisSerArgTrgGlnArgSerLeuGlyProAspAla 720  
 DB 2473 CAGGACAGGCGACCTCCGGGACCCCGACAGCGCGGCGCAACGAGCCCTGGGCCCCGAGATGA 2532  
 QY 721 GluProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPheArgLysIleVal 740  
 DB 2533 GAGCCCGAGCTGTGGCTGGCTTCTGAGAGGCTAATCTGTACACCTTCCGAAAGATTGTG 2592  
 QY 741 AspSerLysTrpPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760  
 DB 2593 GACAGCAAGTACTTGGCCCGGGAATCATGATCCGCTCTGGTCAACACACTAGCATG 2652  
 QY 761 GlyIleGluTrpHisGlnGlnProGlnGluLeuThrAsnAlaLeuGluIleSerAsnIle 780  
 DB 2653 GGCATTCGAATACCCAGAGAGCCCGAGAGGCTTACCAACGCCCTAGAAATCAGCAATC 2712  
 QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTrpGlyProPhe 800  
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 QY 801 GlyTrpIleLysAsnProGlyTrpAsnIlePheAspGlyValIleValIleSerValTrp 820  
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 DB 2953 ACCATGACCAAGTGGCCACCTTCTGCAATGCTGCTTATGCTTTCATCTTATCTTACG 3012  
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 DB 3133 ACCCAGAGGAGCTGGAAACAAAGTCTCTTACAAATGATGGCTTCAAGCTCTTGGGCG 3192  
 QY 941 AlaLeuTrpPheIleAlaLeuMetThrPheGlyAsnTrpValLeuPheAsnLeuVal 960  
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 QY 961 AlaIleLeuValGlyGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980  
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 QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000  
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 QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaIle 1100  
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 QY 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160  
 DB 3724 GATGAAGAGAGAGCTCAAGAGAGAGCGGCGCACGCTGCGGCGAGTGCATCCGCAC 3783  
 QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180  
 DB 3784 AGGAGGTCCTTGAGCGGAGGCGCAAGATTCCTTGACTGCTGCACAGACACTGCAAGT 3843  
 QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGlnHisGlnAspCysAsn 1200  
 DB 3844 CCAGGCTGCATGCACCTGCAGTGCAGGCGCGAGGCTGTCTTGAGACACGAGCTGCAAT 3903  
 QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220  
 DB 3904 GGCATGTCGCTTCAAGGCGCTTGGCCCGGCGCTGCGGCTGCTGATACCCCCCACTGGAT 3963  
 QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeu 1230  
 DB 3964 GGGGATGAGCGCGATGACAGAGGCAACTG 3993

## RESULT 5

US-08-984-709A-49  
 ; Sequence 49, Application US/08984709A  
 ; Patent No. 6320032

## GENERAL INFORMATION:

; APPLICANT: Williams, Mark E.  
 ; APPLICANT: Stauderman, Kenneth A.  
 ; APPLICANT: Harpold, Michael M.  
 ; TITLE OF INVENTION: HUMAN CALCITONIN CHANNEL COMPOSITIONS AND  
 ; TITLE OF INVENTION: METHODS  
 ; NUMBER OF SEQUENCES: 52  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Heller Ehrman White & McCulliffe  
 ; STREET: 4250 Executive Square, Suite 700  
 ; CITY: La Jolla  
 ; STATE: California  
 ; COUNTRY: US

; ZIP: 92037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/984, 709A  
 ; FILING DATE: 02-DEC-1997  
 ; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Seidman, Stephanie L.  
 ; REGISTRATION NUMBER: 33,779  
 ; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 450-8400  
 ; TELEFAX: (619) 587-5360  
 ; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7898 base pairs

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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 249...7307
OTHER INFORMATION:
US-08-984-709A-49

Alignment Scores:
Pred. No.: 0 Length: 7898
Score: 6214.50 Matches: 1367
Percent Similarity: 65.17% Conservative: 212
Best Local Similarity: 56.42% Mismatches: 516
Query Match: 52.21% Indels: 328
DB: 3 Gaps: 59

US-09-611-257A-37 (1-2266) x US-08-984-709A-49 (1-7898)
QY 7 GLVALAGLVALAGLUGLUSERGILYINPROARGSERPHEWETARGLEUENASPLEUSER 26
DB 317 GGGGTTGGTGGGGGCGTCCCGAGAGCCCCG----- 349
QY 27 GLVALAGLYLYARGPROGLYPRO-GLYSER----- 36
DB 350 GGGCGCGGAGCGGAGGCGGAGCGGGGCTCCGAGCTCGGCGTGTCACTCCGAGAGCCC 409
QY 37 -----AAGLULYASPPROGLYSERIALASPSERGLUAGLUGLYLEUPROTYRPROAL 55
DB 410 GGGCGCGGAGCGGCGGAGCGGAGCTGGTCCGACGAGAGCAGCGGCTCCGATACCGGCG 469
QY 55 ALEUALAIPROVALIPHEPHERTYRLEUSERGINASERARGPROARGSERTRPCYSLE 75
DB 470 CTTGGCGGCGCAGCGTCTTCTTCCTCGCTCGGTACAGACCGCGCCGCGAGCTGGTCCCT 529
QY 75 UARGTHRALCYASNPOTRIPHEGLIARGILLESERMETLEUVALILEULEUENANCY 95
DB 530 CCGGCTGTCTGCAGACCCATGCTTCGAGACGCGAGCATGCTGTATCATCTCAACTG 589
QY 95 SVALTHRIEUGLYMERPHENARGPROCGUWASPILEALCYASPSERGLIARGYSAR 115
DB 590 CGGAGCCCTGGGATATGTCCGCGCTGTAGAGAGTGAAGTGGCGCTCCGAGCGCTGCAA 649
QY 115 GILELEUGINALAPHEASPAAPHEILEPHEALAPHEALAVAILUMETVALIY 135
DB 650 CATCTCGAGAGCTTTGACCGCTTCACTTTTCGCTTTTTCGCGTGGAGATGGTATCA 709
QY 135 SNETVALIALALEUGLYILEPHEGLYLYSILYSCYSTYRLEUGLYASPTHTRIPASNA 155
DB 710 GATGGTGGCGCTTGGGCGCTGTCGGGCAAGTGTACTGCGGTGACACGTGMAACAGCT 769
QY 155 UASPPHEPHEILEVALILEALAGLYMETLEUGLYTYRSERLIENASPLEUENALIS 175
DB 770 GGATTTCTTCATGTGTGGCGGCGGAGTGAAGTACTGTTGGAAGCAACAACCTGAG 829
QY 175 RPHESEALAVAILARGTHRVALARGVALILEUARGPROLEUARGALIASNAARGVAL 195
DB 830 CCTCTCGGCTATAGAGACCTGCGGAGTGTGCGGCGCCCTCCGCGCATCAACCGCTGCC 889
QY 195 OSERMETARGILELEUVALTHRLEULEUENASPTHTLEUPROMETLEUGLYASNA 215
DB 890 TAGCATAGCGGATCTGATCACTCTGCTGATGATAGTCCATCTCGGAGAACGTCTCT 949
QY 215 ULEULEUCYSPHEPHEVALPHEPHEILEPHEGLYILEVALIGLYVALILEUENAL 235
DB 950 TCTGCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1009
QY 235 YLEULEUARGASNAARGCYSPHELEUPROGLIENPHESERLIENASPLEUENAL 254

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DB 1010 CCTCTGGGAAACGCTGCTTCTTGACAGTGCCTTTGTACAGAACACAACTGACCTT 1069
QY 255 -LEUGLWARGTYRTRYRGINTHRGLIUSANGIUSPGLUSERPROPHIELIENASERGLIN 274
DB 1070 CTTGGCGGCGTACTTCCAGACGAGAGGAGGAGGAGAACCCGTTCATCTGCTCTTCAAG 1129
QY 274 OARGIUSANGIYMERFARGSERCYARGSERVALPRO-----THRLEUARGLYAS 291
DB 1130 CCGAGACACGAGCATGCAAGAGTCTCGCACATCCCCCGCGCGAGCTGGC----- 1184
QY 291 PGLYGLYGLYLYPROPCYSGLYLEUASPTYRGLIUALATYRASN----- 306
DB 1185 -----ARGCCTTGACCTCGGCGTGGAGGCTTACAGCAGCGCAGAGCCGA 1231
QY 307 -----SERSESERASNTHRTHCYVALASNTTPASNGINTYRTRYRASN 324
DB 1232 GGGGGTGGCGCTGACACCAACGCTGCATCACTGGAACAGTACTCAACGTGTGCCG 1291
QY 324 RLAGLYGLIUSANPROPHELYGLYVALILEASNPHEASPAANILEGLTYRVALAT 344
DB 1292 CTGGGTGACTCCACACCCCGACACGTTGCCATCACTTCACACATCGGCTACGCTG 1351
QY 344 PILEALALEPHEGINVALIETHRLEUGLGLYTRPVALSPILEMETYRPHENALWE 364
DB 1352 GATTCGCATCTTCCAGGTGATCAGCTGGAGAGCTGGGTGAGCATGATGACTACGTAT 1411
QY 364 CASPALAHISERPHETRYRASNPHIELIETRYRHEILEULEULEILEILEVALIGLYSER 384
DB 1412 GGACGCCCATCTATCTCAACCTTCATATTTCACTCTGCATCATCTGGGGTCTCTT 1471
QY 384 EPHEMETILEASNEUCYSELEUVALIILEALATHRGINPHESESGIUTHRGLINAR 404
DB 1472 CTTCTATGATCAACCTGTGCTGTGTGTGTATTCACGAGTTCTGGAGACGAACAGCG 1531
QY 404 GGLUSERGINLEUWETARGIUGLINARGVALIARGPHELEUSERAENALASERTHLEU 424
DB 1532 GGAGAGTACGTGATGCGGAGCAGCGGAGCAGCCACTGTCACACAGACAGCCTGGC 1591
QY 424 ASERPHESERGIUPROGLYSERCYSTRYGLIUSLEULEULYSTYRLEUVALIYRILE 444
DB 1592 CAGCTTCTCCGAGCTGCGACGTGTCTACGAAGTGTCTGAAGTACGTGGGCAATAT 1651
QY 444 UARGLYSALIAALAGARGLEUALAGIINVASERARGIILAGIYVALIARGVALIYLE 464
DB 1652 CCGCAAGGTCAACCGCGCGAGCTTGCCTTACGCCCGCTGCGAGACCGCTGGCGCA 1711
QY 464 ULEUSERSERPROALPROLEUGLYGLINGIUTHRGINPROSESRSERCYSERAR 484
DB 1712 GAAGGTGACCCCAAGTGTGTGCAAGGCCAG-----GATCCCGGAGCACCGCAGCCG 1765
QY 484 GSERHISARGARG--LEUSERVALIHISILEUVAL--HISHSIHISHSIHISHSI 502
DB 1766 GCGAGCGGAGCAGACAGCTCGGTGCACACCTGTGTACCAACCAACATCAACACCA 1825
QY 502 SHISHSIYRHSISLEUGLYANGIYTHRLEUARGIAPROARGALASERPROGLIULE 522
DB 1826 CACACATACATTTTCAAGCATGAGCAGCCCGCGAGCGCCCGCGAGACAGGCGCTG 1885
QY 522 NASPARGASPALAANGIYSEARGIARGLEUWETLEUPROPROSESRSERPROALALE 542
DB 1886 CGAC-----ACAGAGCTGTGCGAGACTGGCGGCGCCCTCGCCACACTTC 1930
QY 542 USERGLYALAPROPROGLYGLYALAGIUSERYALHISERPHETRYRHSIALASPCY 562
DB 1931 CCGAGCGCGGAGACCCCGAGCAGAGTGTGTGACAGCATCTACATGCGCATGCCA 1990
QY 562 SLEUGLU-----PROVALARGCYGLINALAPROPROARGSERPROSERGLIALASE 580
DB 1991 CATTAAGGGGCGCGAGAGAGGCGCGGTGACATGCGCAGCATCTGCGCTGCCAG 2050
QY 580 RGLIYARG--THRVALIGLYSERGLYLYSEVAL--TYRPROTHRAL----- 593

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Db 2051 CCTCAGCTGGCCACAGGGCTGGGCAACATGAACTACCCACGATCCTGGCCCTCAGGGGT 2110  
 QY 594 -----HisThrSerPro-----ProPr 599  
 Db 2111 GGGCAGCGGCAAAAGGACACAGCCCGGACCCCAAGGAGTGGCCGGTGGAGCGCC 2170  
 QY 599 oGUThrLeuIleuIleuValAlaLeuValAlaLeuSerIleuProIleu 619  
 Db 2171 AGGCACC-----GGGGGAGCAGCGCCGTTGACCTT 2200  
 QY 619 uThrSerLeuAsnIleProProGlyProIleuSerSerMetHisIleuLeuGluThrI 639  
 Db 2201 GAACAGC-----CCTGATCCCTTACGAAAGATCCCGGATGGTGGGGAGCA 2248  
 QY 639 nSerThrGlyAlaCysGlnSer-----SerCysIleSerS 652  
 Db 2249 TGAATGGGCGGCGCCCTGGCCATCTGTGGGCTCAGTGTGCCCTGGCCCTGGCCAG 2308  
 QY 652 rProCysLeuValAlaAspSerGlyAlaCysGlyProAspSerCysProIleCysAlaAr 672  
 Db 2309 CCCC-----CCACGGGAGCACAGTACCTGTGAGCTGAAAGAGTCCCGCTACACCCG 2362  
 QY 672 gAla---GlyAlaGlyIleuValGluLeuAlaAspArgGluMetProAspSerAspSerG 691  
 Db 2363 TGCCCTGGAGAGACCCGGAGGAGTGAAGCTCAGCGGCTCGAAAGTGAAGATCTGATGGCCG 2422  
 QY 691 uAlaValIleuIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 708  
 Db 2423 TGGGCTGTATGAAATTCAAGCAGAGAGTCCGACAGTGAACCGTGGAGCCACGACGAC 2482  
 QY 709 -----HisSerArgAlaGlnArgS 715  
 Db 2483 ACCCGTGGCAGCAGACACACAGGCGCCAGCGCCAGCGCCGAGCGGAGCGCA 2542  
 QY 715 rLeuGlyProAspAlaGluProSerSerValLeuAlaPheThrArgLeuIleCysAspTh 735  
 Db 2543 GAGGCGAGCCCGGCGAGCCAGGCTGATGGCGGCTTGGGTACCTTACCGGCA 2602  
 QY 735 rPheArgIleValIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 755  
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 QY 755 lAsnThrLeuSerMetGlyIleGluIleuIleuValIleuValIleuValIleuValIleuVal 775  
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 QY 775 uGluIleSerAsnIleValIleuValIleuValIleuValIleuValIleuValIleuVal 795  
 Db 2723 GGAATTCAGCAACATCGTTCACACAGATGTTCCTTGGAGATGCTGTGAAGCTGCT 2782  
 QY 795 uValIleuValIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 815  
 Db 2783 GGCGTGGCGGCTCTGGGCTACATCCGACACCGGTAACAATCTTTCAGCGGCATCATGCT 2842  
 QY 815 lValIleuValIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 835  
 Db 2843 GGTATCATCAGCTGTGGAGATCGTGGGAGCAGCGGACCGGTGCTGTGTGCTGGCAGC 2902  
 QY 835 rPheArgLeuMetArgValIleuValIleuValIleuValIleuValIleuValIleuVal 855  
 Db 2903 CTTCCGGCTGTGCTGTGGAGCTGTGGAGCTGTTCCTTTCAGCGCCCTGGCGCGCAGCT 2962  
 QY 855 uValIleuValIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 875  
 Db 2963 CGTGTGCTGTGTAAGACATGAGACATGAGACATGAGACATGAGACATGAGACATGAGAC 3022  
 QY 875 eIlePheIleuPheSerIleuGlyMetHisIleuPheGlyCysIleuPheAlaSerGluAr 895  
 Db 3023 CATTTTCATCTTACGATCTGTGGCATGACCTTTTCGGCTGCAAGTTCAACCTGGAAC 3082  
 QY 895 gAsp---GlyAspThrLeuProAspArgIleuValIleuValIleuValIleuValIleuVal 914  
 Db 3083 AGACACCGGAGACACCGTGTCTGACGAGGAGAACTTTCGATCTCCGTGTGTGGCCATCTGT 3142

QY 914 lThrValPheGlnIleuLeuThrGlnGluIleuValIleuValIleuValIleuValIleuVal 934  
 Db 3143 CACCGTGTTCACATCTTGAACCCAGAGAGCTGAAGCTGTGCTGTGTAACAAGCATGTGC 3202  
 QY 934 aSerThrSerSerThrAlaIleuValIleuValIleuValIleuValIleuValIleuVal 954  
 Db 3203 CTCACCTCTCTGTGGCGGCTCTTACTTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 3262  
 QY 954 lLeuPheAsnIleuValAlaIleuValIleuValIleuValIleuValIleuValIleuVal 974  
 Db 3263 GCTTTCACCTGT 3311  
 QY 974 sArgGluAspAlaSerGlyIleuLeuSerCysIleGlnIleuProValAspSerGlnGly 994  
 Db 3312 -----GG 3313  
 QY 994 YAspAlaAsnIleuSerIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 1013  
 Db 3314 CGATGCCACAGATCCGACACGAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 3373  
 QY 1014 -----GlyAspArgIleuValIleuValIleuValIleuValIleuValIleuVal 1025  
 Db 3374 CCAAGCTCAGAGAACTCCAGACACAGAGCTGAAGATGTTCCTTGGCCCTGACGCC 3433  
 QY 1025 uGlyIleuIleuValIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 1045  
 Db 3434 CAACGGGACCTGAGAGGAG 3493  
 QY 1045 aThrProMetSerIleuProIleuValIleuValIleuValIleuValIleuValIleuVal 1065  
 Db 3494 CAGCCCATCTTACCTCCCAAGAGCTACCATCTTGTGATGACAGCCCGCCCTCCAGA 3553  
 QY 3554 CTCTCGCGTGGAGCAGCAGCAGCTCCGGGAGCCGCA-----CTGGAGACAGCAAGGCC 3607  
 Db 1085 rProProSerAlaArgSerIleuProHisSerProIleuValIleuValIleuValIleuVal 1105  
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 Db 1105 rArgArgSerSerArgAsnSerIleuValIleuValIleuValIleuValIleuValIleuVal 1125  
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 Db 1125 rGlyGluArgArgSerIleuLeuSerGlyIleuValIleuValIleuValIleuValIleuVal 1145  
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 Db 1145 rSerGluGluGluArgAlaSerProAla-----GlySerAspHisArgHisArgGlyS 1163  
 QY 3783 -GCTGAGAGCAGCGAGGCG 3841  
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 Db 3902 CGGCGAGGTGTGGCGCTGTGGCGAGCATCTTCTCTGATGAGAGAGCGAGCGAGCGAG 3961  
 QY 1192 rAlaSerGluHisGlnAspCysAsnGlyIleuValIleuValIleuValIleuValIleuVal 1212  
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 QY 1212 uArgProAspAspProIleuAspGlyAspAspAlaAspAspIleuValIleuValIleuVal 1232  
 Db 4022 GAGCCCTTACAGGCC----- 4037  
 QY 1232 sGlyGluArgValArgAlaIleuValIleuValIleuValIleuValIleuValIleuVal 1252  
 Db 4038 -----CAGT 4057



QY	1252	pSerTrpSerAlaYrIlePheProProGlnSerArgPheArgLeuLeuGlyShtSaGIl	1272
Db	4058	GGCCCTGGGGCCCTTACCCCTTCTCCCAACAACCGGTTCCGCGCTTCCTCCGAAGG	4117
QY	1272	eIleThrHisIstysMetPheAspHisValValLeuValIleIlePheLeuAsnGlySht	1292
Db	4118	CATCAACACACAAAGATGTTTATATCAAGTGGTCTCTGTCTTATCTTCTCTCAATCGCTCAC	4177
QY	1292	rIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrIle	1312
Db	4178	CATCGCCCTGGAGAGGCGCTGCATTTGACCCCGGAGACACCGAGCGGCTTCTTCAGAGGT	4237
QY	1312	uSerAsnTrpIlePheThrIleValPheLeuAlaGluMetThrValLysValValAlaIle	1332
Db	4238	CTCCAAATTACATCTTCAACGGCCATCTTCGTGGCGAAGTAGTGTGAAGGTGGTGGCCCT	4297
QY	1332	uGluTrpCysPheGlyGluGlnAlaIstYrLeuArgSerSerTrpAsnValIleuAspGlyLe	1352
Db	4298	GGGGCTGCTGTCCGCGACGACCGCCTTACTGCAAGACGCTGGAACTGCTGTGATGGGCT	4357
QY	1352	uLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyThrLys	1372
Db	4358	GCTGTGCTGGTGTGCCCTGGTGGACATTTGTGTGGCATTGGCCCTGCGTGGTGGCGCA	4417
QY	1372	sIleLeuGlyMetLeuArgValIleuArgLeuLeuArgThrIleuArgProLeuArgValI	1392
Db	4418	GATCCCTGGGTGTCTTCGCGCGTGGCTGCTGTGCGACCTGGCGGCTCTTCAAGGATCAT	4477
QY	1392	eSerArgIleGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProI	1412
Db	4478	CAGCCGGGCGCCGGGCGCTCAAGCTGGTGGTGAAGCGTGATATGTGTGCTCAAGCCAT	4537
QY	1412	eGluAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValG	1432
Db	4538	TGGGAAACATCGTCCCTCATCTGCTGGCCTTTTATCATTTTGTGGCATCTTGGGTGGCA	4597
QY	1432	nLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLys	1452
Db	4598	GCTCTTCAAAAGGAAGTTCTACTACTGCGAGGGCCCGACACACAGAAACATCTCCACCA	4657
QY	1452	sSerAspCysAlaGluAlaSerTrpArgTrpValArgHisIstYrTrpAsnPheAspLeu	1472
Db	4658	GGCAACAGTGGCGGGCGGCCCATACCGCTGGGTGGAGCAAGTCAACATTCGACAACT	4717
QY	1472	uGluValAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMe	1492
Db	4718	GGGCGAGGCGCTGATGTGCTGCTGTCTGTCTGTCAACGAAGATGGATGGTGAACATCAT	4777
QY	1492	tTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTr	1512
Db	4778	GTACGACCGGGCTGATGTCGCTGGTGGTGCACACGAGCGCTGTGCAGAACCAACCCCTG	4837
QY	1512	pMetLeuLeuTrpPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPh	1532
Db	4838	GATGTGTGTGAATTCATCTCTTCCTGCTCATGCTCAAGCTTTCTTGCTGCTCAACATGT	4897
QY	1532	eValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAl	1552
Db	4898	CGTGGCGCTCGTGTGTCGAAACTTCCAAATGTCGGGACGACACCGAGGGCGGAGAGGC	4957
QY	1552	aArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArg-----	1568
Db	4958	GCGGCGGCGAGAGGAGAAAGCGGCTGCGCGCTTACAGAGAGGCGCAGAGCACTTCC	5017
QY	1569	-----LysAlaGlnCysLysProTrpTrpSerAspTrpSerArgPheArgLeuVal	1586
Db	5018	CAGCCCAAGAGGCGCCGCGCGCTTACTATGCCACATCTGCGCCACGCGCGCTCAT	5077
QY	1586	IHisIstLeuGlyTrpHisSerHisIstYrLeuAspPhePheIleThrGlyValIleGlyLeuAs	1606
Db	5078	TCACTCGCTGTGGACCAAGCACTATCTGACCTTTCATCACTTCATCATCTGTGTCA	5137
QY	1606	nValValThrMetAlaMetGluHisIstYrGlnGlnProGlnIleuAspArgAlaLeuLys	1626

[illegible]

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Dh 6089 GCTGCAGAGAGTGAATGAGACCTATGGGCGCGACCC-----TTGGGCTC 6139
Qy 1967 rVAlleuSerValHisSerGlnProAlaAspThrSerTyrIleuGlnLeuProlysAs 1987
Db 6140 CGTTGGCTCTGTGACACTCCGCGCGAGAGTCTGTGCTCCCTCCAGATCCCA----- 6194
Qy 1987 pAlaProHisLeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProIysLeuPr 2007
Db 6195 -----CTGGCTGTGTGCTGCCCGAGAGAGGCGGAGCCCTCCAGCCGCTGTG 6244
Qy 2007 oProProGly-----ArgSerProleuAlaGlnArgProleuArgArgGlnAlaI 2025
Db 6245 CCTTCGGGGAGACAGCCGCTCCCACTCCAGCTCAGCCGCTGTCTGCGAGAGAGGCTGT 6304
Qy 2025 eArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlnAspLeu-----Al 2043
Db 6305 GCACACCGGATTCCTTGGAAGAGGAAG---ATTGACAGCCCTTAGGAGACACCTCGATCCTGC 6361
Qy 2043 aGluValSerGlyProSerPro-----ProleuAlaArgAlaTyrSerPheTyrGly-- 2060
Db 6362 AGAGCCTGTGTAGAAAACCCCGTGTAGGCGGTGACCCAGGGGGGCTCCCTGCAGTCCCC 6421
Qy 2061 ----GlnSerSerThrGlnIaGlnIaHisSerArgSerHisSerIysIleSerIysH 2079
Db 6422 ACCAGCTCCCAACGCGCCGCGACGCTCCGCACTCGTAAGCATAC--TTCCGAGACAGCA 6478
Qy 2079 sMetThrProProAlaPro---CysProGlyProGluProAsnTyrGlySerGlyProPr 2098
Db 6479 CTGCGTCTCAGCCGCGCGGCGGCGCCAGCGGAGAG----- 6515
Qy 2098 oGluThrArgSerSerLeuGlnLeuAspThrGlnLeuSerTyrIleSerGlyAspLeu 2118
Db 6516 -GAGGCGGAGGCTCGGAGCCAGCCAGCGAGAGGTGACGACATCAACAGCTCCGCGCTG 6574
Qy 2118 uPro-----ProGlyGlnGlnGlnGluProPro-----SerPr 2129
Db 6575 CCCCTGGACGCCACAGCCGAGCCGACATGGCCCCGAAAGCTCTCCGGTGGCGCGCGCA 6634
Qy 2129 oATGAspLeuIlyLeuSerCysTyrSerValGlnIaGlnSerCysGlnArgArgProThrs 2149
Db 6635 GCGGAGACTCGCAGCGCTCTACAGCGTGAAGCGTCAGAGGCTTCTTGAGCAAGAGCG--GG 6691
Qy 2149 rTrpLeuAspGlnGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerG 2169
Db 6692 CCGGCGAGAGAGTGTGGCGGCTCGCGAGACTGTGGCGAGCGGAGGAGCTGTGGAGAGC 6751
Qy 2169 nProHisLeuGlyThrAspProSerAsnLeuGlyGlnProleuGlyGlyProGlySe 2189
Db 6752 GAAGGCTGTGGGCGCTGAG-----GCCGAGGCC-----GCTCTGGGTGC 6790
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Db 6791 GCGGAGAAAGAAAGATGAGACCCCTCGATCTCGGTGAGAACCCCTCGCGAGAGAGCA 6850
Qy 2208 nGlyProArgThrProProSerPro-----GlyIleCysLeuArgArgAlaPr 2225
Db 6851 GGGGTGTGGCGGCGCTCCGCGAGAGAGGCGGAGACACACTGAGGCGCAGAGACCC 6910
Qy 2225 oSerSerAspSerIys----- 2230
Db 6911 GTCTCTGAGGCGCCGCTTCACAGGGAATCCTGAGCCCAAGAGGAGCTTAGCGCGCG 6970
Qy 2231 ---AspProleuAlaSerGlyProProAspSerMetAlaIaIaSerProSerPolyIy 2249
Db 6971 GGGGAGACCTTCAGACCAAGGGGAGCGCTGGGCGCAGGCC-----TCCTCCGGGC 7021
Qy 2249 sAspValleuSerLeuSerGlyLeuSerSerAspProAlaAspLeu----- 2264
Db 7022 TGAGCAGCTGACGCTCCCACTTGTCTTGAGCCGCTGAGCCTCGGGGTCCCCAGTGG 7081
Qy 2265 -AspPr 2266
Db 7082 AGACCT 7088
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RESULT 6
US-09-404-650-1
; Sequence 1, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Mcgovern, Paul S.
; APPLICANT: Dietrich, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
; US-09-404-650-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.30% Conservative: 213
Best Local Similarity: 51.44% Mismatches: 506
Query Match: 46.14% Indels: 449
DB: 3 Gaps: 55

US-09-611-257a-37 (1-2266) x US-09-404-650-1 (1-6816)
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Qy 51 -----LeuProTyrProAlaLeuAlaProValAlaPhePheTyrLeuSerGln 66
Db 324 GGTGATCTCATGATCCACACCCAGACCTGGCGCTTATGCTTCTTCTGCTGCGCAGAG 383
Qy 67 AspSerArgProArgSerTyrPyrCysLeuArgThrValCysAsnProTyrPheGluArgIle 86
Db 384 ACCAGCAGCCCGCGAACTGTGCATCAAGATGTGTGCAACCGGTGATTGAATGTGTC 443
Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db 444 AGCATGTGTGATCTCTGTGAATCTGCTGACACTTGTGGATGTACAGCCGCTGAGAGCAG 503
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Qy 127 PhePheAlaValGlnMetValIlyIysMetValAlaLeuGlyIlePheGlyIlyIysCys 146
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Db 624 TACCTCGGGAGACATGGAACCGCTGGAATTTCTTCACTGTCAATGAGAGGATGTGTGAG 683
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Db 684 TACTCCCTGTGACCTTGAGACATCAACCTGTCAAGCATCCGCAACCGGCGCGCTCTGAGG 743
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Db 744 CCCCTCAAAACCATCAACCGCGGCCAGATGCGGATCTGTGTGAACCTGTCTGTGGAC 803
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OY	1640	rValPheYsLeuValAlaPheGIYPheArgArGPheGlnAspArgTPAsenGlnE	1660
Db	4668	TGTGTGAAGCTGGATGGCATTTGGTCTGAGGCGCTTCTTCAAGACCGATGGACCACT	4747
OY	1660	uAspLeuAlaIleValLeuLeuSerIleMeCGlyIleThrLeuGIuIleGIuValAs	1680
Db	4748	GGACCTGGCCATTGTGCTACTGTGAGTCATGGGATCATCCCTTGAGAGAGATCGAGTCAA	4807
OY	1680	nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr	1700
Db	4808	TGCGGCTGGCCCAATCCACCATATCCGATATCCGATCATAGAGGGTCTTGCCCATTTGCCG	4867
OY	1700	qValLeuYsLeuLeuYsMetAlaValGIYMeCArgAlaLeuLeuAspThrValImeGI	1720
Db	4868	AGTCTGAAGCTGTGAAGATGCGCACAGAAATCGGGCCCTGCTGGACAAGGTGTGCA	4927
OY	1720	nAlaLeuProGIuValGIYAsnLeuGIYLeuLeuPheMetLeuLeuPhePheIlePheAl	1740
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OY	1740	aAlaLeuGIYValGIuLeuPheGIYAspLeuGIuCYsAspGIuThrHisProCYsGIuGI	1760
Db	4988	TGCTCTCGGGGGTGAAGCTCTTTGGAGACTGTCTGCACAGCAAGAACCCGTGGAGGG	5047
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OY	1780	lSerThrGIYAspAsnTPAsenGIYIleMetIleAspThrLeuArgAspCYs--AspGI	1799
Db	5108	CTCCACGGGTGACCACTGAACGGGATCATGAAAGCAACGCTGGGAGCTGCACCCACA	5167
OY	1799	nGIuSerThrCYsTYrAsnThrVal-----IleSerProIleTYrPheAlaSerPheVa	1817
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OY	1817	lLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetIysIleuGI	1837
Db	5228	GCTCACCGCGAGTTCTGTCTCATCACTGTGTGTGTGCTGTGCTCATGAAGCACCTGGA	5287
OY	1837	uGIuSerAsnIysGIuAlaIYsGIuGIuAlaGIuLeuGIuAlaGIuLeuGIuIleuGIuMe	1857
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Db	5405	C---CGAGGGCGGGAGGGGCGGGCGGGGCGACACCGAGGGCGGCTTGTGCGGCG	5461
OY	1885	--SerProIysProGIYAlaLeu--	1891
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OY	1901	r-----HisPheSerLeuGIuHisProThrMetGlnPro	1912
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OY	1930	-----	ValSerArgThriHisSerLeuProAsn---AspSerTyMetCysArgHi	1945
Db	5762	CTTCTTCCCTTCCTGCTCTCTACGGCGCTGCGCGGATCCAGAGAACTCTGTGTGATG	5821	
OY	1945	sglySerThrAlaGlulGlyProLeuGlyIhiSarGlyTYrGlyLeuProLysAlaGlnSe	1965	
Db	5822	GGAGAGATCCCATTCACCTCTGC-----CGTCTCTGG-----CTGAAACATGCAG	5869	
OY	1965	rglySerValLeuSerValHisSerGlnProAlaAspThrSerTyxIleuGlnLeuP	1985	
Db	5870	CAGTCAGACACCCCAAGCTCTTCTCCCGATGCTCCAGAGCTTCTCTGCCCATGCC	5929	
OY	1985	olysAspAlaProHis-----	1999	LeuLeuGlnProHisSerAlaProth
Db	5930	AGCCGAGTCTTCCACCTCGACGTCTGCCACGACGAAAGGCCGAGAAAGGCACTGG	5989	
OY	1999	rTrpGlyThrIleProLysLeuProProProGly-----	2014	ArgSerProle
Db	5990	CACGGAACCTCCCAAGATTGGCTGACGAGGGCTCTGGGACATCTCGCGGTACCAAG	6049	
OY	2014	uAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThiAspSerLeuAspAlaGlnI	2034	
Db	6050	GGTCAACTGTAACTCTCTCCCGGACGACCGGAGGACACAGCTCGTGGAC-----	6101	
OY	2034	ylEuGlySerArgLysAspLeuAlaGluValSerGlyProSerProProLeuAlaAr	2054	
Db	6102	-----	6127	GCAGGCCCAAGACGCTCCGCGGGCAG
OY	2054	gAlaTySerPheTrpGlyGlnSerSerThrglnAlaGlnIhiSerArgSerHisSe	2074	
Db	6128	CCTGCAGACCCACGCTCGACGACAGCTGACCTTGACGACAGACCCCGCGGTGCC-----	6182	
OY	2074	rLysIleSerIyHisMetThrProProAlaProCysProGlyProGluProAsnTrpIleSe	2094	
Db	6183	-----	6226	CTGGGCGCGCCCGCGCTCTCCAGAACCCCGCGCGCGCTGTC
OY	2094	ylYsGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSe	2114	
Db	6227	C-----	6254	CCGCGCGCTGCGCGCGCTGAGCTG-----
OY	2114	rgLysAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuYsLy	2134	
Db	6255	-----	6274	CGGCGCGGGGCGCTTTCAG
OY	2134	sCyTySerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluI	2154	
Db	6275	CCTCGCGGCGCTCGCGGCG-----	6298	CATCA
OY	2154	naArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyTh	2174	
Db	6299	GCGCAGCCACAGCAGCGGAGGCTC---ACCAGCCGGGCTGCACCCACACACACTCAT	6355	
OY	2174	rAspProSerAsn-----	2191	LeuGlyGlyGlnProLeuGlyGlyProGlySerArgPr
Db	6356	GGACCCCTCGGACACGAGAGGGCGGGTGGCGCGGGGGGGGGCGCGGACGACGA	6415	
OY	2191	olYalysylsLeuSerProProSerIleThr-----	2208	IleAspProProGluSerGly
Db	6416	CTCGAGACCTCTGACGACCTCTGCTACCTCTTCTTGCCCGCGCC-----	6467	
OY	2208	nglyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs	2228	
Db	6468	-----	6517	CCGCGCGCAGCCCGCGGCTTCACGCCGCCAGGAAGTTCAGCAGCACAG
OY	2228	pSer-----	2244	LysAspProLeuAlaSerGlyProProAspSerMetAlaIaSe
Db	6518	CAGCTGGCGCGCCCGCGCGCGCCACAGCGCGCGCTTGCCACAGCGCTGGCGCGGAG	6577	
OY	2244	rProSerProLysAlaAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLe	2264	

Db 6578 CCCCTCGTGGCGCGGAC-----CGCAGCAAGGACCCCGCGCG 6619  
Qy 2264 uaapPro 2266  
Db 6620 GGCACCG 6626

RESULT 7  
US-09-935-541-1  
Sequence 1, Application US/09935541  
Patent No. 6589787  
GENERAL INFORMATION:  
APPLICANT: Dietrich, Paul S.  
APPLICANT: McGivern, Joseph G.  
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
TITLE OF INVENTION: AND USES  
FILE REFERENCE: R043B-RG sequence listing  
CURRENT FILING DATE: 2001-08-23  
PRIOR FILING DATE: 1999-09-23  
PRIORITY APPLICATION NUMBER: 09/404,650  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 6816  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (192)..(6716)  
US-09-935-541-1

Alignment Scores:  
Pred. No.: 0 Length: 6816  
Score: 5492.50 Matches: 1236  
Percent Similarity: 60.30% Conservative: 213  
Best Local Similarity: 51.44% Mismatches: 506  
Query Match: 46.14% Indels: 449  
DB: 4 Gaps: 55

US-09-611-257a-37 (1-2266) x US-09-935-541-1 (1-6816)

Qy 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGly 50  
Db 264 CAGCCCGGACCCCGGAGCCCATCTCCCGCAGCGCTGAGAGAGCCCTGGAATG 323  
Qy 51 -----LauProTyrProAlaLeuAlaProValAlaPhePheTyrLeuSerGln 66  
Db 324 GCTGATCTCATGTCCTCACACCGACCTGGCGCTTCTTCTGCTCGACAG 383  
Qy 67 AspSerArgProGlySerTyrCysLeuArgThrValCysAsnProTyrPheGluArgIle 86  
Db 384 ACCACCGACCCCGGAACTGCTGATCAAGATGCTGCAACCCGCTTTGAAATGTC 443  
Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106  
Db 444 AGCATGCTGGATGCTGCTGAACCTGCGTGAACCTTGCCATGTACAGCCGTCGACGAC 503  
Qy 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126  
Db 504 ATGACATGCTGCTCGACCGCTGCAGAGTCTTGCGCTTTGATGATCTTATTC 563  
Qy 127 PhePheAlaValGluMetValValIleCysValAlaLeuGlyIlePheGlyLysLeuCys 146  
Db 564 TTCCTTGCATGAGATGCTGCTCAAGATGCTGCGCTGGGATTTTGGCAAGAGTC 623  
Qy 147 TyrLeuGlyAspThrTyrPheAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166  
Db 624 TACCTCGGGGACACATGAGACCGCTGGATTTCTTCATGCTATGAGCGAGGATGGTCAG 683  
Qy 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186  
Db 684 TACTCTCGACCTTCAGAACATCAACTGTCAGCATCCGACCGTGGGCTCTGAGG 743

Qy 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAsp 206  
Db 744 CCCCTCAAGCCATCAACCGCGCGCCAGATGCGGATCTGTGAACCTGCTCCGAGAC 803  
Qy 207 ThrLeuProMetLeuGlyAsnValIleLeuLeuCysPhePheValPhePheIlePheGly 226  
Db 804 ACACTGCCATGCTGGGAAATGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTT 863  
Qy 227 IleValGlyValGlnLeuTyrPheAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246  
Db 864 ATCATAGTGTGACGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 923  
Qy 247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266  
Db 924 TTCACCATCAAGAGGATGGCTGCTGCCCATCTACCAAGCGGAGAGATGATGAG 983  
Qy 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286  
Db 984 ATGCCCTTCATCTGCTCTCTGCTGCGGACATGGATATGGGCTGCCATGATCCCC 1043  
Qy 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300  
Db 1044 CCGCTCAAGAGGAG-----GGCGGAGTGTGCTGTCCAAAGACAGAGCTCTAC 1094  
Qy 301 AspTyrGluAlaTyrAsnSerSerSerThrThr-----CysValAsnTyrAsnGln 318  
Db 1095 GACTTGGGGCGGGGCGCCAGACCTCAATGCCAGCGGCTGTGTCAATGAAACCGT 1154  
Qy 319 TyrTyrThrAsnCysSerAlaGlyGluIleAsnProPheLysGlyAlaIleAsnAsp 338  
Db 1155 TACTACATGTGTGCGGACGCGGAGCGGACCCCAAGAGGTGCCATCACTTTGAC 1214  
Qy 339 AsnIleGlyTyrAlaTyrPheAlaIlePheGlnValIleThrLeuGluGlyTyrPheValAsp 358  
Db 1215 AACATGGTTATGCTTGATGATTCATCTTCAGATGATCACTCGAAGAGCTGGTGGAG 1274  
Qy 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu 378  
Db 1275 ATCATGTACTACGTGATGATGATGCTCACTCTTCAACATTCATCACTTCACTGCTT 1334  
Qy 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPhe 398  
Db 1335 ATCATAGTGGCTCTTCTTCATGATCACTGAGCTGCTGCTGCTCATAGGACCCAGTTC 1394  
Qy 399 SerGluThrLysGlnArgGlnSerGlnLeuMetArgGlnArgValArgPheLeuSer 418  
Db 1395 TCGGAGACCAAGCAACGAGGACACCGGCTGATGCTGAGACGAGCGGACGCTACTGTC 1454  
Qy 419 AsnAlaSerThrLeuAlaSerPheSerGlnProGlySerCysTyrGluGluLeuLeuLys 438  
Db 1455 ---TCCAGACAGGCGGACCTACCGCGACCTGGCCACATGCTCAACGAGAGATCTTCAG 1511  
Qy 439 TyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAla 458  
Db 1512 TATGTCGCCACATCTCGCCCAAGGCCAAGCCG-----CGGCGCTG 1553  
Qy 459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnPro 478  
Db 1554 GGCTTACCAAGGCGCTCGAGAGCGCGGCGGCGGCGCTGGGG----- 1595  
Qy 479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisIleValHisHisHis 498  
Db 1595 ----- 1595  
Qy 499 HisHisHisHisHisHisTyrHisIleGluGlyAsnGlyThrLeuArgAlaProArgAlaSer 518  
Db 1595 ----- 1595  
Qy 519 ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer 538  
Db 1596 -----CCGAG 1601

QY 539 ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheThrHis 558  
 Db 1602 GCGCCGGGCC-----CCCGCAAACTGGAGCC-----CAC 1631  
 QY 559 AlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGlu 578  
 Db 1632 GCCAAG-----GAGCCCCGGCAGTACAGAGCTGTGCCCGCAATAGCCCCCTGGAT 1682  
 QY 579 AlaSerGlyArgThrValGlySerGlyValValTyrProThrValHisThrSerProPro 598  
 Db 1683 GCGAGCCCCCAACCCCTG-----GTGCAGCCCATC 1712  
 QY 599 ProGluThrLeuArgGlyLysValAlaLeuValGluValAlaAlaSerSerGlyProProThr 618  
 Db 1713 CCGGCCACGCTG----- 1724  
 QY 619 LeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuGluThr 638  
 Db 1724 ----- 1724  
 QY 639 GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp 658  
 Db 1724 ----- 1724  
 QY 659 SerGlyAlaCysGlyProAspSerSerCysProTyrCysAlaArg----- 672  
 Db 1725 -----GCTTCGATATCCCGCAGCTGCTTGTCTGCTGCAGCATGAGAGCGGCCGCCGCC 1778  
 QY 673 AlaGlyAlaGlyGlyValGluLeuAlaAspArgGlyMetProAspSerAspSerGluAla 692  
 Db 1779 TCGGGCGTGGGAGCAGCAGCAGC---TCGGGCGAGAGAGGGCTCGGGAGCTCCGCT 1835  
 QY 693 ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerAspArg 712  
 Db 1836 GGTGGCGAG-----GACGAGCGGATGGGAGCGGGCCCGGAGCAGCAGCAGCAGCGAGCC 1889  
 QY 713 GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu----- 726  
 Db 1890 TCCTCAAACTGGGAG 1949  
 QY 727 -----AlaPheTrrPheLeuIleCysAspThrPheArgLysIleValAspSerLysTyr 744  
 Db 1950 TCGGGGAGATGTGTGGCGGAGAGCGGAGCCAAAGCTCGCGGCAATCGTGAGACAGCAAGTAC 2009  
 QY 745 PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGlyTyr 764  
 Db 2010 TTCAAACGGGGCATTCATGATGGCCATCTGGTCAACAACCTGCAATGGAGCATGAGCAGC 2069  
 QY 765 HisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer 784  
 Db 2070 CACGAGCAGCCGAG 2129  
 QY 785 LeuPheAlaLeuGluMetLeuLeuLeuValTyrGlyProPheGlyTyrIleLys 804  
 Db 2130 ATGTGTGCGCTGAGATGATCTCGAAGCTGGCGTGCATTTGGGCTCTTCACTACCTGCGCT 2189  
 QY 805 AsnProTyrAsnIlePheAspGlyValIleValIleSerValIleProGluIleValGly 824  
 Db 2190 AACCCCTACAACATCTTCGACAGCATCTTGATCATGACATCGAGAGATCGTGGAG 2249  
 QY 825 GlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu 844  
 Db 2250 CAGGCGGAGCGGTGGGT 2309  
 QY 845 ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn 864  
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 QY 865 ValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMet 884  
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 QY 944 PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeu 963  
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 QY 964 ValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSer 983  
 Db 2670 GTGAGGGGCTTCAGCGGAG----- 2690  
 QY 984 CysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGluPro 1003  
 Db 2691 -----GCTGACGCCAATCGCTCTACTCGGACGAG 2720  
 QY 1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013  
 Db 2721 GACCAAGCTCATTCACAATGAGAGATTGTGATAGCTCCAGAGAGCGCTGACAGCAGC 2780  
 QY 1014 GlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033  
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 QY 1034 SerLeuLeuProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSer 1053  
 Db 2826 -----CTGAGACCC-----AGTCTCCACTGGGT 2849  
 QY 1054 ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThr----- 1069  
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 QY 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080  
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 QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrrSerAlaAla 1100  
 Db 2970 TATGACACAGCTCTCTGTCCAGCTCCGAGCTCTTACTAGGGCCATGGGGCCGAC 3029  
 QY 1101 SerSerTrrPheSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
 Db 3030 GCGGCTGGGCGACGCTGCTCCAGCTGGAAC-----AGCTCAAG 3071  
 QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu---GlyGlnGluSer 1139  
 Db 3072 CACAACCGCCGCTCGCGGAGCATGATCCCTGCTCTTGGGAGCGGCGGCGGCGGCG 3131  
 QY 1140 GlnAspGluGluGluSerSerGlyGlu-----GluArgAlaSerProAlaGlySerAsp 1157  
 Db 3132 CGGGTCTGAGAGTTGCCGCGAGCAGAGGGCGCGCGGCGGCGACCTCTGACACCCCA 3191  
 QY 1158 His-----ArgHisArgGly 1162  
 Db 3192 CAGCGCCACCAATTCATCAGCGGCCCATCTGGCGCACCGGCACCGCACCGCGCGG 3251  
 QY 1163 SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182  
 Db 3252 AGCTGTCTCTTCACAAAGAGATCGGTGACCTGGCGGAGCTGTGCTCCGCGGTGGG 3311  
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 Db 3312 GCCCAACCCCGGGCGGCTGAGAGGGCGGAGGCGCGGCGCGCGGCGCATGAGAGCTGCAAT 3371  
 QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeu---As 1220



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Qy 1220 pgiYAspAalAaspArglulYAsnLeuSerLyseGlyGluArgValAlaTPrI 1240  
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Db 3488 CGACGCTATTAAGCCCACTGGTGGCGAGGTCGCGAAAGACTGGTGTCTACTACTTCTC 3547  
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Db 3548 TCCGGAACAAGTTCGCGGCTGTGTGTCAGACCATTAATGCCAACAACCTTCGACTA 3607  
Qy 1280 sValValLeuValIleIlePheLeuAsnCyseIleThrIleAlaMetGluArgProLyS 1300  
Db 3608 CGTGCCTCGGCTTCATCTTCTCAACTGCATCACATCGCTCGAGCGGCTCGAGAT 3667  
Qy 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTrpIlePheThrAlaVa 1320  
Db 3668 CGAGCGCGGCGACCGAAGCATTTCTACCGTGTCCAACTACATCTTCACGCGCAT 3727  
Qy 1320 lPheLeuAlaGluMetThrValIleValAlaLeuGlyTrpCySPheGlyGluGlnAl 1340  
Db 3728 CTTCGTGGCGAGATGACATTGAAGGTAAGTCTCGCTGGGCTGTACTTCGCGAGACAGC 3787  
Qy 1340 aTyTrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360  
Db 3788 GTACTCTACGAGCAGCTGGAAAGCTGTGATGGCTTCTTGTCTTCGTGCATCATCGA 3847  
Qy 1360 pIleLeuValSerMetValSerAspSerGlyThrLySIIleleuGlyMetLeuAlaGValle 1380  
Db 3848 CATGTGGTGTCTTCGCGCTGAGCGCGGAGCCCAAGATCTTGGGGGTCTCCAGTCTT 3907  
Qy 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIIeserArgIaGlnGlyLeuLySle 1400  
Db 3908 GCGGCTCTGCGACCTTACGCCCCCTGCTGTCTATCAGCGGCGCGCGGCTGAAAGCT 3967  
Qy 1400 uValValGluThrLeuMetSerSerLeuLySProIIleGlyAsnIIleValValIIeCyG 1420  
Db 3968 GGTGTGGAGACATCATCTCTCCCTCAAGCCCATCGGCAACATCGTCACTCTGTG 4027  
Qy 1420 sAlaPhePheIleIlePheGlyIIleleuGlyValGluLeuPheLySIIlySPhenPheVa 1440  
Db 4028 TGCCTTCTTCACTCTTGTGCACTCTGGAGTGCAGCTCTTCAAGGCAAGTCTTCA 4087  
Qy 1440 lCyseGlnGlyGluAspThrArgAsnIIleThrAsnLySerAspCySAlaGluIleSerTy 1460  
Db 4088 CTGTCTGGGCGTGAACACCGCAACATCACACCGCTCGGACTGCATGGCGGCAACTA 4147  
Qy 1460 rArgTrpValIArgHisLySIIyTrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh 1480  
Db 4148 CCGCTGGTTCATCAACAATCAACTTCGACACCTGGGCGAAGCTCGATGTCCTCTT 4207  
Qy 1480 eValLeuAlaSerLySAspGlyTrpValAspIIleMetTyAspGlyLeuAspAlaValG 1500  
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Qy 1500 yValAspGlnGlnProIIleMetAsnHisAsnProTrpMetLeuLeuTrpPheIIleSerPh 1520  
Db 4268 TGTGACACGAGCTGTGACCAACCAACACCGCTGGAGTGGCTGTACTTCTCTCT 4327  
Qy 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValIleGluAsnPh 1540  
Db 4328 CTGTGTACTGTCAAGCTTCTTGTGTCTCAACATGTTGTGGTGTGCGTGAAGAACT 4387  
Qy 1540 eHisLyCySArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLySArgle 1560  
Db 4388 CCACAAATGTCCGCGACCAAGAGGCTGAAGAGGACAGCGCGCTGAGGAAGCGGCT 4447  
Qy 1560 uArgArgLeuGluLySArgArgArgValGlnCySAspProTyTrpSerAspLySle 1580  
Db 4448 GCGGCGCTGGAGAAAGCGCGGAGGCGCAAGCGGCTGCCCTTACTATGCCACTTATG 4507

Qy 1580 rArgPheArgLeuLeuValHisIleuCystrSerHisTyTrLeuAspLeuPheIleTh 1600  
Db 4508 TCACACCGGCTGTCTACTACATCCATGTCACACCACTGACACTTCACTTCACTAC 4567  
Qy 1600 rGlyValIIleGlyLeuAsnValValThrMetAlaMetGluHisTyTrGlnGlnProGlnII 1620  
Db 4568 CTTCATCATCTGTGCTCAAGCTGTGTACCATATGTCCTGGAGCACTACATCAGCCAGTC 4627  
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Qy 1640 rValPheLyLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnle 1660  
Db 4688 TGTGTGAAGCTGTGGCATTTGTGTGAGGCGCTTCTTCAAGAGCCGATGAACAGCT 4747  
Qy 1660 uAspLeuAlaIleValLeuLeuSerIIleMetGlyIleThrLeuGluGluIIleGluValAs 1680  
Db 4748 GGAATGTGCATTTGTGTACTGTCAATGAGCATGAGCATCACCTGGAGAGATCGAGATCA 4807  
Qy 1680 nAlaSerLeuProIIleAsnProThrIleIleArgIIleMetArgValLeuArgIIleAla 1700  
Db 4808 TGGCGCCCTGCCATCATCCACATCATCCCATCATGAGGTTCTGTGCAATGGCCG 4867  
Qy 1700 gValLeuLyLeuLeuLySMetAlaValGlyMetArgAlaLeuLeuAspThrValIleMetG 1720  
Db 4868 AGTGTGAAGCTGTGAAGATGGCCACAGAAATGGCGGCTCTGTGACAGCGGAGTGCA 4927  
Qy 1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl 1740  
Db 4928 AGCTTGTCCCAAGTGGGCAACTGGGCTCTCTTCAATGTCTCTTCTTCAATCATAGC 4987  
Qy 1740 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCySAspGluThrHisProCySglul 1760  
Db 4988 TGTCTGTGGGTGAGCTCTTGTGGAAGCTGTGTCGAAAGAGAGAACCCGTGGAGG 5047  
Qy 1760 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1780  
Db 5048 CATGAGCGGCAATGCCCTTTCAGAACTTGTGGATGAGCTTCTTCACTTTCAGAT 5107  
Qy 1780 lSerThrGlyAspAsnTrpAsnGlyIIleMetLySAspThrLeuArgAspCyS---AspG 1799  
Db 5108 CTCCACGGGAGCAACTGGAACGGGATCATGAAGAGCACTCTGGGATCGAACCCAGCA 5167  
Qy 1799 nGluSerThrCySTrpAsnThrVal-----IleSerProIIleTyPheValSerPheVa 1817  
Db 5168 CGAGCGAGCTGTGAGAGAGCTGTGAGCTTGTGTGCGCGCTGTACTTGTGAGCTTGT 5227  
Qy 1817 lLeuThrAlaGlnPheValLeuValAsnValIleAlaValAlaLeuMetLySIIleuG 1837  
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Qy 1837 uGluSerAsnLySgluAlaLySgluGluGluGluLeuGluAlaGluLeuGluIleuGluMe 1857  
Db 1857 t---LySThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProG 1876  
Qy 1857 t---LySThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProG 1876  
Db 5348 GCGCCATGAGCTGTGGCGCTGTGGCGGAGGCTGTACCGGCTCCCGGCGGCC---CTGTG 5404  
Qy 1876 yValGluGlyProAspSerProAsp----- 1884  
Db 5405 C---CGAGGCGCGGAGAGGCGGCGGCGGCGGACACCGAGGCGGCTTGTGCCGCG 5461  
Qy 1885 -----SerProLySProGlyAlaLeu----- 1891  
Db 5462 CTGTACTTGTGCTGCCAGACTCTTGTGAGGGAGAGCTACATCATCGAACACTGTG 5521  
Qy 1892 -----HisProAlaAlaHisAla----- 1897  
Db 5522 GGGCTCATCTTCCACCACTACTCTGTGCGCGGCTGAGAGAGTGTACACAGCA 5581

QY 1898 -----ArgserAlase 1901  
DB 5582 GCAGAGTGCAGCTGGCTGAGACGAGGCGCTTCTCCCTGAAGCTCAGACAGGCTCTGTC 5641  
QY 1901 r-----HisPheSerLeuGlnHisProThrMetGlnPro----- 1912  
DB 5642 CATCTGTGTGGTGCAGCTAGTCTCGAGAGACCCACAGCTGCGCCACTGGCCGCA 5701  
QY 1913 ----HisProThrGlnLeuProGlyProAspLeuThrValArgLysSerGly----- 1929  
DB 5702 GCACAGCAAGGGTGTGAGCTGACCCACCTGAGCCGCTGTGTGGAGACTGGGCGAATG 5761  
QY 1930 -----ValSerArgThrHisSerLeuProAsn-----AspSerTyrMetCysArgHis 1945  
DB 5762 CTCTCTTCCCTTGTCTCTTAAGGCGCTTCCGCGATCCAGAGAACTTCTGTGTAGAT 5821  
QY 1945 sglYserThrAlaGlnGlyProLeuGlnHisArgGlyTyrGlyLeuProLysAlaGlnSe 1965  
DB 5822 GGAGAGATCCCATTCACCTGTCTC-----CGTCTCTG-----CTGAAACATGACAG 5869  
QY 1965 rglYserValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuPr 1985  
DB 5870 CAGTCAAGACACCCCAAGTCCCTTCTCCCGGATGCTCCAGCCCTCTCTGCGCCATGTC 5929  
QY 1985 olYsAPAlaProHis-----LeuLeuGlnProHisSerAlaProth 1999  
DB 5930 AGCGGAGTCTTCCACCTGCAATGCTGCGCAGCAAGAAAGGCCCAAGAGGCACTGG 5989  
QY 1999 rTyrGlyThrIleProLysLeuProProGly-----ArgSerProle 2014  
DB 5990 CACTGGAACCTCTCCCAAGATTGCGCTGCAGGGGCTCTGGGCACTCTGCGTCAACAG 6049  
QY 2014 uAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnI 2034  
DB 6050 GGTCAACTGTACCTCTCGGAGGACCGGAGCGACACCTCTGCTGAC----- 6101  
QY 2034 yLeuGlySerArgGluAspLeuAlaGlnValSerGlyProSerProProLeuAlaAr 2054  
DB 6102 -----GCCAGCCCAAGACGCTCCGCGGCGAG 6127  
QY 2054 galATYserPheTyrGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSe 2074  
DB 6128 CTGCAGACACGCTCGAGGACGCTGACCTGACGACGACGACGCGCGCTGTC----- 6182  
QY 2074 rlySIIleSerLysHisMetThrProProAlaProCysSProGlyProGlnProAsnTrp 2094  
DB 6183 -----CTGGGGCGCGCGCGCTGTCTCAAGACCCGCGGCGCGCTGTC 6226  
QY 2094 yLysGlyProProGluThrArgSerSerLeuGlnLeuAspThrGlnLeuSerTrpIleSe 2114  
DB 6227 C-----CCGCGCGCTGCGCGCGCTGAGCTG----- 6254  
QY 2114 rglYAspLeuLeuProProGlyGlyGlnGlnGluProProSerProArgAspLeuLysLy 2134  
DB 6255 -----CGGCGCGCGCGCTGTC-----CGGCGCGCGCGCTTTCAG 6274  
QY 2134 sCysTyrSerValGlnAlaGlnSerGlnArgArgProThrSerTrpLeuAspGlu 2154  
DB 6275 CCTGCGGGGCGCTGCGGCG-----CATA 6298  
QY 2154 nATGATGHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisleuGlyTh 2174  
DB 6299 GCGGACCCACAGAGAGCGGGGCTCC---ACGAGCCCGGGCTGACCCACACGACTCCAT 6355  
QY 2174 rAspProSerAsn-----LeuGlyGlyGlnProLeuGlyGlyProGlySerArgPr 2191  
DB 6356 GGAACCCCTCGAGAGAGAGGCGCGGTGCGCGGCGGCGGCGGCGGCGAGCGAGCA 6415  
QY 2191 olYsLySlyLeuSerProProSerIleThr-----IleAspProProGluSer 2208  
DB 6416 CTCGAGAGCCCTTCAGAGCTCTGCTCACTCCCTTCTGCGCCGCGCC----- 6467  
QY 2208 nglYProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs 2228

DB 6468 -----CCGCGCGCAAGCCCGGCGCTCAAGCGCCGCGCAAGAGTTCAAGAGACAG 6517  
QY 2228 pSer-----LyAspProLeuAlaSerGlyProProAspSerMetAlaAlase 2244  
DB 6518 CAGCTGTGCGAG 6577  
QY 2244 rProSerProLysLyAspAPValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLe 2264  
DB 6578 CCCCTGTGTGGCGCGGAC-----CGCAGCAAGACCCCGCGCGCG 6619  
QY 2264 uAspPro 2266  
DB 6620 GGCACCG 6626  
RESULT 8  
US-09-404-650-3  
; Sequence 3, Application US/09404650  
; Patent No. 6309858  
; GENERAL INFORMATION:  
; APPLICANT: Dietrich, Paul S.  
; APPLICANT: McGiven, Joseph G.  
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
; TITLE OF INVENTION: AND USES  
; FILE REFERENCE: R00438-REG sequence listing  
; CURRENT APPLICATION NUMBER: US/09/404,650  
; CURRENT FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 6855  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (192) .. (6755)  
US-09-404-650-3  
Alignment Scores:  
Pred. No.: 0 Length: 6855  
Score: 5484.00 Matches: 1237  
Percent Similarity: 59.93% Conservative: 211  
Best Local Similarity: 51.20% Mismatches: 507  
Query Match: 46.07% Indels: 462  
DB: 3 Gaps: 56  
US-09-611-257A-37 (1-2266) x US-09-404-650-3 (1-6855)  
QY 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGlnAlaGlnGly 50  
DB 264 CAGCCCGAGACCCCGAGACCCCATCTCTCCCGCAGGCGCTGGAGAGCTTGTGATGA 323  
QY 51 -----LeuProTyrProAlaLeuAlaProValPhePheTyrLeuSerGln 66  
DB 324 GGTGATTCATGATGCCACACACCAAGACTGGGCGCTATTGCTTCTTCTGCTGCGAGAG 383  
QY 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPhGlnArgIle 86  
DB 384 ACCACACGCCCCGAGACTGTGCATCAAGATGTGTCAACCCCTGTGTGTGAATGTCTTC 443  
QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGlnAsp 106  
DB 444 AGCATGTGTGTATCTCTGTAAGTGGCTGTACACTTGGCATGTATACACCGCGAGAGAG 503  
QY 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126  
DB 504 ATGAGCTGCTGTTCGACCGCTGCAAGATCTGCGAGGCTTGTGATGACTTCATCTTATTC 563  
QY 127 PhePheAlaValGlnMetValValLysMetValAlaLeuGlyIlePheGlyLysCys 146  
DB 564 TTCCTTGGCATGGAATGTGTCAAGATGTGTGGCGCTGGGAGATTTTGGCAAGAGTGC 623  
QY 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166



QY 865 ValAlaThrPheCysMetLeuMetLeuPheIlePheSerIleLeuGlyMet 884  
 |||||  
 DB 2370 GTGGCCACTTCTGCATGCTGCATGCTCTTATCATCTTCACGACCTTGGGAAG 2429  
 QY 885 HisLeuPheGlyCysIlePheAlaSerGluArgAsp---GlyAspThrLeuProAspArg 903  
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 DB 2430 CATATTTTGGCTGGCAAGTTTCAAGCTCCGACGGACACTGGAGACACGGGTGCCGACAG 2489  
 QY 904 LysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGlu 923  
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 DB 2490 AAGAACTTCGACTCCCTGCTGGGGCCATCGTCACTGTCTTCAGATCTCCACCCGAGAG 2549  
 QY 924 AspTrpAsnLysValLeuTrpAsnGlyMetAlaSerThrSerSerTrpAlaIleLeuTrp 943  
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 DB 2550 GACTGGAAAGCTGCTCTTCAACAATGGCAATGGCTCCACTTCTCCCTGGGCTCTCTAC 2609  
 QY 944 PheIleAlaLeuMetThrPheGlyAsnTrpValLeuPheAsnLeuValAlaIleLeu 963  
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 DB 2610 TTTGTGCTCTCATGACCTTGGCACTATGTCTCTTCACTGCTGGGTGGCATCTTG 2669  
 QY 964 ValGlnGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlyIleLeuSer 983  
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 DB 2670 GTGGAGGGCTTCCAGCGCGAG----- 2690  
 QY 984 CysIleGlnLeuProValAspSerGlnGlyIleAspAlaAsnLysSerGluSerGluPro 1003  
 |||||  
 DB 2691 -----GGTACGCCAATGCTCTACTGGAGAG 2720  
 QY 1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013  
 |||||  
 DB 2721 GACCAAGAGCTCATCCAAATAGAAAGTTTGAATAGCTCCAGAGAGCTCGACACAG 2780  
 QY 1014 GlyAspArgLysLeuCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033  
 |||||  
 DB 2781 GGAAGATCCCAAGCTCGCCCAATCCCAATGACCCCAATGGGCAC----- 2825  
 QY 1034 SerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSer 1053  
 |||||  
 DB 2826 -----CTGGACCCC-----AGTCTCCACTGGGT 2849  
 QY 1054 ThrSerThrGlyLeuGlyAlaLeuGlyProAlaSerArgArgThr----- 1069  
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 DB 2850 GGGCACTAGTCTGCTGGGGCTGGGACCTGCCGCCGACTCTACCTGACGACCGGAC 2909  
 QY 1070 -----SerSerSerGlySerAlaIleProGlyAlaIle 1080  
 |||||  
 DB 2910 CCCATGCTGGTGGCCCTGGGCTCCGAAAGACAGATGTCATGCTCTAGGAGATGAC 2969  
 QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaIle 1100  
 |||||  
 DB 2970 TATGACACAGGCTCTGCTGCACGCTCCGAGCTCTTACTACGGGACATAGGGCCGAC 3029  
 QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
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 DB 3030 GCGGCTGGGGCCAGCGGTGCTCTCAGCTGGAC-----AGCTCCAG 3071  
 QY 1121 ArgArgSerProSerGlyLysArgArgSerLeuLeuSerGlyLys---GlyGlnGluSer 1139  
 |||||  
 DB 3072 CACAAACCCCGCTGGCGAGCATGATCCTGCTCTGCGGAGCGCGCGCGCGCG 3131  
 QY 1140 GlnAspGluGlnGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157  
 |||||  
 DB 3132 CGGGTCTGGAGGTTCCCGGAGCAGAGGGCGCGCGCGGACCCCTGCACACCCCA 3191  
 QY 1158 His-----ArgHisArgGly 1162  
 |||||  
 DB 3192 CACGCCCAACCATTCATCAGCGGCCCATTCGGGCAACGCGCACCGCACACCGCGG 3251  
 QY 1163 SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182  
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 DB 3252 ACGTGTCTCCTCGAACAAGGAGCTCGGTGACCTGGCCGAGCTGTGGCCCGCGGTGGGC 3311

QY 1183 LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisLeuAspCysAsn 1200  
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 DB 3312 GCCCAACCCCGGGCGGCTGGAGGGCGGACGGCCCGCGGCAATGAGAGCTGCAT 3371  
 QY 1201 GlyLysSerAlaSerGlyArgGluAlaArgAlaLeuArgProAspAspProLeu---As 1220  
 |||||  
 DB 3372 GGCAGAGAT-GCCCAACATGCG---CAAGAGCTCTTCAACAAGATGGGCGACCGGGGGA 3427  
 QY 1220 PglYAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240  
 |||||  
 DB 3428 TCGCGGGAGGATGAGAGAAATGACCTACACCTGTGCTTCCGCTGCGCAAGATGAT 3487  
 QY 1240 eArgAlaArgLeuProAlaCysTrpLeuGluArgAspSerTrpSerAlaTrpIlePhePr 1260  
 |||||  
 DB 3488 CGACGCTATAAGCCCACTGGTGGAGGTCCGGCAAGACTGTCTGTCTACCTTCTTC 3547  
 QY 1260 obProLysSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280  
 |||||  
 DB 3548 TCCGAGAAACAGGTTCCGGGTCTGTGCAGACATTAATGGCCCAAACTTTCAGACTA 3607  
 QY 1280 eValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300  
 |||||  
 DB 3608 CGTGTCTGGCTTCATCTTCTCACTGATCCACATCGCTCGAGCGGCTCAGAT 3667  
 QY 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTrpIlePheThrAlaVal 1320  
 |||||  
 DB 3668 CGAGGCGCGGACACCGAAGCGATCTTCTCAACGCTGTCAACTACATCTTCAACGCCAT 3727  
 QY 1320 ILeuLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAl 1340  
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 DB 3728 CTTCTGGGCGAGATGACATTAAGATGATCGCTGGGCGCTGTACTTCCGGGACAGGC 3787  
 QY 1340 eThrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360  
 |||||  
 DB 3788 GTACCTAGCGACACTGGAGATGCTGATGAGCTTCTGTCTTCGTGATCATGCA 3847  
 QY 1360 PLeuLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe 1380  
 |||||  
 DB 3848 CATCGTGGTGTCCCTGGGCTCAGCGGGGAGCCAAAGTCTTGGGGTCTCCAGTCTT 3907  
 QY 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400  
 |||||  
 DB 3908 GCGGCTCTGCGCACTTACGCCCCCTGCTGTCTACAGCGGGGCGCGGCTTAAGCT 3967  
 QY 1400 uValValGluThrLeuMetSerSerLeuLeuProIleGlyAsnIleValIleCysCys 1420  
 |||||  
 DB 3968 GGTGTGGAGACATCATCTCTCTCAAGCCCATCGGCAACATGATCTATCTGCTG 4027  
 QY 1420 sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440  
 |||||  
 DB 4028 TGCCCTTCTTCATCATCTTGGCATCTGGAGTGCAGGCTCTTCAAGGGCAAGTTCTACA 4087  
 QY 1440 lCysGlnGlyLysAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTr 1460  
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 DB 4088 CTGTCTGGGCGTGACACCCGCAACATCAGCAGCTCGGACTGCATGCGCCCAACTA 4147  
 QY 1460 rArgTrpTrpValArgHisLysTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh 1480  
 |||||  
 DB 4148 CGGTGTGGTCCATCAAAATACAACTTGACCACTGGGCGCAGGCTCGATGATCTCTCT 4207  
 QY 1480 eValLeuAlaSerLysAspArgLysTrpValAspIleMetTrpAspGlyLeuAspAlaValGln 1500  
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 DB 4208 TGTCTGGCATTCAGATGATGTTGGGTGAACATCATGTAACAATGACCTGGATGCTGTGC 4267  
 QY 1500 uValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTrpIleSerTrp 1520  
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 DB 4268 TGTGACAGAGAGCTGTGACCAACCAACCCCTGATGCTGTGCTTCTATCTCTCT 4327  
 QY 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPh 1540  
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 DB 4328 CCTGTCTATCGCACTTCTTGTGTCTCAACATGTTTGTGGGTGTGCGGTGGAAACTT 4387  
 QY 1540 eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluLysArgLe 1560

[illegible]

Db	5462	CTGCTACTCGCTCCGACGAGAACTGTGGCTGGACAGGCTCTTTATCATCAAGGA	5521
Qy	1884	-----AppserProlyProGlyAlaLeuHis-----	1892
Db	5522	CTCCCTGGAGGGAGGAGCTGACCATCATCGACAACCTGTGGGCTCATCTTCCACACTA	5581
Qy	1893	-----ProAlaIaIa-----	1895
Db	5582	CTCCTCGCTGCGGGCTGCAGAAAGTGTCAACAGACAGACAGAGAGGTGCAGCTGGCTGA	5641
Qy	1896	-----HisAlaArgSerAlaSer-----	1903
Db	5642	GACGGAGGCGCTTCTCCCTGAACCTAGACAGAGTCTGTCCATCTCTGGGTGACGACCT	5701
Qy	1903	eSerLeuGlnHisProThrMetGlnPro-----HisProThrGlnLeuPro	1918
Db	5702	GAGCTCGAGAGACCCCAACAGCTGCCCCACCTGCGCGCAAGACAGCAAGAGGTGAGCTGA	5761
Qy	1918	oGlyProAspLeuLeuThrValArgLysSerGly-----ValSerArgTh	1933
Db	5762	CCCACTGAGGCCCATGGGTGTGGAGAACCTGGGGGAATGCTTCTTCCCTTCTCTCTAC	5821
Qy	1933	rHisSerLeuProAsn---AspSerTyrMetCysArgHisGlySerThrAlaGlnGlyPr	1952
Db	5822	GGCGGCTCGCGCGGATCCAGAGAACTTCTGTGTGAATGAGAGAGATCCCATTCACACC	5881
Qy	1952	oLeuGlnHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerValLeuSerValHis	1972
Db	5882	TGTC-----CGTCCCTGG-----CTGAACAATGACAGCAGTCAACACCCCAAGTCC	5929
Qy	1972	sSerGlnProAlaAspThrSerTyrTyrLeuGlnLeuProLysAspAlaProHis-----	1990
Db	5930	CTTCTCCCGGATGCTCCACGCCCTCTCTGCCCCATGCAACGCGAGTCTTCCACCTGC	5989
Qy	1991	-----LeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProLysLe	2006
Db	5990	AGTGTCTGCCCAAGCAAGAAAGGCCCAAGAAAGGACAGTGGCACTGGAACTCCCCCAAGAT	6049
Qy	2006	uProProProGly-----ArgSerProLeuAlaGlnArgProLeuArgAr	2021
Db	6050	TGGCGTGCAGGGGCTCTCGGCGATCTGCGGCTGACCAAGGGTCAACGTGACCTTCCTCG	6109
Qy	2021	gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlnAspLe	2041
Db	6110	GCAGGCCCAACGGAGCAGACAGTGGCTGGAC-----	6140
Qy	2041	uLeuAlaGluValSerGlyProSerProProLeuAlaArgLarTyrSerPheTyrGly	2061
Db	6141	-----GCCAGCCCCAGAGACTCCGGGGGAGAGCTGCAGACACAGCTCGAGGA	6187
Qy	2061	nSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetTh	2081
Db	6188	CAGCTGTGACCTTGAGGCAGACAGCCCCCGGCGTGGC-----CTGGG	6226
Qy	2081	rProProAlaProCysProGlyProGluProAsnTyrGlyLysGlyProProGlnPAr	2101
Db	6227	GCGGCGGCGGCTGCTCCAGAGACCCCGGAGCGGCGCTGTC-----CCGCGCGCTCG	6277
Qy	2101	gSerSerLeuGlnLeuAspThrGlnLeuSerTyrPheSerGlyAspLeuLeuProProGly	2121
Db	6278	CCGCGCGCTTGAGCTGG-----	6293
Qy	2121	YgLYglnGlnGluProProSerProArgAspLeuLysLysCysTyrSerValGlnAlaGly	2141
Db	6294	-----CGCGGCGCGGGGCTTTCAGCCTCGGGGGGCTCGCGGGGCG--	6323
Qy	2141	nSerCysGlnArgArgProThrSerTyrLeuAspGlnGlnArgArgHisSerTyrIleAlaVal	2161
Db	6333	-----CANTCAGCGCAGCACAAGCAGACGCGGGG	6358
Qy	2161	lSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn-----	2178
Db	6359	CTGC-----ACGAGCCCGGGCTGACCAACAGACTCATGAGACCCCTTGGAGCGAGAGGG	6415



Db 1554 GGCCTTACCAAGCCCTGCAGAGCCGCCAGCCCTGGCC----- 1595  
 Qy 479 SerSerSerCySerSerArgSerSerHisArgArgLeuSerValHisValLeuValHisValHis 498  
 Db 1595 ----- 1595  
 Qy 499 His 518  
 Db 1595 ----- 1595  
 Qy 519 ProGluLeuLeuGlnAspArgAlaAsnGlySerArgArgLeuMetLeuProProProSer 538  
 Db 1596 ----- 1601  
 Qy 539 ThrProAlaLeuSerGlyAlaProProGlyGlyValGluSerValHisSerPheTyHis 558  
 Db 1602 GCCCGGCC-----CCCGCAAACTGGGCC-----CAC 1631  
 Qy 559 AlaAspCyHisValLeuGluProValArgCyGlnAlaProProProArgSerProSerGlu 578  
 Db 1632 GCCAAG-----GAGCCCCGGCACTACCACTGTGCGCAACATAGCCCTTGAT 1682  
 Qy 579 AlaSerGlyArgThrValGlySerGlyValValTyProThrValHisThrSerProPro 598  
 Db 1683 GCCAGCCCAACACCTG-----GTGCAGCCCATC 1712  
 Qy 599 ProGluThrLeuLeuGlyValAlaLeuValGluValAlaAlaSerSerGlyProProThr 618  
 Db 1713 CCGCCCAACCTG----- 1724  
 Qy 619 LeuThrSerLeuAsnHisLeuProGlyProTySerSerMetHisValLeuLeuGluThr 638  
 Db 1724 ----- 1724  
 Qy 639 GlnSerThrGlyAlaCyGlnSerSerCyValSerHisSerSerProCyLeuValAlaAsp 658  
 Db 1724 ----- 1724  
 Qy 659 SerGlyValaCyGlyProAspSerCyAspProTyCyAlaArg----- 672  
 Db 1725 -----GCTTCGGATCCCGGCAAGCTGCCCTTGCTGCAGCATGAGAGAGCGCGCGGCC 1778  
 Qy 673 AlaGlyAlaGlyValGluValAlaLeuValAspArgGluMetProAspSerAspSerGluAla 692  
 Db 1779 TCGGGCTGGGGCAACACCGAC---TCGGGCAAGAGGGCTCGGGCTCGGGAGCTCCGCT 1835  
 Qy 693 ValTyArgLysPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg 712  
 Db 1836 GGTGGCGAG-----GACGAGGCGGATGGGAGCGGGCCCGAGACGAGACGAGAC 1889  
 Qy 713 GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu----- 726  
 Db 1890 TCCTCAGAACTGGGGAAAG 1949  
 Qy 727 -----AlaPheTPArgLeuHisCyAspThrPheArgLysHisValAspSerLysTy 744  
 Db 1950 TGCAGGAGATGTGGCGGAGAGACCGAGCCAACTGCGCGCATCTGAGACAGCAAGTAC 2009  
 Qy 745 PheGlyArgGlyHisMetHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 764  
 Db 2010 TTCAACGGGGCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2069  
 Qy 765 HisGluGlnProGluGluLeuThrAsnAlaLeuGluHisSerAsnHisValPheThrSer 784  
 Db 2070 CACAGAGAGCGGAG 2129  
 Qy 785 LeuPheAlaLeuGluMetLeuLeuValLeuValValTyArgLysProPheGlyTyHis 804  
 Db 2130 ATGTTTGCCCTGGAGATGATCTGAAAGCTGGCTGATTTGGGCTTTCGATACCTGATGCT 2189  
 Qy 805 AsnProTyArgHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 824  
 Db 2190 AACCCCTCAACATCTTCAGAGAGATCATCTGATCATCATCATCATCATCATCATCATCATCAT 2249

Qy 825 GlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu 844  
 Db 2250 CAGCGGAGAGGTGGGTGTGTGGGTGGGACCTTCCGCTGTGGCGGTGGAACCTG 2309  
 Qy 845 ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn 864  
 Db 2310 GTGGCTTCATGCTCTCCCTCGCGGCGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2369  
 Qy 865 ValAlaThrPheCysMetLeuLeuMetLeuPheHisPheHisSerHisLeuGlyMet 884  
 Db 2370 GTGGCACCCTTCGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATGCTGTGATG 2429  
 Qy 885 HisLeuPheGlyCysValSerPheAlaSerGluArgAsp---GlyAspThrLeuProAspArg 903  
 Db 2430 CATATTTTGGCTGCAAGTTCAAGCTCCGCAAGAGACTGGAACACTGGAACAGCGCCGACAGG 2489  
 Qy 904 LysAsnPheAspSerLeuLeuThrAlaHisValHisValPheGlnHisLeuThrGlnGlu 923  
 Db 2490 AAGAACTTCGATCTCCCTGCTGTGGGCAATGCTACTGTGTTCAGATCTTCACACCGAGAG 2549  
 Qy 924 AspTrpAsnLysValLeuTyArgGlnHisValAlaSerThrSerSerTrpAlaAlaLeuTy 943  
 Db 2550 GACTGGAAGGTGCTTCTTACATGAGCATGAGCTCCACATCTTCCTCGGGCTCCCTCTAC 2609  
 Qy 944 PheHisAlaLeuMetThrPheGlyAsnTyValLeuPheAsnLeuValAlaHisLeu 963  
 Db 2610 TTTGTGCTCTCATGACCTTGGCAACTATGTCTTCAACTGTGTGTGGGCAATCTG 2669  
 Qy 964 ValGluGlyPheGlnAlaGluGluHisSerLysArgGluAspAlaSerGlyGlnLeuSer 983  
 Db 2670 GTGAGGGCTTCCAGGGAG----- 2690  
 Qy 984 CysHisLeuProValAspSerGlnGlyValAspAlaAsnLysSerGluSerGluPro 1003  
 Db 2691 -----GTGAGCGCAATGCTCTACTCGAGCAG 2720  
 Qy 1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013  
 Db 2721 GACCAAGCTCATCAACATGAGAAGATTGATAGCTCCAGAGAGCGCTGACAGCAGC 2780  
 Qy 1014 GlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033  
 Db 2781 GGAATGCCAAGCTCTGCCAATCCCATGACCCCAATGGGAGAC----- 2825  
 Qy 1034 SerLeuLeuProProLeuLeuHisHisHisHisHisHisHisHisHisHisHisHisHis 1053  
 Db 2826 -----CTGGAACCC-----AGTCTCCCACTGGGT 2849  
 Qy 1054 ThrSerThrGlyLeuGlyAlaLeuGlyProAlaSerArgArgThr----- 1069  
 Db 2850 GGGACCTAAGTCTCTGCTGGGCTGGGAGCTGCGGCCCGCCCGCACTTCACAGCAGCGGAC 2909  
 Qy 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080  
 Db 2910 CCATGCTGTGTGGCTCGGCTCCGAAAGAGAGATGATCATGCTCTAGGAGAGATGAC 2969  
 Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProHisSerAlaAla 1100  
 Db 2970 TATGACAGAGGCTCTCCGTGACAGCTCCCGAGGCTCCACTACAGGAGCATGGGGCGGAGC 3029  
 Qy 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
 Db 3030 GCGGCTGGGCGAGCGCTCCCTCAGCTGAGAC-----AGCTCAAG 3071  
 Qy 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu---GlyGlnGluSer 1139  
 Db 3072 CACAAGCGCGCTGGGGGAGCATGACTCCCTGCTCTTCGAGAGCGCGCGCGCGCC 3131  
 Qy 1140 GlnAspGluGluGluSerGluGlu-----GluArgLysSerProAlaGlySerAsp 1157  
 Db 3132 CCGGTCTGCAAGGTTCGCGGAGAGAGAGGCGCGCGCGGCGCGCACCCCTGCACACCCCA 3191



QY	1158	His-----	-----ArgHisLeuGly	1162
Db	3192	CACGCCCAACCAATTCATCAAGGCCCCCTGTGGCAACCGCCACCGCCACCGCCGCGG	3251	
QY	1163	SeuLeuGIuArGvGIuAlaIySeSerPheAspLeuProAspThrLeuGIuAlProGIy	1182	
Db	3252	ACGCTGTCCCTCGACACAGGAACTCGGTGAACTGGGCCCAAGCTGGTCCCGCGGTGGC	3311	
QY	1183	LeuHISArGThraIaSerGIyArg-----GlySerIaSerGIuHISgInAspCyAsn	1200	
Db	3312	GCCACCCCCCGGGCGCGCTGGAGGGCGGCAAGCCCGGCCCGGCATAGAGACTCGAAT	3371	
QY	1201	GIyIySeSerIaSerGIyArgLeuAlaArgAlaLeuArgProAspProIleu-As	1220	
Db	3372	GCGAGGAT-GCCCGACATCGC---CAAGAGCTTCCACCAAGATGGCGACCGCGGGA	3427	
QY	1220	PGIyAspAspAlaAspAspGIuGIyAsnLeuSerIyGIyIuArgAlaArgAlaTrpI	1240	
Db	3428	TCCGGGGAGATAGAGAGAAATCGATTACACCTGTGCTTCCGCGTCGCAAGATAT	3487	
QY	1240	eArgAlaArgLeuProAlaCyTyIyLeuGIuArgAspSerTrpSerAlaTyIlePheP	1260	
Db	3488	CGACGCTATTAAGCCCGCATGTGGAGAGTCGGGAAGACTGCTGTCTATACCTTCTC	3547	
QY	1260	oProGISeArArgPheArgLeuLeuCyHisArgIleIleThrHISyIySePheAspH	1280	
Db	3548	TCCCAAGAAACAGTTCGCGGTCTGTGTCAACCATTAATCCCAAACTCTTCGACTA	3607	
QY	1280	eValIyLeuAlaIleIlePheLeuAsnCyAlleThrIleAlaIleMetGIuArgProIyS	1300	
Db	3608	CGTCCCTCGGCTTCATCTTCTCATCTGATACCATCGCCCTGGAGCGGCTTCAGAT	3667	
QY	1300	eAspProHISerIaGIuArgIlePheLeuThrLeuSeArAsnTyIlePheThrAla	1320	
Db	3668	CGAGCGCGGACAGCACCGAAGCATCTTTCTCACCGTGTCCAATCAATCTTCAAGGCAT	3727	
QY	1320	IlePheLeuAlaGIuMetThrValIyValAlaLeuGIyTrpCySpPheGIyGIuAla	1340	
Db	3728	CTTCTCGGCGCAGATGACATTTGAAGGTGTGTCTGCTGGCCCTGTATCTTCGCGGACGAGC	3787	
QY	1340	aTyIleuArgSerSerTrpAsnValIleuAspGIyLeuLeuValIleuIleSeValIleAs	1360	
Db	3788	GTACTTACGACAGCACTGAAACGTGTGATGCTTTTGTCTTCTCGTGTCAATCATCGA	3847	
QY	1360	PileuLeuIleSerMetValSerAspSerGIyThyIySileuGIyIleMetLeuArgValle	1380	
Db	3848	CATGTGTGTCTCCCTGGCTCAAGCGGGGAGCCAAAGTCTTGGGGGTCTCCAGTCTT	3907	
QY	1380	uArgLeuLeuArgThrIleuArgProLeuArgValIleSeArAlaGIuGIyLeuIySle	1400	
Db	3908	GCGGCTCTCGGCAACCTTACGCCCTCGTGTATCAGCGGGCGCGCGGCTCGAAGCT	3967	
QY	1400	uValIyAlaGIuThrIleuMetSerSerLeuIyProIleGIyAsnIleValIleIleCyS	1420	
Db	3968	GGTGTGTGAGACATCATCTCTCCCTTAACCCATCGCAACATCGTGTCAATCTCTGTG	4027	
QY	1420	sAlaPhePheIleIlePheGIyIleLeuGIyValGIuLeuPheIyGIySlyPhePheVa	1440	
Db	4028	TGCTCTTTCATCATCTTGTGGCATCTTGGAGTGTGAGTCTTTCAAAGGCAAGTCTTACA	4087	
QY	1440	IySgInGIyGIuAspThrArgAsnIleThrAsnIySeSerAspCyAlaGIuIaSerTy	1460	
Db	4088	CTGTCTGTGGCGGTGAGCACCCGGAACATCACCAACGCTCGGACTGAGCGCGCAACTA	4147	
QY	1460	rArgTrpValArgHISlyGIyTrAsnPheAspAsnLeuGIyGIuAlaIleuMetSerLeuP	1480	
Db	4148	CCGCTGGGTTCATCAACAATCAACTTGTGAACAACCTGGGCGCAGGCTCGAGTCTCCCTT	4207	
QY	1480	eValIleuIaSerIyAspGIyTrpValAspIleMetTyIyAspGIyLeuAspAlaValGI	1500	
Db	4208	TGTCTTGGCATCAAGAGATGTGTGGTGAACATCATGTACATGATGACTGTGCTTGC	4267	
QY	1500	yValAspGIuGIuProIleMetAsnHISAsnProTrpMetLeuLeuTyIlePheIleSerP	1520	

Db	4268	TTGTGGACCGAGCCTCTGTGAACCAACCAACCCCTGGAATCTGTGTACTTCACTTCTCTT	4327
QY	1520	eLeuLeu1IeVala1aPhePheValLeuAanMetPheValGlyVala1Vala1GluAenph	1540
Db	4328	CTGTCTACTGTGTGACGCTTCTTTTGTGCTCAACATGTTTGTGGTGTGTGTGGAGAACTT	4387
QY	1540	eH1LyCysArgGlnH1seGln1Glu1Glu1Glu1a1aArgArgArg1Glu1Glu1Arg1e	1560
Db	4388	CCACAAGTCCGGGACGACCAAGGAGGCTGAAAGGCGCGGGCGGTGAAGAGAGCGGCT	4447
QY	1560	uArgArgLeuGlu1uArg1uArg1aGlyVala1aGln1CysLysProTyrTyrSerAspTyrSe	1580
Db	4448	GCGGCGCTGTGAGAGAAAGCGCGGAAAGCCCAAGCGCTGCTTACTATGCACTTATG	4507
QY	1580	rArgPheArgLeuLeuValH1sh1sLeuCysThrSerH1eTyrLeuAspLeuPhe1IeTh	1600
Db	4508	TCACACCCGGGTGTCTTCCACTCCATGTGCACACAGCACATCACTGGAACATCTTCATCAC	4567
QY	1600	rGlyVal1IeGlyLeuAanVala1ThrMetAlaMetGluH1eTyrGln1ProGln1I	1620
Db	4568	CTTCATCATCTGCTCAACGATGGTGCACCAATGCTCCTGGACACTACATCAAGCCCAAGTC	4627
QY	1620	eLeuAspGlu1aLeu1uArg1IeCysAenTyr1IePheThrVal1IlePheVal1LeuGluSe	1640
Db	4628	CTGTGAGACAGCCCTCAAGTACTGCAACTATATGTTACCACTGTCTTGTGTGAGAGGC	4687
QY	1640	rValPhe1uArgLeuVala1aPheGlyPheArgArgPhePheGlnAspArgTyrAanGluSe	1660
Db	4688	TGTGTCTGAAGCTGTGTGCATTTGTGTCTGAAGCGCTTCTTCAAGGACCGATGGAACGAGCT	4747
QY	1660	uAspLeuVala1IeValLeuLeuSer1IeMetGly1IeThrLeuGlu1Glu1IeGluVala	1680
Db	4748	GGACTCTGACCTGTGTGTCTACTGTGTGACATATGGGATCAACCTGAGAGAGATCGAAGTCAA	4807
QY	1680	nAlaSerLeuPro1IeAanPro1H1e1IeArg1IeMetArgVala1LeuArg1IeAlaAr	1700
Db	4808	TGCGAGCCCTGCCCACATCAATCCACATCATATCCGATATAGGGTTTGGCGATTGCCCG	4867
QY	1700	gValLeu1uArgLeuLeu1uArg1IeMetArgAlaLeuLeuAspThrValMetG1	1720
Db	4868	AGTCTGTGAAGCTGTGTAAGATGGCCACAGAAATCGGGCCCTGTGTGACACGGTGTGCA	4927
QY	1720	nAlaLeuProGlnVala1uArg1uArg1IeLeuLeuPheMetLeuLeuPhe1IePheAl	1740
Db	4928	AGCTTTGGCCCGAGGTGGGCAACCTGGGCGCTCTCTTATCTGCTCTTCTTCATCTTATGC	4987
QY	1740	aAlaLeuGlyVala1GluLeuPheGlyAspLeuGlu1uArg1uArg1IeProCysGlu1	1760
Db	4988	TGCTCTCGGGGTGAAGCTCTTTGGGAAAGTGTCTGTGACAGCAACAGAACCCGTGTGAGGG	5047
QY	1760	YLeuGlyArgH1sa1aThrPheArgAanPheGlyMetAlaPheLeuThrLeuPheArgVa	1780
Db	5048	CATAGACCGGATGCCACCTTCGAGAACTTCGGATGGCTTCTTCTACACTCTTCCAGGT	5107
QY	1780	1SerThrGlyAspAanTyrAanGly1IeMetLysAspThrLeuArgAspCys--AspG1	1799
Db	5108	CTCCACGGGTGACAACTGGAACGGGATCATGAAGAGCACCTGTGGGAGCATGCCACCGCA	5167
QY	1799	nGluSerThrCysArg1rAanThrVal-----1IeSerPro1IeArgPheValSerPheVa	1817
Db	5168	CGAAGCGGAGCTGCTGAGCAAGCCGTGCAAGTTGTGTCCGCTGTACTTCGTGAGACTTCGT	5227
QY	1817	1LeuThrAlaGlnPheValLeuValAanVala1Vala1aValLeuMetLysH1sLeuG1	1837
Db	5228	GCTCACCGCGCAGTCTGTCTCATCAACATGATGTGTGTGTGTGTCTCATGAAGCACTGTGA	5287
QY	1837	uGluSerAsn1uArg1uArg1uArg1uArg1uArg1uArg1uArg1uArg1uArg1uArg1u	1857
Db	5288	CGACGAGCAACAGGAGCGGAGGAGGACCGCGAGATGATGATGCGAGACTCGAGCTGTGAGAT	5347
QY	1857	t---LysThrLeuSerProGlnProH1sSerProLeuGlySerProPheLeuTyrProG1	1876

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Db      5348 GGGCCATGCGCTGGGCGCTGGCCCGAGGCTGCTACCGGCTCCCGGCGCC---CTGG 5404
Qy      1876 yValgluglyProAsp-----1881
Db      5405 C---CGAGGGCCGGAGAGGGGCGGGCGGGGGGACACCGAGGGCGGCTTGTGCGCGG 5461
Qy      1882 -----SerPro-----1883
Db      5462 CTGCTACTCGCTGGCCCGAGAGAACCTGTGCTGACAGCGCTCTTTAATCATCAAGA 5521
Qy      1884 -----AapserProlyeProglYalaueuhis-----1892
Db      5522 CTGCTTGAGGGGAGTGAACATCATGACAACTGTGGGCTCCATTTCCACACTA 5581
Qy      1893 -----ProAla1a-----1895
Db      5582 CTGCTGGCGCTGGCGGCTGCAAGAGTGTCAACAGCAAGAGAGGTGAGCTGCTGA 5641
Qy      1896 -----HisAlaArgserAlaSer-----Hisph 1903
Db      5642 GACGAGGCGCTTCTCCCTGAACCTGACAGAGTCTCTGTCATCTCTGGGTGACGACT 5701
Qy      1903 eSerleugluHisProthmetGlnPro-----HisProthrgluueupr 1918
Db      5702 GAGCTCTGAGAGACCCCAAGCTGCGCACTGGCCGCAAGAGACAGCAAGGCTGAGCTGA 5761
Qy      1918 oglyProAspleuethrValArglysergly-----ValserArgth 1933
Db      5762 CCGACGAGGCCATGATGCTGTGGGAGACCTGGGGAAATGCTTCTCCCTTGTCTCTAC 5821
Qy      1933 rHisserleuproAsn---AapserlyMetCyValgHiglySerthralagluylpr 1952
Db      5822 GGGCGTCTCCCGGATCCAGAACTTCTGTGTGAGATGAGAGAGATCCCATTTCAACC 5881
Qy      1952 oleugluHisArgglyTrglYleuProlyValaglnSerglySerValleuserValh1 1972
Db      5882 TGTC---CGGCTCTGG---CTGAACATGACAGAGCTACAGCACCCCAAGTCC 5929
Qy      1972 sSerGlnProAlaAspThrserTyrIleleuglnleuProlyAspAlaProhis-----1990
Db      5930 CTCTCTCCCGGAGTCCCTCCAGCCCTCTCTGCCATCCAGCGAGTTCCTTCCACCTGC 5999
Qy      1991 -----LeuleuGlnProHisserAlaProthTrglYThrIleProlyle 2006
Db      5990 AGTGTCTGCCAGCCAGAAAGGCCAGAAAGGCGACTGAGCACTGGAACTCTCCCAAGAT 6049
Qy      2006 uProProProglY-----ArgserProleuAlaglnrgrProleuAagAr 2021
Db      6050 TGGCTGCGAGGGCTCTGGGCGATCTCTGGGTCACTCAAGGCTCAATGTAACCTCTCTCG 6109
Qy      2021 gGlnAlaAlaIleArgThrAspSerleuAspValglnIlyleuGlyserArgluAsple 2041
Db      6110 GCAGGCCACCGGAGGACGACACGTGCTGAC-----6140
Qy      2041 uLeuAlaGluValserglyProserProProleuAlaArgAlaTyrSerPheTrglYgl 2061
Db      6141 -----GCCAGCCCAAGCACTCCGCGGAGAGCTGACAGCAAGCTGAGGA 6187
Qy      2061 nSerSerThrlaInlaInlnHisSerArgserHisSerlyglIleSerlyHisMetth 2081
Db      6188 CAGCTGACCTGAGCCAGCAAGCCCCCGGCGGTGC---CTGGG 6226
Qy      2081 rProAlaArProCyArProglYProgluProAvnTrpGlyLyserglyProProgluInThrAr 2101
Db      6227 GCGCGCGCGCTCTCTCAAGAACCCCGGCGCGCTGTC---CCCGCGGCTCG 6277
Qy      2101 gSerSerleuGluLeuAspThrTrglYleuSerTrpIleSerglyAspleuLeuProProgl 2121
Db      6278 CCGCGCGCTGAGCTG-----6293
Qy      2121 yGlyGlnGlnGluProProserProArgAspleuAspleuAspleuValglnIle 2141
Db      6294 -----CGCGCGCGGCGCTCTTCAAGCTTGGCGGCGCGGCG---6332

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Qy      2141 nSerCyGlnArgArgProThrSerTrpLeuAspGlnArgArgHisSerIleAlaVa 2161
Db      6333 -----CATCGCCGAGCCAGACGACGCGGAG 6358
Qy      2161 lSerCyLeuAspSerSerIleSerInProHisleuglyThrAspProSerAsn-----2178
Db      6359 CTCC---ACCAAGCCGAGGCTGACACCAACGACTCATGACACCTTGGAGACAGAGG 6415
Qy      2179 -LeuglyGlyGlnProleuGlyIlyProglYserArProlyValYleuSerProPr 2198
Db      6416 CCGCGGTGGCGGCGGCGGCGGCGGCGGCGGAGCACTGAGAGACCTGACGAGCT 6475
Qy      2198 oSerIleThr-----IleAspProProgluSerGlnIlyProArgThrProProse 2215
Db      6476 CTGCTACCTCTCCCTCTTCTGCGCGCGCGCC-----CCGCGCGCAGC 6517
Qy      2215 rProglYIleCyLeuArgArgAlaProserSerAspSer-----LysAs 2231
Db      6518 CCGCGGCTCTACGCGCGCCGAGAGTTTCAAGACACACAGACGCTGAGCGCGCGCGCG 6577
Qy      2231 pProleuAlaSerGlyProProAspSerMetAlaAlaSerProSerProlyleAspVa 2251
Db      6578 CCGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6635
Qy      2251 lLeuSerleuSerGlyLeuSerSerAspProAlaAspleuAspPro 2266
Db      6636 -----CGCAGCAAGAGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6665

RESULT 10
US-09-404-650-12
; Sequence 12, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-404-650-12

Alignment Scores:
Pred. No.: 0
Score: 5418.50
Percent Similarity: 60.47%
Best Local Similarity: 51.57%
Query Match: 45.52%
Gaps: 53

US-09-611-257A-37 (1-2266) x US-09-404-650-12 (1-6503)
Qy      27 GLyAlaGlyLyArgProglYProglYserAlaGlnLyAspProglYserAlaAspSer 46
Db      320 GGAATCACTGAGAGCGCGGCGCGCGAGTCCCTTCATCTCCATCAGGCTGAGAGAG 379
Qy      47 GlnAlaGlnGly-----LeuProTyProAlaLeuAlaProValAlaPhePhe 62
Db      380 CCAATTGGAAGAGAACCAACCTGACGTCCACATCCAGACTGCTCTGTGTGCTTCTTC 439
Qy      63 TyrLeuSerGlnAspSerArProArgSerTrpCyLeuArgThrValCyAsnProTrp 82
Db      440 TGCCTGCGCAGACACAGAGCCCAAGAACTGTGATCAAGATGATTGTAAACCGCTGG 499
Qy      83 PheGlnArgIleSerMetLeuValIleLeuLeuAspCyValThrleuglyMetPheArg 102

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Db 500 TTGAGATGTGTGAGCATGCTGATTCTTGCTGAACGTGTGACCTCGGGCATGTACGAG 559  
 QY 103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAsp 122  
 Db 560 CCATGTGATGACATGAGAGTGCCCTGTGGAACCGTTGCAAGATCTCGACAGGCTTCGATGAC 619  
 QY 123 PheIlePheAlaPhePheAlaValGluMetValValMetValAlaLeuGlyIlePhe 142  
 Db 620 TTGATCTTCACTTCTTTGCTGATGAGAGTGTGCTTAAGTGTGGCCCTCGGACATTTT 679  
 QY 143 GlyIysLysCysPheIleuGlyAspThrTrpAsnArgLeuAspPheIleAlaIleAla 162  
 Db 680 GCGAAGAAGTGACTACTCGGAGACACATGGAACCGCTGGAATTTCTTCAATGTCATGGCA 739  
 QY 163 GlyMetLeuGluTyrSerIleuAspLeuGlnAsnValSerPheSerAlaValArgThrVal 182  
 Db 740 GGGATGGTTGAGTACTCTGTGACCTACGAAACATCACTGACACCTGACACCTCGACTG 799  
 QY 183 ArgValLeuArgProMetArgAlaIleAsnArgValProSerMetArgIleLeuValThr 202  
 Db 800 CGTGTCTGAGGCTCTCAAGGCCATCAACCGTGTACCAAGATGCGGATCCTGTGTGAAC 859  
 QY 203 LeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhe 222  
 Db 860 CTGCTCTCGACACGCTGGCCCATGTGGGGAACGTGCTCTGCTGTTTCTTCGTCTTC 919  
 QY 223 PheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPhe 242  
 Db 920 TTCATCTTGGGCATCATGCGGTGACGCTCTGGGCGGCTGCTACGGAACCGCTGCTTC 979  
 QY 243 LeuProGluAsnAspPheSerLeuProLeuSerValAspLeuGluArgTyrTrpGlnThr 262  
 Db 980 CTGGAAGAAGATCTTCAACCATCAAGGGGATGTGGCTGCCCCCTTAATTAACCAACGAG 1039  
 QY 263 AsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCys 282  
 Db 1040 GAGATGACGAGATGCGCTTATCTGCTCCCTGACTGGGGAACAATGGCATMGAGCTGC 1099  
 QY 283 ArgSerValProThrLeuArgIleAspGlyGlyGlyProProCysGlyLeu----- 300  
 Db 1100 CACGAGATCCCGCACTGAAGAGCAG-----GGCCGGGAAGCTGCTGTCCAAA 1150  
 QY 301 -----AspTyrGluAlaTyrAsnSerSerAsnThr-----CysVal 314  
 Db 1151 GATGATGTGATATCATTTGGGGGCGGGGCGCCAGAGACTCAAGCCAGCGGTCTGTCTGC 1210  
 QY 315 AsnTrpAsnGlnTyrTrpThrAsnCysSerAlaGlyGluHisAsnProPheIysGlyAla 334  
 Db 1211 AACTGGAACCGCTACTACAAACGTCTGCGGACGGGCAACGCCAACCTCAAGAGGCGCC 1270  
 QY 335 IleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlu 354  
 Db 1271 ATCAACTTTGACAAACATGGCTATGCGGGATGTGATTTTCCAGGTGATCACTGTGAA 1330  
 QY 355 GlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyr 374  
 Db 1331 GGTGGGTGAGATCATGTACTATGTGATGAGCGCATTTCTTTCAACAATCTTCACTAC 1390  
 QY 375 PheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuCysLeuValIle 394  
 Db 1391 TTCATTTCTGCTCATATGAGGCTCTTCTTCAATGATCAATGTCCTGTTGTCAAT 1450  
 QY 395 AlaThrGlnPheSerGluThrIlysglnArgGluSerGlnLeuMetArgGluGlnArgVal 414  
 Db 1451 GCAACCCAGTTCTCTAGACCAAGCAACGGGACACCGCTATGTGTGAGCAACCCGAG 1510  
 QY 415 ArgPheLeuSerAsnIleSerThrLeuAlaSerPheSerGluProGlySerCysTyrGlu 434  
 Db 1511 CGCTACTGTCTC---TTCAGACAGGTGGCCAGTTAGCGTGAAGCCGGTATGCTATGAG 1567  
 QY 435 GluLeuLeuIysTyrLeuValTyrIleLeuArgValAlaAlaArgArgLeuAlaGlnVal 454  
 Db 1568 GAGATCTTCCAAATATGTCTGTACATCTTTCGCAAGGCCAAGGCGCTGAGCCCTC 1627

QY 455 SerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGln 474  
 Db 1628 TACAGGCCCTGCAGAACCGG----- 1648  
 QY 475 GluThrGlnProSerSerSerCysSerArgSerHisArgArgLeuSerValHisIleu 494  
 Db 1648 ----- 1648  
 QY 495 ValHisHisHisHisHisHisHisIleTyrHisIleuGlyAsnGlyThrLeuArgAla 514  
 Db 1648 ----- 1648  
 QY 515 ProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeu 534  
 Db 1649 -----GCGCAGGCCATAGGCG----- 1663  
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 Db 1664 -----CCGGGACACACAGCC-----CCTGCCAAGCCTGGGCCC----- 1696  
 QY 555 SerPheTyrHisAlaAspCysHisIleuGluProValArgCysGlnAlaProProArg 574  
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 QY 575 SerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHis 594  
 Db 1739 AGCCCCCTGGAC-----CCCACTCCAC 1762  
 QY 595 ThrSerProProProGluThrLeuLysGluLysAlaLeuValGluValAlaIleSerSer 614  
 Db 1763 ACACGTGGCAGGCC----- 1777  
 QY 615 GlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLys 634  
 Db 1777 ----- 1777  
 QY 635 LeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCys 654  
 Db 1778 -----ATCTCTCCATT 1789  
 QY 655 LeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672  
 Db 1790 CTGGGCTCTGAC-----CCAGCAGACTGCCCTCACTGCGACAGCAGGCA 1834  
 QY 673 -----AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSer 688  
 Db 1835 GGCAGCGGCGCTCTGGGCGCTGGGCGACACTGAC--TCAGGCCAGAAAGGCTCAGATTCT 1891  
 QY 689 AspSerGluAlaValTyrGluPheThrGlnAspAla---GlnHisSerAsp-LeuArgAs 707  
 Db 1892 GGTGGCTCTGCAGAGCGCGAAGCCAAATGGGATGATCTCCAGAGCATGAGGATGGGTC 1951  
 QY 707 PProHisSer-----ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSer 724  
 Db 1952 TCCTGAGACTGGGGAAGAGAGAGACAGACAGCGGG-----CAGCCCGCACTG 2002  
 QY 724 rValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerIleTyr 744  
 Db 2003 TGTGGG-GATGTGTGGCCGAGACACGAAAAAGCTGGGGCATCTGTGACAGCAAGTA 2061  
 QY 744 rPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGlyTyr 764  
 Db 2062 CTTCAACAGAGTATCATGATGATCTATCTGTGTGAACAGTCACACATGGGATGAGAGA 2121  
 QY 764 rHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer 784  
 Db 2122 CCACGAACAGCCCGAGAGCTGACCAACATCTTGGAGATTCGAAATGTGTCTTACCAG 2181  
 QY 784 rLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLys 804  
 Db 2182 TATGTTTGGCCCTGGAGATGATCTGAAATGCGCCGCTTGGGCTTTCGACTACTCGG 2241



Db	4237	CTGGGCGCAGGCAATTGATGTCCTTTGCTTGGCTTCCAGGACGGCTGGTGAACAT	4236
Qy	1491	emcETyAsp1yLeuaspAlaVal1g1Val1AspGln1Pro1leuEAsn1AsenPr	1511
Db	4297	CATGTATATATGATTGAATGCTGTTGGCTGTGGACAGAGCACTGAAACCAACCAACC	4356
Qy	1511	oTyrMetLeuLeuTyrPhe11eSerPheLeuLeu11eVal1AlaPhePheVal1LeuAsnMe	1531
Db	4357	CTGATGCTACTGTAACCTTATTTGGTTCTGCTCATGTCTGACGCTTCTTGTGCTCAACAT	4416
Qy	1531	tPheVal1g1Val1Val1Val1G1uAsnPhe11eVal1yCyArg1nhi1g1nG1uG1uG1	1551
Db	4417	GTTTGCGGCGCTGGTCTGGAGAACTTCCAAAGTGGCCGGAGCAACAGAGGCTGAGAA	4476
Qy	1551	uAlaArgArgArg1uG1u1y1sArgLeuArgArgLeuG1u1y1s1y1sArgArg1y1sAlaG1	1571
Db	4477	GGCCCGAGGCGTGAAGAGAAACGGCTCGGGCGCTGGAAAGAAAGCGCCCTAAGGCTCA	4536
Qy	1571	nCyAluAspTyrTyrSerAspTyrTyrSerArgPheArgLeuLeuVal1h1s1leuCySth	1591
Db	4537	GAGCGTGCCCTACTATGATGTAACCTACCTGCTCCCAAGGCTGCTCATCTCACTCACTGATGCAC	4596
Qy	1591	rSerH1sTyr1LeuAspLeuPhe11eTnrg1yVal11eG1yLeuAsnVal1Val1TnMetAl	1611
Db	4597	CAGCCACTACCTGGACATCTTCACTTACCTTATCATCTGCTCATATGTGTGCACCATGTC	4656
Qy	1611	ameG1uH1sTyrGlnGlnProGln11eLeuAspG1uAlaLeu1y1s11eCyAsenTyr11	1631
Db	4657	CTGGAGACACTAACCAACGCTTACATCCCTTGAAGACAGGCTTAAAGTACTGCAACTACAT	4716
Qy	1631	ePheThrVal11ePheVal1LeuG1uSerVal1Phe1y1sLeuVal1AlaPheG1yPheArgAr	1651
Db	4717	GTTCAACCACTGCTTTGGTGTGAGAGGCTGTGCTGAAGCTGGTGCACTTGGCTCGAAGCG	4776
Qy	1651	gPhePheGlnAspArgTnrg1PasnG1nLeuAspLeuAla1e1Val1LeuLeuSer11eMetG1	1671
Db	4777	TTTCTTCAAGAGCCGATGGAAACAGCTGGACCTGCACTGTGTGCTGTCCGTCAAGG	4836
Qy	1671	Y11eThrLeuG1uG1u1eG1uVal1AsnAlaSer1eLeuPro11eAsnPro11e11eAr	1691
Db	4837	CATCACTGAGAGAGATCGAGATCATGATCCGCCCTTCCATCAACCCACATCATTCG	4896
Qy	1691	g11eMetArgVal1LeuArg11eAlaArgVal1Leu1y1sLeuLeu1y1sMetAlaVal1G1yMe	1711
Db	4897	TATCATGGGTGTTGCGGTATCGCCGGGTGTGAAGCTATTGAAGATGGCCACAGAAAT	4956
Qy	1711	tArgAlaLeuLeuAspThrVal1MetGlnAlaLeuProG1nVal1G1yAsnLeuG1yLeu1e	1731
Db	4957	GCGGGCCCTGCTGGACACAGTGGTAAACAGGCTCTGCCCAAGGTGGCAACCTGGGCTGCT	5016
Qy	1731	uPheMetLeuLeuPhePhe11ePheAla1aLeuG1yVal1G1uLeuPheG1yAspLeuG1	1751
Db	5017	CTTCACTGCTCTTCTTCACTCATCTATGCTGCTCTGGAGTGAAGCTCTTGGAAAGCTGCT	5076
Qy	1751	uCyAspG1uThrH1sProCy1sG1uG1yLeuG1yArgH1sAlaThrPheArgAsnPheG1	1771
Db	5077	CTGCAATAGACAGAAACCGGTGTGAGGGGATGAGCGGGACGCCACTTTGAAAACCTTCGG	5136
Qy	1771	yMetAlaPheLeuThr1eLeuPheArgVal1SerThG1yAspAsnTnrg1y11eMet1y	1791
Db	5137	CATGGCCCTTCTCAACGCTCTTCCAGAGCTTCCACAGGCGCATTAACCGAATGAATTAAGA	5196
Qy	1791	aAspThr1eLeuArgAspCy1s---AaspG1nG1uSerThCy1sTyrAsnThrVal1-----11	1808
Db	5197	GGACACCCCTGGAGAGCTGTAACCATGATGAAGCGACGCTTAAGACAGCCCTGCAGTTTGT	5256
Qy	1808	eSerPro11eTyrPheVal1SerPheVal1LeuThrAlaGlnPheVal1LeuVal1AsnVal1a	1828
Db	5257	GTCACCGCTCACTTGTGTGAAGCTTGTGCTCAACAGCTCAAGTTGCTGCTCAACAGCGGT	5316
Qy	1828	111eAlaVal1LeuMet1y1s1eLeuG1uSerAsn1y1sG1uAla1y1sG1uG1u1aG1	1848
Db	5317	GGTGGCCCTGCTGATGAACATCTGATGAACAGAAACAGAGGCCCCGAGAGATGACAGA	5376

1848	uLeuGlnAlaGlnLeuGlnLeuGlnMet--LysThrLeuSerProGlnProHisSerP	1867
1849		
5377	GATGGATGGCTGAGATCATCGATGAGATGGCCCATGGAGCTCGAGCCCTGCTT	5428
1867	oleuGlySerProPheLeuTrpProGluValGlnGlyProAspSerProAspSerPro	1887
5429	-----	5436
1887	sProGluValAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGlnI	1907
5437	CCCTGGT-----	5443
1907	sProThrMetGlnProHisProThrThrGluLeuProGluProAspLeuLeuThrVal	1925
5444	---CCCTGGCCCTGCCCCCTGGCCCTGGCTGTGGCCCGAGGCTCCCACTGATCC	5502
1926	-----ArgLysSerGlyValSerArgThrHisSerLeuProAspAspSerTy	1941
5503	TGGGGCTCCGGGGCGAGAGATCGGAGAGGGGAGAGTGTCCAGAGC---GACACCGAGATCA	5559
1941	rMetCysArgHisGlySerThrAlaGlnGlyProLeuGlnHisArgGlyTrpLeuLeuP	1961
5560	CTGTGTCCCG-----	5569
1961	oLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyI	1981
5569	-----	5569
1981	eLeuGlnLeuProLysAspAlaProHisLeuGlnProHisSerAlaProThrTrpG	2001
5570	-----CACTGCTATTGCTCCGACCAGAGACCCCTGTGG-	5602
2001	yThrIleProLysLeuProProGluValArgSerProLeuAlaGlnArgProLeuArgA	2021
5603	-----CTGACAG	5610
2021	gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlnsP	2041
5611	CGTCTTTATATCATCAAGACATCTTGGAG-----GGAGAGCTGACCAT	5655
2041	uLeuAlaGlnValSer-GlyProSer-ProProLeuAlaArgAlaTrpSerPheTrpGly	2060
5656	CATTGACAACTGTGTGGTCCGCTTCCACCACTACGCTCACTGACGGCTGTGGCAA	5715
2061	GlnSerSerThrGlnAlaGlnGlnHisSerArgSer-----HisSerLysIleSer	2077
5716	GTGTCAACATGACAAAGCAAGACAGAGCTTTCATCATCTGTGGGGAGTACACTGAT	5775
2078	LysHisMetThrProProLapProCysProGlyProGlnProAsnTrpGlyLysGlyPro	2097
5776	---CTTGAGAGACCCACGAGCTGGCCA-----CAGGGGCC	5808
2098	ProGlnThrArgSerSerLeuGlnLeuAspThrGlnLeuSerTrpLieserGlyAspLeu	2117
5809	AAGAGAGGACAG-----GATGAACTA	5829
2118	LeuProProGlyGlnGlnGlnProProSerProArgAspLeuLysCysTyP--	2136
5830	GAGCTCCG-----GAGCCATGACAGCTGGAAGACTGGATGAATGCTTTGG	5877
2137	-----SerVal-----	2138
5878	CCCTTTGCCAAGCGAGCCAGTGTCCACAGGCCAGAGAGCTGTGTGCGAATGGGGGC	5937
2139	---GlnAlaGlnSerCys-GlnArgArgProHisSerTrpLeuAspGlnAlaArgArgH	2157
5938	CATTCACTTAAACCTGTCCAG-----TCTGTGCTCAACACAGACAGACGCCA	5985
2157	sSerIleAlaValSerCysLeuAspSerGlySerGlnPro-----	2170
5986	AGACACCCCAAGGCTTTCTCCCGAGTGGCTCCAGGCTCTCTGTAAGTGGCTGTGA	6045



[illegible]

QY	844	UVALANGPhaLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetLaspAs	864
Db	2362	GGTGGCGGTTGATCGGGCGCTGGCGCCAGCTCGTGGTCTCATGAAGCAATGACAA	2421
QY	864	nVALaLAtPhcEysMetLeuMetLeuPheIlePheISerLileuGlyMe	884
Db	2422	CGTGGCCACTTCTGCATGCTACTCAATGCTTCACTTCACTTCACTGATCTCTGGAT	2481
QY	884	CHISLeuPheGlyCYalysPheAlaSerGluArgAsp--GlyAspThrLeuProAspAr	903
Db	2482	GCAATATCTTGGCTGGCAAAATTCAGCCCTCCGACGAGACACGGGAGACACCGTCTCGACAG	2541
QY	903	GLYAspAsPheAspSerLeuLeuThrAlaIleValIThrValPheGlnIleLeuThrGlnI	923
Db	2542	GAAACAATTGATTCTTACTGCTGGGCACTGTCACAGTGTCCAGATCTCTCACTACAGA	2601
QY	923	UAspTrpAsnLysValLeuTyraAngiMetAlaSerThrSerSerTrpAlaAlaLeuTy	943
Db	2602	GGACTGGAAAGTTTGCTGCTGATCAATGAGCATGCGCTCCACACCCCGGGCGCTTCCCTTA	2661
QY	943	rPheIleAlaLeuMetThrPheGlyAenTyrrValLeuPheAsnLeuLeuValAlaIle	963
Db	2662	TTTGTGTGCCCTCAATGACCTTGGCAACTACGTTCTTAATCTCTGTGGGTAACTCT	2721
QY	963	UValIGluGlyPheGlnIaGluIleSerLysArgGluAspAlaSerGlyGlnLeuSe	983
Db	2722	GGTAAAGGGTTTCCAGCTGAG--	2743
QY	983	rCYaIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluPr	1003
Db	2744	CGTAAAGGTTTCCAGCTGAG--GGTAAAGGTTTCCAGCTGAGTTCTGATGTA	2772
QY	1003	oASPPhaPheSerProSer--	1013
Db	2773	GGACCAAGCTCATCCCAATTGGAGAGATTGACAGACTCCCAAGAGGCTGGACAAACAG	2832
QY	1013	pGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGlnLeuArgLys	1033
Db	2833	TAGAGATCTCAAGCTGCGCCCAATACCAAGACACCCAAATGACAC--	2878
QY	1033	sSerLeuLeuProProLeuIleIleHisThrAlaAlaIThrProMetSerLeuProLysSe	1053
Db	2879	CTGAGACCT--AGCTTCCCT--	2896
QY	1053	rThrSerThrGlyLeuGlyAlaLeuGlyProAla--	1065
Db	2897	CTGGGTGGCATCTGGGTCCTGCTGATACCATGGGTACTGCCCCCG	2943
QY	1066	--SerArgArgThrSerSerSe	1072
Db	2944	CGTCTCACTGACGACGACCGGATAGTGGCCCTAGACTCTCGAAAAGCAATGTCAT	3003
QY	1072	rGlySerAlaGluProGlyAlaAlaHisgIuMetLysSerProProSerAlaArgSerSe	1092
Db	3004	GTCCTCGGGACG--ATGACCTATGATCAGACATCTTGTCCACAGTCTCCGGAAGCTC	3057
QY	1092	rProHisSerProITrpSerAlaAlaAspSerITrpThrSerArgArgSerSerArgaSe	1112
Db	3058	CTACTACAGGGCCCTGGGGCGGACGTGGAGACTGGGCGCTACCGCGCTCCAGCTGAAAC--	3115
QY	1112	rLeuGlylArgAlaProSerLeuLysArgArgSerProSerGlyGlyLysArgArgSerLeuLe	1132
Db	3116	AGCTGAAACACAAGCGCGCTCAGCTGATGATGATGATGATCTTAACT	3159
QY	1132	uSerGlyGluGlyGlnGlnSerGlnAspGluGlu--GlnLysSerGluGluGlu--	1149
Db	3160	GTCCTGGGAGGGGTGGAGTACTGCTCCGACAGGCGCTGTGAAGGCGCCGGGAGGAGGGGCC	3219
QY	1150	ArgAlaSerProAlaGlySerAspHis--	1158
Db	3220	AACCTGGACCGCAGCTCTGATGCTTCCACACGCGCACACGCGACCATGAGACCCCACT	3279



QY 1159 -----ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAs 1173  
DB 3280 GGCACACCGTACCCGACACACCGCCGCGACTGTGCTCCCTTGATACAGGGACTCTGTGA 3339  
QY 1173 PleuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer-----GlyArgG1 1191  
DB 3340 CTTGGAGAGACTGGTGGCCGTGGTGGTGGCCACTACCGGGCCGCTTGGAGGGGGGGGG 3399  
QY 1191 ySerAlaSerGluHisArgGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAl 1211  
DB 3400 TCAGGGCCCTGGGGCAGAGAGACTGCATATGGCAGAAATGCCAACATACCAAGATGCTT 3459  
QY 1211 AlaMetArgProAspAspProLeuMetArgGlyAspAspAlaAspAspGluLysLeuLeuSe 1231  
DB 3460 CACCAAGATGATGATACCGCCGCGACCGCGGGGAGAGAC---GAGAGAGAGATGCATATAC 3516  
QY 1231 rLysGluArgLysValArgAlaTrpIleArgAlaArgLeuProAlaCysTrpLeuGluArg 1251  
DB 3517 CTTGTGTTTCCGGGGTCCGCAAGATGATTGATGTGTACAGCCGGACTGTGGCCAGATCCG 3576  
QY 1251 GAAspSerTrpSerAlaTrpIlePheProGlnSerArgPheArgLeuLeuCysHisArg 1271  
DB 3577 CGAGGATGGTGGTGTACTCTTCTCCCGGAGAACAGTTCGGATCCGTGTGCAGAC 3636  
QY 1271 gLleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysI1 1291  
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QY 1291 eThrIleAlaMetGlnArgProLysIleAspProHisSerAlaGluArgIlePheLeuTh 1311  
DB 3697 CACCATTGCTCTGGAGAGACCCAGATTGAACCTGTAGGACTGAGGCACTTCTCTCAC 3756  
QY 1311 rLeuSerAsnTrpIlePheThrAlaValPheLeuAlaGluMetThrValLysValValAl 1331  
DB 3757 GGTGTCTAATCACTACTTTCACAGCCACTTCTGTGGGAGATGACATGAAAGGTGCTTC 3816  
QY 1331 AlaGluGlyTrpCysPheGlyGluGlnAlaTrpLysLeuSerSerTrpAsnValLeuAspG1 1351  
DB 3817 TCTGGGCTGTACTTGTGTGAGCAGCGGTACTGCTGTAGCAGCGTGAATGACTGAGTGG 3876  
QY 1351 yLeuLeuValLeuLeuSerValIleAspIleAlaValIleValSerMetValSerAspSerGlyTh 1371  
DB 3877 TTTCTCGGTCTTGTGTGCATCATCGATATCGATGTGTGTGCGTCTGTGTGGGGAGCC 3936  
QY 1371 rLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgVal 1391  
DB 3937 CAAGATTCTGGGGGTCTCCGGGTCTGTGGCTCTCTGTACTTACTTGTCTTGAAGGT 3996  
QY 1391 L11SerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysPr 1411  
DB 3997 TATCAGCCGGGGCCCTGGGCTGAAGCTGTGTGAGAACGCTCATCTTCTCCCTCAAGCC 4056  
QY 1411 cLleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyVal 1431  
DB 4057 CATTGGGAACATCGTCTCATCTGTCTGTCTTTCATCTCTTGTGGCATCTCTGGGGGT 4116  
QY 1431 gLntLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAs 1451  
DB 4117 GCAGCTTTTCAAGAGCAAGTTCTTACATGTGTGGAGTGAGACCCGAAACATCACCA 4176  
QY 1451 nLysSerAspCysAlaGlnAlaSerTrpArgTrpValArgHisLysTrpAsnPheAspAs 1471  
DB 4177 CCGATCTGACTGCGTGGCGGCACTACCGCTGGGTGCATACCAATACAACTTTGACAA 4236  
QY 1471 nLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerTrpAspGlyTrpValAspI1 1491  
DB 4237 CTTGGGCGAGGATGATGCTCTCTTGTGTGTGTGCTTCAAGGACGGCTGGGGAACAT 4296  
QY 1491 eMetTrpAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnPr 1511  
DB 4297 CATTTATATATGATTTAATGTGCTGTGTGTGACCAAGCAGCATGACCAACCAACCC 4356  
QY 1511 cTrpMetLeuLeuTrpPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMe 1531

DB 4357 CTGGATGCTACTGTAATCTTATTTGTTCTGTCTCATCGTACAGTTCTTGTGTCAACAT 4416  
QY 1531 rPheValGlyValValValGluAsnPheHisLysCysArgGlnHisArgGluGluGluG1 1551  
DB 4417 GTTGTGGCGGTGTGTGTGAGAACTTCCAAAGTGCCTGGGAGACACCAAGGCTTAGGA 4476  
QY 1551 uAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArguArgAlaG1 1571  
DB 4477 GGGCGGAGGCGGAGAGAAACCGGTGGCGGCTGGAAAGAAACCGCGTAAAGGCTCA 4536  
QY 1571 nCysLysProTrpTrpSerAspTrpSerArgPheArgLeuLeuValHisIleLeuCysTrp 1591  
DB 4537 GAGGCTGCCCTTACTTACTTACTTACTTCTGTCCCAAGGCTGTCTATCATCTCATGTGCAC 4596  
QY 1591 rSerHisTrpLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAl 1611  
DB 4597 CAGCCACTACCTGGAATCTTCTTACTTACTTCTTCTCATCTGCTCATATGTTGTCCATGTC 4656  
QY 1611 aMetGluHisTrpGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTrpTr1 1631  
DB 4657 CTTGAGGCACTACCAACACGACTTACATCCCTAGAGACAGCCCTTAACTACTGCACTTACAT 4716  
QY 1631 ePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArg 1651  
DB 4717 GTTCCACCACTGTCTTGTGTGTGAGGCTGTGTGAAAGCTGTGTGCACTTGTGCTGAGGCC 4776  
QY 1651 gPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetG1 1671  
DB 4777 TTTCTTCAAGGACCGATGGAGACAGCTGGACCTGGCATGTGCTGTGCTGTGCTCATGGG 4836  
QY 1671 yLleThrLeuGluGluIleGlyValAsnAlaSerLeuProIleAsnProThrIleIleArg 1691  
DB 4837 CATCACACTGAGAGATGAGATGATCAATGCGCGCTTCCATCAACCCCACTCATCTCCG 4896  
QY 1691 gLleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuMetAlaValGlyLys 1711  
DB 4897 TATCATAGCGTGTCTGTGTGTGATCCCGGGGTGTGAAGCTTGAATGAGATGGCCACAGAA 4956  
QY 1711 rArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyLysLeuGlyLeuLe 1731  
DB 4957 GCGGGCCCTGTGACACAGGTGTACAGGCTGTGCCACAGGTGGCAACTGTGGCCGTGT 5016  
QY 1731 uPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyLysPheG1 1751  
DB 5017 CTTCATGCTGCTCTTCTTCTCATCTATGCTGTCTGTGAGAGTGAGACTCTTGGAAAGCTGT 5076  
QY 1751 uCysAspGluThrHisProCysGluGluLeuGlyArgHisAlaThrPheArgAsnPheG1 1771  
DB 5077 CTGCATAGACGAGAACCCGTTGTAGGGCATGAGCCGGGACGCCCACTTTGAACAACTTCCG 5136  
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QY 1791 sAspThrLeuArgAspCys---AspGlnGluSerThrCysTrpAsnThrVal-----I1 1808  
DB 5197 GGAACACCTGTGAGACTGTACCCATGATGAGCCAGCTGTCTTAGAGCAAGCTGTGAGTTGT 5256  
QY 1808 eSerProIleTrpPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValVa 1828  
DB 5257 GTACCGCTTACTTGTGTGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5316  
QY 1828 L11LeuAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaG1 1848  
DB 5317 GTGGCGCGTCTGATGAACATCTGATGACACCAACAGAGAGCCCAAGAGATGCAGAG 5376  
QY 1848 uLeuGluAlaGluLeuGluLysLeuGluMet---LysThrLeuSerProGlnProHisSerPr 1867  
DB 5377 GATGAGATGCTGAGATGAGCTGAGATGGCCCATGGCTCTGGCCCTCGCCCT----- 5428  
QY 1867 oLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProLy 1887

Db 5429 -----GGCCCCCTG 5436  
QY 1887 sProgluYalaleuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHis 1907  
Db 5437 CCCTGGT----- 5443  
QY 1907 sProThrmGlnProHisProThrcGluLeuProGlyProAspLeuLeuThrVal----- 1925  
Db 5444 -CCCTGCCCCCTGCCCCCTGCCCCCTGCTGCTGAGCCCGAGAGCTGCCCACTAGTTCAACC 5502  
QY 1926 -----ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTy 1941  
Db 5503 TGGGGCTCCGGGGCAGAGATCGGAGGAGGACAGTCTGGAGGC---GACACCGAGAGTCA 5559  
QY 1941 rMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTyrProGlyLeuP 1961  
Db 5560 CCGTGTCCCG----- 5569  
QY 1961 oLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrl 1981  
Db 5569 ----- 5569  
QY 1981 eLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTyrP 2001  
Db 5570 -----CACTGCTATTCTCCAGCCCGAGAGACCCCTGTG-- 5602  
QY 2001 yThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgAr 2021  
Db 5603 -----CTGGACAG 5610  
QY 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAsp 2041  
Db 5611 CGCTCTTAATATCATCAGAGACCTCTTGAG-----GGGAGCTGACCAT 5655  
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Db 5656 CATTTGCAACCTGTCTGGGTCCGCTTCCACCACTAGCCTCAGCGCTGTGGCAA 5715  
QY 2061 GlnSerSerThrGlnAlaGlnHisSerArgSer-----HisSerLysIleSer 2077  
Db 5716 GTGTCCATCATGACACAGACAGACAGCTCTTCATCCATCTGCTGGGAGATGACCTGACT 5775  
QY 2078 LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpLysGlyPro 2097  
Db 5776 -----CTTGAGAGACCCCAAGCGCTGCCA-----CAGGSCCC 5808  
QY 2098 ProGluThrArgSerSerLeuLeuAspThrGluLeuSerTrpLieserGlyAspLeu 2117  
Db 5809 AAGGAGAGCAAG-----GGTGAACTA 5829  
QY 2118 LeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysCysTyr--- 2136  
Db 5830 GAGCCTCCG-----GAGCCCATGACAGCTGAGACCTGATATAATGCTTTGG 5877  
QY 2137 -----SerVal----- 2138  
Db 5878 CCCTTGCCAGAGGACAGCTGTCCACAGGCCAGAGAGCTGCTGGAGATGGGGGC 5937  
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Db 5938 CATTCATTCACACCTGTCCAG-----TCTGGCTCAACACAGAGAGCAGCCCA 5985  
QY 2157 sSerIleAlaValSerCysLeuAspSerGlySerGlnPro----- 2170  
Db 5986 AGCACCACAGAGCCCTTTCTCCCGGATGGCTCAGCCCTCTCTGTATGATGCTGCTGA 6045  
QY 2171 -----HisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProG 2188  
Db 6046 GTTCTTTCACCCCTGCTGTCTGCCAGCAGAGGGGAGAGAACCGGGCATAGTGCAGG 6105  
QY 2188 ySerArgProLysLysLysLeuSerProProSerIleThrIleAspProGluSerG 2208  
Db 6106 AACCTGCCCCAAGATGACACTTCAG-----GGGTCTCG 6138

QY 2208 nGlyProArgThrProProSerProGlyIleCysLeuArgArgArgAlaProSerSerAs 2228  
Db 6139 GGCATCGCTGAGAGTACCGAGTGTCACTGCACCTCTTGGCCCGAGGCTACTGTAGTGA 6198  
QY 2228 pSerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProly 2248  
Db 6199 CACGTCC-----TTGATGTCAGTCTTACAGAGCTCAGCGGAGCCTTACAGACCACT 6252  
QY 2248 sLysAspValLeuSerLeuSer 2255  
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RESULT 12  
US-09-949-016-15601  
Sequence 15601, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
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PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15601  
LENGTH: 70308  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-15601  
Alignment Scores:  
Pred. No.: 2,336-127 Length: 70308  
Score: 2237.00 Matches: 730  
Percent Similarity: 21.93% Conservative: 25  
Best Local Similarity: 21.20% Mismatches: 64  
Query Match: 18.79% Indels: 2626  
Gaps: 19  
US-09-611-257A-37 (1-2266) x US-09-949-016-15601 (1-70308)  
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Db 9554 GATGAGGAA-----GCTGGGTCCAGAGAGGTGAGATGACCAAGTGGGACTCCCT 9604  
QY 18 SerPheMetArgLeuAsnAspLeuSerGlyAlaGlyValArg-----ProGlyProGly 35  
Db 9605 TCTCTGATGAGAGTCTGGGCTG---GGGGCTGTCTGCGTATGTCAAGGCTCTGGC 9661  
QY 36 SerAla-----GluLysAspProGly----- 42  
Db 9662 ACCACACTGCTTACCTTCAGATGAGCCAGAGGTAACAGAGAGAGGTCTTAGGGCG 9721  
QY 43 SerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValAlaPhePhe 62  
Db 9722 GGGTGGGGGGCGGGCTCAGCTCCAGCTTGGCCAGCTGTTCC----- 9766  
QY 63 TyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrp 82  
Db 9767 -----TTGACTGCCAGTACTCG 9784  
QY 83 PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArg 102  
Db 9785 TTGAGCGGATAGAGATGTGTCTCATCTTCTCAACTCGTGAACCTCGGAGATGTTCCGG 9844  
QY 103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeu----- 117

Db 9845 |||||CCATGGAAGACATCGCTGTGACTCCAGCGCTGCAGATCCTGAGGTGTGTGT 9904  
 QY 117 ----- 117  
 Db 9905 GT 9964  
 QY 117 ----- 117  
 Db 9965 CCTCTACTCTCTGCAAGAGCCCTGACCCACTGTGTGGAGCTAGGGTGGACTAGAGG 10024  
 QY 118 -----GlnAlaPheAsp 121  
 Db 10025 GTATTCCTTCACCCACGCTCAAGTTTCAGCCACTCTTGTCCCACTCAGCGCTTGTAT 10084  
 QY 122 AspPheAlaPheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyIle 141  
 Db 10085 GACTTCATCTTGTGCTTGTGCTTGTGCGTGAAGATGTGTGATGTGTGTGTGTGTGTGT 10144  
 QY 142 PheGlyLysIleGlyCysTyrIleGlyAspThrTyrAsnArgLeuAspPhePheIleValIle 161  
 Db 10145 TTTGGGAAAAAGTGTATCTGGGAGACATTGGAACTGGCTTGTATCATGTGATC 10204  
 QY 161 ----- 161  
 Db 10205 GCAGGGTGAAGACCTGGGCTGTGGGTGGAGAGCAATGATCAGATCGATCCCTTCCCGG 10264  
 QY 161 ----- 161  
 Db 10265 GGCCAGGGTTCGTGGGCTGTGACTCTCAGCTCCAGCCAGTTACAGACCACCTTTCTCC 10324  
 QY 161 ----- 161  
 Db 10325 CTGGCTATCTCTGAGGGGTCTGAGGCTGCGCTGCTAGAGACTGTAGCTATATCTAA 10384  
 QY 161 ----- 161  
 Db 10385 ATTCCAAGGCCCTATTCCTAATTCGCCCCCTCTGTATGGGCAATGTGCTTGTCTC 10444  
 QY 161 ----- 161  
 Db 10445 GGGGTAGCTTGTGCCCCCAGACAGAGCCGGAATCTTCAGGGTCCCTTGGTGAAGAA 10504  
 QY 161 ----- 161  
 Db 10505 GAGGAGTCAAGGTCATCTGCTGCCCCCTAAAGCAGAGATTCCTATGACCTTGTGA 10564  
 QY 162 -----AlaGlyMetLeu 165  
 Db 10565 CCCCACTGTGGCCTCAGACTCAAGAGGCCCTCTTGTGGCCCCCTCCCTGAGGATG-CTG 10623  
 QY 166 GlnTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeu 185  
 Db 10624 GAGTACTCGCTGACCTGCAAGACGTCACTTCAGCTGTCAAGACAGTCGCTGTGCTG 10683  
 QY 186 ArgProLeuArgAlaIleAsnArgValProSer----- 196  
 Db 10684 CGACCGCTCAGGGSCATTAAACCGGTGCCAGTGAAGAACCCCTCAGCGCTCAGCCCTG 10743  
 QY 196 ----- 196  
 Db 10744 AAGAGAGCCCCAGAGAGAAATGTGAACTCTCAGACCACCTCTACTGTGTCTCA 10803  
 QY 196 ----- 196  
 Db 10804 CTTGACCCCTCAGAGGCCCTCTCAGAGAGGCTCACTGGGAGCTGGGATTCGTGAAC 10863  
 QY 196 ----- 196  
 Db 10864 AAAATGGAACCTCGAATGTGGCACTATGGAGTTACTGTGGAAAAACCCACTCATTTT 10923  
 QY 196 ----- 196

Db 10924 AGCTTGCTTTAGTGTCAAGTGTCAAGAAATCTCAGATGACCCCTTCTTCACTAGA 10983  
 QY 196 ----- 196  
 Db 10984 TGACACTCCCCAGAGAGATAGGGGTGTGGGACTGAGAGGCTGACAGCGAAGAGT 11043  
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 Db 11044 GAGCGAAAGTCTAATGCGCTTTTCTTAGCCAGAACAGCCTCTCATGTACTGTCTT 11103  
 QY 196 ----- 196  
 Db 11104 GCTGTGAGACAGCTGGCCAGCGCTGAAGTACTTCTCTCAAGACAAAGGCCACTCAG 11163  
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 Db 11164 TCTCACCTCCGCTGTGCCCTTCTCCTTCCGCCCCCTTCAACCATTTGAGTAA 11223  
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 Db 11224 CTGCCGGGCCATTATCTAAATTAACTGCATTTGTTCTGAGCCAGCGAGCTTTGGC 11283  
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 Db 11344 CAACCTACAAAGCTGCAAGTGTGCCGTGTGTCTTAGAGAGTGGGTGTGGCGAG 11403  
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 Db 11404 GAATGATGTTCTGGGGCTCAGTGCCTGTTGTACTGATGTAGACAGACCCTCTG 11463  
 QY 196 ----- 196  
 Db 11464 CGCTGT 11523  
 QY 196 ----- 196  
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 Db 11584 GTGTAAACAGAGCTCCAGAAAGGGCATGCTCGCTCTCTCCCGCCAGGTGATG 11643  
 QY 196 ----- 196  
 Db 11644 GCTGGCAGATTATAGGCTCTGTCTTAACCCGGGTAAATCCCTTAATGCAACCTGT 11703  
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 Db 11704 AGGAATTGATCTCAGTTGAGACACAGAAAGCTGAAGGGGATGGGTAGAGAGGGGG 11763  
 QY 196 ----- 196  
 Db 11764 AGGAGACTGAGTGAAGAAACTGGGCTGGAGGGCGAGGCTGGCTGACGTACCAA 11823  
 QY 196 ----- 196  
 Db 11824 GAGGTTAATTAGCTGTGCTTAGCAGCTTTTGTCCCTGAGGGGCCAGGGGGCCATATGAT 11883  
 QY 196 ----- 196  
 Db 11884 GGCACCTTGGGGGTGAAGCCAGCCATTAGATCTGTCTGTGACGAGGGCTTGGCGGA 11943  
 QY 196 ----- 196  
 Db 11944 CTGGGGCTGTGTTCAAGCAATTTGGGCCGTTGAGTTCTAGACTGTGAGTACGAGAGAG 12003  
 QY 196 ----- 196  
 Db 12004 GGAAGTAACCTTAACAGGGCTTTTGAAGAGGGGTTTCACTGCTTTCCCTATGAGGGG 12063

QY	196	-----	-----	196	QY	249	-----	249
Db	12064	GTTGTAATTGATGACTTCTGAGAAAGACAGTATTGTATCTTTCAGGTCCTGATTTGGG	12123	Db	13144	CTGGGTGCACCTCCAGAGATTCTGATTTTCATTTGCTGTGGGGCTCAGCTTGAGTGAAG	13203	
QY	196	-----	-----	196	QY	249	-----	249
Db	12124	GATCTGACCAAGCAGGAAATGTTTCAGGGAGACAGGGCTCAGAGCCATAGTAGACAC	12183	Db	13204	ATTTTTCAACCCCTCCAGTACTCTAACTTGAGTGAATTTGAAATCACTATTCCAG	13263	
QY	196	-----	-----	196	QY	249	-----	249
Db	12184	AGGGATTTGGCCCTGCTAGAGAGTGGCTCAAAATGAGATTCTGCTGTGTCA	12243	Db	13264	GATGTACCTTCAACATCTGAGTGTGAGTTTCCCACTCAGGCTCATGCTCTGTGT	13323	
QY	196	-----	-----	196	QY	249	-----	249
Db	12244	TTCCTCTGAGATTGCTGCTCAGTTTCCCTAATGACTCTGTGTGATTAAGAAA	12303	Db	13324	GCCCAAAATCCCTGCGCCAGTCCCTTCCCACTTCTGTGTTCTGCGCTGTCAACC	13383	
QY	196	-----	-----	196	QY	249	-----	249
Db	12304	GGTCAGTACTGTGCTGTTGAGAGAAAGATAGGAGTGTGGGTGATGTG	12363	Db	13384	TATATGCTCGAGCATGTGTGCATCTCTCCCTTCTGGGCCCTCTCCCTGAGAGCCA	13443	
QY	196	-----	-----	196	QY	250	-----	256
Db	12364	TGCGGGTGTGGGTGTGTGTGAGAGGAGTTCGAAAGCCAAAGCTGGGTTCGATTCG	12423	Db	13444	CTCCCAAGTCTACCCCTGTTCCCTCCATCTCTGACAGCCCTGAGCGTGAAGCTGGA	13503	
QY	196	-----	-----	196	QY	256	UARGTYTYTGTGlnThrgluasngluaspluserProphelieCyserglnProargl	276
Db	12364	TGCGGGTGTGGGTGTGTGTGAGAGGAGTTCGAAAGCCAAAGCTGGGTTCGATTCG	12423	Db	13504	GGCTATTACAGACAGAGAAAGAGATGAGAGCCCTTCATCTGTCTCCAGCCAGCGGA	13563	
QY	196	-----	-----	196	QY	276	UasnglYweLarSerCySarSerValProThrlenuarglYaaPglYglYglYglYPr	296
Db	12424	GCACTTACCTTAGCAGCTGTGTGATACTGGGTGATCAAGTCAATTTCTCCAAAGCTCAG	12483	Db	13564	GAACGGCATGCGGTCTGTGAGAAAGGTGCCACGCTGCGGGGAGCGGGGGGGGGCCCC	13623	
QY	196	-----	-----	196	QY	296	OProCysglYleuAapTYTgluaAlaTYrAsnSerSerAenThrTYrCyValAsnTr	316
Db	12484	ACTTTCATCTGTGAATTGGAGATGATTAATTCACATGTGATGATGTGTGGAGAGTAG	12543	Db	13624	ACCTTCGGGTCTGAGACTATGAGGCTTACACAGCTCCAGCAACACCACTGTGTCACTG	13683	
QY	196	-----	-----	196	QY	316	pAsnglTYTYTThrAsnCySserAlaglyuhisasnProphelysglYalaIleas	336
Db	12544	GAGGGGCAACATTTCCCACTCACTGTGTGTGACTGTGAGATTACCTGGGCAAG	12603	Db	13684	GAACCAGTACTACCACTGCTCAGCGGGGAGCAAACTTCAAGGGGCGCATCA	13743	
QY	196	-----	-----	196	QY	336	nPhelaSpasnIleglYTYTAlaTTPllalaIlePheglh-----	349
Db	12604	CCACAAGGGGAAGTGGTGGGGCAAGGGCTCAGAGGCTATCTGGGAGTCAAGAGCTG	12663	Db	13744	CTTTGACAACATTTGGCTATGTGCTGTGATGCCATCTTCCAGGTGGGAGAGCTGGCCCCG	13803	
QY	196	-----	-----	196	QY	349	-----	349
Db	12664	TCTGTGTGTCTCCCTCCAGCTTGAAGCCGGGCGGTCTCAGAGCTCAGAGTCCCTGTGGGG	12723	Db	13804	GGAAGTTCCTCCAGAAACACAGCCCAAGACACAGCCAGATCCGAGTGTGTCTCAG	13863	
QY	196	-----	-----	196	QY	349	-----	349
Db	12724	CCCCTCCGGAGTGTCTGCCGGCCGTGGCAGTCAAGCTTACCCCGGCGCAGCTGTGTCCC	12783	Db	13864	GGTTGGGGTGGGGGTCAAGGCTCTGAGAGACTGAAGAGATTGGTGGGCCATAG	13923	
QY	197	-----	-----	208	QY	350	-----	361
Db	12784	CAGCGTGGCTTCTGCCCCCAGAGGCATGGCATCTTGTCAAGCTTGTGCTGAGTACGCT	12843	Db	13924	TCAGCTGCCCCCTTGCACCCCTTAGATCATACCTGAGAGGGTGGGTGCACATCATGT	13983	
QY	208	uProMettLeuglYasnValleuLeuLeuCySphelPheValPhePheIlePheglYlleVa	228	Db	361	YrPheValIweLarSpaIahIserPheTYrAsnPhelIeTYrPheIleuLeuIlele-	380	
Db	12844	GCCCATGTGGGCAAGTCTGCTGTCTGCTTCTTCTTCTCATCTTCCGCAATCCG	12903	Db	13984	ACTTGTGATGAGTGTCTCATTTCTTCTACAAATTTCACTTCTCATCTCTCATCAT-C	14042	
QY	228	IglYValIglInleuTTPAlagIyleuLeuArghasnArgCySphelLeuProglUasnPhese	248	QY	380	-----	-----	380
Db	12904	CAGCGTCCAGCTGTGGGCAAGGGCTGTTCGAAACCATGTCTTCTCACTGAGAAATTTTCAG	12963	QY	380	-----	-----	380
QY	248	rLeu-----	249	Db	14043	GTGATGACTCTCAAGATCCCGGTGGGATGGGCATCTGTGGGACACCTGTGGGGGAG	14102	
Db	12964	CTGTGTAGTGTGAGACAGGTCAGGGAGAGACTGGAGTGTATAGGGCTGGGACACC	13023	QY	380	-----	-----	380
QY	249	-----	249	Db	14103	TCCAGAGAGGGATAGTTTGTCTGTCTGAAATTTTAACTTCTCAGACAAAGTCTTAG	14162	
Db	13024	CCCAAGTTCTCATTCCGGTTGTACTGACATATCTGTTTCAACATCTGAGACATATTC	13083	QY	380	-----	-----	380
QY	249	-----	249	Db	14163	AGAGGCATCCATCATATATGTAGTGAAGGACACCAATGTCAAGTCAAGAGAAATCCAA	14222	
Db	13084	TGTTCTCAAACTTGCTACCATTTGAAACCACTGGGAGTTTAAAAATGATCTGATGC	13143	QY	380	-----	-----	380

Db 14223 GTCAGGCGGAGCTTAAGTCTATTGGGACCTTGGCAGTCAATTCATGAGGCTCC 14282  
QY 380 ----- 380  
Db 14283 AGCACTGCTCTGGGCTCTGTCTTCTTCATGGGTAAATGAATGGTTCTCAACTGAGATG 14342  
QY 380 ----- 380  
Db 14343 ATACCACTCTCCAGAGGGCATTGGAAATGGGAAGGGTGAATTCGTTTGAATTTT 14402  
QY 380 ----- 380  
Db 14403 TTTAATAGCTTTATGAGACATTAATCATATTCATCCCTTGAATGATC 14462  
QY 380 ----- 380  
Db 14463 CAGTGTCTTTAAGCATGTTTACAGAGTTCTGTTTTTTGTAAGACAAAGGGAGTCA 14522  
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QY 380 ----- 380  
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QY 380 ----- 380  
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QY 380 ----- 380

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QY 381 -----ValGlySerPhePheMetIleAsnLeuCysL 391  
 Db 16443 ATTTCCTCTTCCTGTCGCCACCCCTTACAGAGTGGGCTCTTCTTCAATGATCACTGTGTGC 16502  
 QY 391 euValValIleAlaThrGlnPheSerGluThrLysGlnArgIleuSerGlnLeuMetArg 411  
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 QY 411 InGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlyS 431  
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 Db 16683 TGGCTCAGGCTCTCTGGGGCAGCAGTGTGGGGTTGGGGCTGTCAAGCAGCCAGCAGCCCC 16742  
 QY 471 euGlyGlyGlnGluThrGlnProSerSerSerCysSerArgSerHisArgArgLeuSerV 491  
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 QY 571 roProProArgSerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrP 591  
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 QY 641 ----- 641  
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 Db 18303 ATTCTGTATCAAGCTGATTTAAAGGACATTGATGCTTTGGGCTAGGTCCTGAAGTG 18362  
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 Db 18363 TGTGGCACAGATGATCTAGTATCGGTATGCGTCTATGTCCATGAAAGGGGTCCAGTG 18422  
 QY 641 ----- 641  
 Db 18423 TGTGTGTGTGCGTGTGTGATGACAGTGTCTGTGTATATGATGATGATGTGACATGT 18482  
 QY 641 ----- 641  
 Db 18483 GCTTATGTGTAGTGTGATGTGCGATGTGAAGCTTTTCTTGTGTGTGTGATGTG 18542  
 QY 641 ----- 641  
 Db 18543 TGCATATGTCTGGCATAATGTGCGGTGTGTGAATGTGTTTGACACATGTGTGTATG 18602  
 QY 641 ----- 641

Db	18603	TGCATGATATGATGTCCTCATATGGTGGGTGTCCAATATGATATATCATATGTCACAGATGTC	186662
Qy	641	-----	641
Db	18663	GCATCTGAGACACGTGTGAGGTGACAGTGTCTGTGTGGGTGTGTGTGCAAGTGACGT	187222
Qy	641	-----	641
Db	18723	GTGTGGCGGTGTCTTAAGGATCCCATGGAAGTGTGTCTCAGAAACGTGTTATGTAGTC	187822
Qy	641	-----	641
Db	18783	CTGGCTTCTGGGAAGGGGAAGGGAGCGAGCTCTTGTGTGAAGCAGCTAGATATAGG	188422
Qy	641	-----	641
Db	18843	AGCTGTCCAGGACCTCAGAGACATCCAGGCCACTCTCTAGAGCCCGAGAGACATTCAGCA	189022
Qy	641	-----	641
Db	18903	GTGACTGTCAATGAAGTGCTATTGACATTTAGGGCACTTGTGGGTCAAGATGCCACT	189622
Qy	641	-----	641
Db	18963	TGCCTGACATTACAGACCCCTGGCCCACTAAGTGCTAGACCCCATCACTGTAACAAC	190222
Qy	641	-----	641
Db	19023	CCAGACTCCCTGACTCATTTTACATATCTACAGAGGAGGTAGCCAGGTACAGAC	190822
Qy	642	-----GlyAlaCysGlnSerSerCysIle	650
Db	19083	TCTGGAGCCTTCACTCTACTCTCTGTTCAGGTGCTGCCAAGCTCTTGCAAGATC	191422
Qy	651	SerSerProCysLeuIysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCys	670
Db	19143	TCCAGCCCTTCTTGAAAGCAGACAGTGGAGCCTGTGTGTCCAGACAGCTGCCCTCTGT	192022
Qy	671	AlaArgAlaGlyAlaGlyGluValGluLeuAlaAspArgIleMetProAspSerAspSer	690
Db	19203	GCCCGGCGGGGAGGAGGTGAGCTGCGCACCTGAATATGCTGTACTAGACAC	192622
Qy	691	GluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSer	710
Db	19263	GAGGCACTTATGAGTTTACACACAGATGCCAGACAGGCACCTCCGGAGACCCCAACAG	193222
Qy	711	ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheTyrArg	730
Db	19323	CGCGGCGCAACGAGACCTGGGCGCCAGATGACAGAGCCAGCTGTGTGCGGCTTCTGAAG	193822
Qy	731	LeuIleCysAspThrPheArgGlyIleValAspSerTyrThrPheGlyArgGlyIleMet	750
Db	19383	CTAATCTGTGTGACACCTTCCGAAGAATTGTGACAGCAAGTACTTGTGCGGGCAATCCAG	194422
Qy	751	IleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGln	770
Db	19443	ATCCGCATCTCTGTGTACACACTACGATGGGATCTCAATACACAGACAGGTAGAGAGG	195022
Qy	771	LeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMet	790
Db	19503	TGGGCAAGGCA-----GGGCTCTCGGCAAGCTGCTTTT	195352
Qy	791	LeuLeuIysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePhe	810
Db	19536	CGCCTCGGGGCTG-----GGGCTTCTTACTCTCTCCGACCCCTCTCTGTAGCTC	195862
Qy	811	AspGlyValIleValIleValIleSerValTyrGluIleValGlyGlnGlnIyGlyIle	830
Db	19587	AGCTTCTCTCTCATAGCTGTCTAGCCCACTGCGACAGTGAAGGGAGGTGTGATATGA--	196442
Qy	830	userValLeuArgThrPheArgLeuMetArgValLeuIysLeuValArgPhe-----	847

[illegible]



Db 62 GCGGTGAGATGCTCATCAAGATGTTGGCGCTTGGCGGCTGTTGGCGAGAAAGTTACTCG 121  
 QY 149 G1YASPTHTTTPASNAIrgLeuAspPhePhe11eVal11eAlaGlyMetLeuGluTyrSer 168  
 Db 122 GGTGACACGTGGAACAGCGCTGATTTCTTCATGCTGGCGGAGATGAGTACTCG 181  
 QY 169 LeuAspLeuGluAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeu 188  
 Db 182 TTGGACGACACACACATGAGCTTCTGGCTATACGACCGTGGGTGGTGGCGCCCTTC 241  
 QY 189 ArgAla11eAsnArgValProSerMetArg11eLeuVal1ThrLeuLeuAspThrLeu 208  
 Db 242 CCGGCATCAACCGCTGCTGCTAGCATCGCGATCTGTGCTGCTGCTGCTGCTGCTGCTG 301  
 QY 209 ProMetLeuG1YAsnValLeuLeuLeuGlySerPhePheVal1PhePhe11ePheG1Y11eVal 228  
 Db 302 CCCATCTCGGGAACCTCTTCTGCTGCTTCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCT 361  
 QY 229 G1YValG1LeuThrAlaG1LeuLeuArgAsnArgCysPheLeuProGluAsnProSer 248  
 Db 362 GGGGTCACTCTGGCTGGCTGCTGCGAACCGCTGCTTCTGGACAGTGCCTTTGTC 421  
 QY 249 LeuProLeuSerValAsp---LeuG1YArgTyrTyrG1nThrG1YAsnGluAspGluSer 267  
 Db 422 AGGAACAACAACCTGACCTTCTCGCGGCGGTACTACACAGCGAGAGGCGGACGAGAAC 481  
 QY 268 ProPhe11eCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro--- 286  
 Db 482 CCGTTCATCTGCTCTCCACGCGCAGAACCGGCATCAGAGATGCTCGCACATCCCCGCGC 541  
 QY 287 -----ThrLeuArgG1YAspG1YG1YProProCysG1YLeuAspTyrG1YAla 304  
 Db 542 CCGCGGAGCTGGC-----ATGCCCTGCACCTTGGGTGGAGGGCC 583  
 QY 305 TyrAsn-----SerSerSerAsnThrThrCysValAsnTPAsn 317  
 Db 584 TACACGACGCGCAGCGGCGGAGGTGGGCGTGCAGCAACGCTGCATCAACTGGAAC 643  
 QY 318 G1nTyrTyrThrAsnCysSerAlaG1YGluHisAsnProPheG1YAla11eAsnPhe 337  
 Db 644 CAGTACTACAAACGTGGCGCTGCGGTGACTCCAAACCCCAACGAGTGCATCAACTTC 703  
 QY 338 AspAsn11eG1YTrAlaTTP11eAla11ePheG1YAla11eThrLeuGluG1YTPVal 357  
 Db 704 GACAACTGGCTTACGCTGGATTGCCATTTCCAGGTATCCAGGTATCCAGGTATCCAGGT 763  
 QY 358 Asp11eMetTyrPheValMetAspAlaHisSerPheTyrAsnPhe11eTyrPhe11eLeu 377  
 Db 764 GACATCATGTACTACGTCAATGACGCGCCACTCATTTCAACAATTCAATTTCAATTCCTG 823  
 QY 378 Leu11eT11eValG1YSerPhePheMet11eAsnLeuCysLeuVal11eAla11eThrGln 397  
 Db 824 CTCTATCATCTGGGCTCTTCTTCAATGATCAACCTGCTGCTGATTTGGCAGCGAG 883  
 QY 398 PheSerGluThrTyrGlnArgG1YAsnArg11eLeuMetArgGluGlnArgValArgPheLeu 417  
 Db 884 TTCTCGAGCGAGAGCGCGAGAGTCACTGATGGAGGAGCGGAGCGGACCCCACTCG 943  
 QY 418 SerAsnAlaSerThrLeuAlaSerPheSerGluProG1YSerCysTyrGluGluLeu 437  
 Db 944 TCCAAAGACAGCAGCGCTGGCACTTCTCCGAGCCTGGAGCTGTACGAAAGCTG--- 1000  
 QY 438 LysTyrLeuValTyr11eLeuArgLysAlaAlaArgArgLeuAlaGlnValSerAla 457  
 Db 1000 ----- 1000  
 QY 458 AlaG1YValArgValG1YLeuLeuSerSerProAlaProLeuG1YG1YnG1nThrGln 477  
 Db 1000 ----- 1000  
 QY 478 ProSerSerSerCysSerArgSerHisArgArgLeuSerValHis11eLeuValHisHis 497  
 Db 1000 ----- 1000

QY 498 HisHis11eHis11eHis11eTyrHis11eLeuG1YAsnG1YThrLeuArgAlaProArgAla 517  
 Db 1000 ----- 1000  
 QY 518 SerProGlu11eGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProPro 537  
 Db 1000 ----- 1000  
 QY 538 SerThrProAlaLeuSerG1YAlaProProG1YAlaGluSerValHisSerPheTyr 557  
 Db 1000 ----- 1000  
 QY 558 HisAlaAspCysHis11eLeuGluProValArgCysGlnAlaProProProArgSerProser 577  
 Db 1000 ----- 1000  
 QY 578 GluAlaSerG1YArgThrValG1YSerG1YValTyrProThrValHisThrSerPro 597  
 Db 1001 -----CCGTACTGCAC----- 1012  
 QY 598 ProProGluThrLeuGlyGluValAlaLeuValGluValAlaAlaSerSerGlyProPro 617  
 Db 1012 ----- 1012  
 QY 618 ThrLeuThrSerLeuAsn11eProProG1YProTyrSerSerMetHis11eLeuLeuGlu 637  
 Db 1012 ----- 1012  
 QY 638 ThrGlnSerThrG1YAlaCysGlnSerSerCysLys11eSerSerProCys-LeuYAla 657  
 Db 1013 -----CCGAGCCCTGAGGA 1027  
 QY 657 AspSerG1YAlaCysG1YProAspSerCysProTyrCysAlaArgAlaG1YG1 677  
 Db 1028 CCGGAGGGT----- 1037  
 QY 677 ValG1YLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheTh 697  
 Db 1038 ---GAGCTCAGCGGCTCGGAAGATGAGACTCAAGATGGCCGCTGATGAATTCAC 1093  
 QY 697 rGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuG1 717  
 Db 1094 GCAGAGCGTGGCAACGGTGAACCGCTGGGAGCCC-----ACCGCAACC 1135  
 QY 717 YProAspAlaGluProSerSerValLeuAlaPheTyrArgLeu11eCysAspThrPheAr 737  
 Db 1136 ACCCGG-GGCGAGCCAGGCTGGATGGCGGCGCTGCGGTACTTCAAGCGGCAAGCTGCG 1194  
 QY 737 GlyVal11eValAspSerLysTyrPheG1YArgG1Y11eMet11eAla11eLeuValAsnTh 757  
 Db 1195 CCGCATCGTGAACAGAGTACTTCAGCCGTGGCATCATGATGGCCATCTTGTCAACAC 1254  
 QY 757 rLeuSerMetG1Y11eGluTyrHis11eGluGlnProGluGluLeuThrAsnAlaLeuGlu11 777  
 Db 1255 GCTGAGCATGGGCGGAGTATCATGAGAGCGGAGGAGCTGAATGCTGGAAGT 1314  
 QY 777 eSerAsn11eVal11eThrSerLeuPheAlaLeuGluMetLeuLeuVal11eVal11eVal 797  
 Db 1315 CAGCAACATCGTGTTCACACGATGTTCCTCGAGATGCTGTGAAGCTGCTGGCCCTG 1374  
 QY 797 rG1YProPheG1YTyr11eLysAsnProTyrAsn11ePheAspG1YVal11eVal11eVal 817  
 Db 1375 CCGCCCTCGGCTCATTCGGAACCCGTACAAKATCTTCGACGGCATATCTGTGTCAT 1434  
 QY 817 eSerValTyrGlu11eValG1YnGlnG1YG1YLeuSerVal11eArgThrPheAr 837  
 Db 1435 CAGGCTGCGAGATCGTGGGCGAGCGGAGCGTGAGCTTGTGTGTCGCGACCTTCGCG 1494  
 QY 837 rLeuMetArgVal11eLysValLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValVa 857  
 Db 1495 GCTGCTGCTGTGCGAAGCTGTGCGCTTCTGCAAGCCCTGCGGCGGCAACTGCTGTGT 1554



QY 517 AlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgMetLeuProPro 536  
 Db 1436 ---GCAAGAGAGGAGAGACCGGTTTGCAGAT----- 1465  
 QY 537 ProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPhe 556  
 Db 1465 ----- 1465  
 QY 557 TyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProArgSerPro 576  
 Db 1465 ----- 1465  
 QY 577 SerGluAlaSerGlyArgThrValGlySerGlyLeuValTyrProThrValHisThrSer 596  
 Db 1465 ----- 1465  
 QY 597 ProProProGluThrLeuLeuGlyGlyAlaLeuValGluValAlaAlaSerSerGlyPro 616  
 Db 1465 ----- 1465  
 QY 617 ProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLeuLeu 636  
 Db 1465 ----- 1465  
 QY 637 GluThrGlnSerThrGlyAlaCysGlnSerSerCysLeuValIleSerSerProCysLeuLys 656  
 Db 1466 -----CTCTGTGCTGTGTGATCCCTTCGCCGCC 1495  
 QY 657 AlaAspSerGlyAlaCysGlyProAspSerSerProTyrCysAlaArgAlaGlyAlaGly 676  
 Db 1496 GCCAGGCTCAAGACCGGAAAGACAGAGAGCTGCTCACTTCCGGAG----- 1543  
 QY 677 GluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPhe 696  
 Db 1544 -----AAGGAGAAGATGTTCCCGTTT 1564  
 QY 697 ThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeu 716  
 Db 1564 ----- 1564  
 QY 717 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 736  
 Db 1565 -----TTATTC 1570  
 QY 737 ArgGlyIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn 756  
 Db 1571 CGCGCATGTGTGAAGCTCAGAGCTTCTACTGGGTGTGTGTGCGTGTGGCGCCGTAAC 1630  
 QY 757 ThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu 776  
 Db 1631 ACACGTGTGTGGCCATGTGCTACAAACACAGCCCGCGGCTTACACAGACCTGTAT 1690  
 QY 777 IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuVal 796  
 Db 1691 TTTCGAGAGTTTCTTTCCGGGTCCTTCTCACAAGATGTCCTGAAGATGTATGG 1750  
 QY 797 TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal 816  
 Db 1751 CTGGGGCCCGAAGCACTTCCCGTCTCTCAACTGCTTGCATTGGGGCATCCG 1810  
 QY 817 IleSerValTrpGluIleValGlyGln-----GlnIleGlyGlyLeuSer 831  
 Db 1811 GGGAGGCTTTTAAGGTGTGGGCGGCATCAAGCCGGGAAGCTCTTTGGGATCAGT 1870  
 QY 832 ValLeuArgThrPheArgLeuMetArgValIleuLysLeuValArgPheLeuProAlaLeu 851  
 Db 1871 GTGCTGGGGCCCTCGCGCTGTGAAGATCTTCAAAGTCAAGAAATCGAGACTCCCG 1930  
 QY 852 GlnArgGlnLeuValValLeuMetLysTrpMetAspAsnValAlaThrPheCysMetLeu 871  
 Db 1931 CGGAACCTGTGTGTGCTGTGAATCCATGAAGTCCATCATCACTGCTCTTCTTG 1990  
 QY 872 LeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPhe 891

Db 1991 CTCTTCCTCTTCAATTGTGTGTCTTCCCTGCTGGGAGATGACAGCTGTTGGGGAAGTTC 2050  
 QY 892 AlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrp 911  
 Db 2051 AACTTCACGAGATGAGATCCAC-----ACCACTTCGACACCTTCCCTGCC 2098  
 QY 912 AlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTrpAsn 931  
 Db 2099 GCCATCTCACTGTCTTCAATCTGTGAAGGAGAGACGTGAAGTCAAGTATGTATCAC 2158  
 QY 932 GlyMet-----AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAla 946  
 Db 2159 GGGATCGAATCCGACAGCGCGCTCAGCAAGGCAATGTCCTCTTACTTCACTTGTTC 2218  
 QY 947 LeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGly 966  
 Db 2219 CTGACACTGTTCGAAACTACACTGCTGAATGCTTCTTGGCCATCGCTGTGACAAAC 2278  
 QY 967 Phe---GlnAlaGluGluIleSerLys-----ArgGluAspAlaSerGlyGln 981  
 Db 2279 CTGGCCAAAGCCCAAGAGCTGACCAAGATGAAGAGAGATGAAGAAAGCCCAATCAG 2338  
 QY 982 -----LeuSerCysIleGln 986  
 Db 2339 AAGCTTGCTTGCAAAAGGCCAAAGAGTGCCTGAAGTCAGGCCCATGCTTCCCGCAAC 2398  
 QY 987 LeuProValAspSerGlnGlyValAspAlaAsnLysSerGluSerGluProAspPhePhe 1006  
 Db 2399 ATCTCATGCGCGGACGACGAGAACTCGGCCAAGCGCGCTCGGTGTGGACGACGCG 2458  
 QY 1007 SerProSerLeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGly 1026  
 Db 2459 GCCACGACGTAAGCTGTGCAAACTGTGGGCGACGTGTGAGGCGCTGTACGCAAGATG 2518  
 QY 1027 Glu-----HisProGluLeuArgLys 1033  
 Db 2519 GACCCGAGAGAGCGGCTGCGCTTCCGCACTAGCGGCCACCTGCGGCCGACATGAAGACG 2578  
 QY 1034 SerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuPro----- 1051  
 Db 2579 CACTGTGAACCGGCGCTGTGTGTGAGCTGTGGCCGACGCGCGCGGCGCGCTGGGA 2638  
 QY 1052 -----LysSerThrSe 1055  
 Db 2639 GGCAAAAGCCGACCTGAGGCTGCGAGGCGCCCGAGGCGCTGACCTCCGGCAGGCAC 2698  
 QY 1055 rThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThrSerSer----- 1071  
 Db 2699 CACCGGACCGGACAGGACAAAGACCCCGCGGCGGAGAACAGACCGAGCAGAGGCC 2758  
 QY 1072 -----SerGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProBr 1087  
 Db 2759 CCGAAGCGGAGAGCGGGAGCCCGGTGCTCCCGGAGGAGCGGCCCGCGCCGACGACG 2818  
 QY 1087 oSerAlaArg-----SerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe 1105  
 Db 2819 CACAGCAAGAGAGCGCGCGGAGCGCCCGAGGCGCGAGCGAGCGGCGGAGGCCAGGC 2878  
 QY 1105 rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSe 1125  
 Db 2879 CCGAGAGGCGGCGGCGGACACCGGCGGCTCC-----CGAGAGGCGGCGGAG 2932  
 QY 1125 rGlyGlu----- 1127  
 Db 2933 CGGAGAGCCCGACGACCGCGGACCGGACCGGACCGAGATCCGAGTCCGCGCG 2992  
 QY 1127 ----- 1127  
 Db 2993 GCCAAGGCGAGCGCGCGCGGACCGGCGGCGCGCCCGAGCGGAGCGCGGAGGCG 3052  
 QY 1128 -----ArgArgSerLeuLeuSe 1133

Db 3053 GAGAGCGGGGAGGAGCGCGCGCGGACCGGCGGACGAGGCGGACCTGCTCAC 3112  
 Qy r-glygluglyglu-glugsergluaspugluglusergsergluglugluatgalaaser 1152  
 Db 3113 GAGGCTGTGGAGAGAGAGACAGAGAGAGAGAGCGGACGAGAGAGAGAGAGAGATAGT 3172  
 Qy 1153 ProAlaGlySerAspHisValGlyHisArgGlySerLeuGluValAlaValSerSerPhe 1172  
 Db 3173 GAAGCCCAAGCAAGAAAG 3232  
 Qy 1173 AspLeuProAspThrLeuGluValProGlyLeuHisValThrAlaSerGlyArgGlySer 1192  
 Db 3233 GAGACGAGTGGAGAGTGTGATCTGTGAGTCCATGACACATGCTCCAGCACTGTCTCCAG 3292  
 Qy 1193 AlaSerGluHisArgGluAspGlySerGlyLeuSerAlaSerGlyArgGlyLeu 1212  
 Db 3293 AAGGTGAG 3352  
 Qy 1213 ArgProAspAspPro-----ProLeuAsp 1220  
 Db 3353 CAGCCCGGAG 3412  
 Qy 1221 GlyAspAspAlaAspAspGluGlyAspLeu-----SerLeuGlyGluArg 1235  
 Db 3413 GAAGCCAGGCTGCTCCAGAGTGTGATGATCCAGATGATCCAGAGAGAGAGAGAGAG 3472  
 Qy 1236 -----ValArgAlaThrPheAlaArgAlaArgGlyProAlaCysArg 1248  
 Db 3473 GAGGTGAG 3529  
 Qy 1249 LeuGluArgAspSerThrSerAlaThrLeuPheProPheGlnSerArgPheArgLeu 1268  
 Db 3530 -----TCCATGTTCTGTTTAAAGCCCGGACCAACCTGCTCGCGCTCTC 3571  
 Qy 1269 CysHisArgGlyLeuThrHisLeuMetPheAspHisValValLeuValIleIlePheLeu 1288  
 Db 3572 TGCCATGATCATCTGAG 3631  
 Qy 1289 AsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIle 1308  
 Db 3632 AGCAGCATCGCGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3688  
 Qy 1309 PheLeuThrLeuSerAsnThrIlePheThrAlaValIlePheLeuAlaGluMetThrVal 1328  
 Db 3689 GCTCGAATGATCTGATTAATTAATTTTCACTGCTGCTTACCTTGAATGATGTTAAAG 3748  
 Qy 1329 ValValAlaLeuGlyTTPCyPheGlyGluGluAlaThrLeuArgSerSerThrAsnVal 1348  
 Db 3749 ATGATGCACTTGGAGCTGCTGCTTCAACCTGAGAGCTTATTCGGGAGACTTGGAGAAC 3808  
 Qy 1349 LeuAspGlyLeuLeuValIleSerValIleAspIle-----LeuValSerMetValSer 1367  
 Db 3809 CTGACCTTCATTTGCTGATGAGGCGCCCTGGAGGCTTGGCTTCTGAGGCTGTGGGA 3868  
 Qy 1368 AspSerGlyThrLysIleLeuGlyMetLeuArgValIleAspGluLeuArgThrLeuArg 1387  
 Db 3869 GGATTCGAAGGAGAAAGATCAATACATCAAGTCTGAGAGGCTTCTGCTGCTGCGG 3928  
 Qy 1388 ProLeuArgValIleSerArgAlaGlnIleGlyLeuLysLeuValValGluThrLeuMetSer 1407  
 Db 3929 CCCCCTCAAGACCTCAAAAGCGCTGCCCAAGCTCAAGGCTGTGTTGACTGTGTGGTAAAC 3988  
 Qy 1408 SerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGly 1427  
 Db 3989 TCCCTGAAGAGATGCTCTCAACATCTTGAATGCTCAATGCTCTTCAATTCATATTCC 4048  
 Qy 1428 IleLeuGlyValIleGluPheLysGlyLysPhePheValCysGlyGlyGlu----- 1444  
 Db 4049 GTCATTGGCGGTGACACTCTTCAAAAGGAAATTTTCTACTGACAGAGAAATCCAAAGAG 4108  
 Qy 1445 -----AspThrArgAsn-----IleThrAsnLysSerAspCysValGluAlaSer 1459  
 Db 4109 CTGAGAGAGGACTGAGAGGAGTCAATTTGATTTAGAAAGAGAAAGTGGAACTGAC 4168

Qy 1460 TyrArg-----TrpValArgHisLysTyrAsnPheAspAsnLeuGluAlaLeuMetSer 1478  
 Db 4169 CCCAGGAGAGGAGAAAGAAATTCAGATTTCACTACAGAGAAATGCTGTGGGCTGTGAGC 4228  
 Qy 1479 LeuPheValLeuAlaSerLysAspGlyTTPValAspIleMetTyrAspGlyLeuAspAla 1498  
 Db 4229 CTGTTCAAGTGTCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4288  
 Qy 1499 ValGlyValAspGlnIleProIleMetValHisAsnProThrMetLeuThrPheIle 1518  
 Db 4289 ACCATGAG 4348  
 Qy 1519 SerPheLeuLeuIleValAlaPhePheValLeuAspMetPheValGlyValValIleGlu 1538  
 Db 4349 GTCTACTTGTGGCTTTCTCCCTTCTTCTGTAACAATTTTGTGCTTGAATCATC 4408  
 Qy 1539 AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLys 1558  
 Db 4409 ACCTTT-----CAGAGCAGGAGGAGCAAGGATGTGTGA----- 4444  
 Qy 1559 ArgLeuArgArgLeuGluLysLysArgArgLysAla-----GlnCysLys 1573  
 Db 4445 -----TGACGCTGAG 4498  
 Qy 1574 ProTyr-----TyrSerAspTyrSerArg-----PheArgLeuLeuValHisLysLeu 1589  
 Db 4499 CCCCCTGACAGGATACATGCCCCCAAAACCGGAGAGAGAGAGAGAGAGAGAGAGAG 4558  
 Qy 1590 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValIleThr 1609  
 Db 4559 GTGGTCTCCCCGCTTGAATACCTTCATCATGAGCCATGATAGCCCTCAACAGCTGTGCTG 4618  
 Qy 1610 MetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsn 1629  
 Db 4619 CTGATGATGAAGTTATGATGATGACACCTATGATGATGATGATGATGATGATGATGAT 4678  
 Qy 1630 TyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPhe 1649  
 Db 4679 ATCGTGTTCACATCCAGATTTCTCCATGAAATGCGTGTGAAGATCATCGCTTGTGGGCTG 4738  
 Qy 1650 ArgArgPhePheGlnAspArgTTPAsnGlnLeuAspLeuAlaIleValLeuSerIle 1669  
 Db 4739 CTGAACATTTTCAGAGATGCGCTGGAATGCTTGAATCTTGTGCTGCTGCTGCTGCTGCTG 4798  
 Qy 1670 MetGlyIleThrLeuGluGluIle-----GluValAsnAlaSerLeuProIleAsnProThr 1688  
 Db 4799 ACTGATATTTTATGAAACAGAGATTGGGAAACGAA-----AATTGCATC 4843  
 Qy 1689 IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAla 1708  
 Db 4844 AACCTGAGCTTCCCTCCCTCTTTCGAGCTGGCGGCTGATCAAGCTGCTCGGACGAGGC 4903  
 Qy 1709 ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu 1728  
 Db 4904 TACACCATTCGATCTGCTGTGAGACCTTGTCCAGTCTTCAAGGCCCTGCTGCTGCTGCTG 4963  
 Qy 1729 GlyLeuLeuPheMetLeuLeuPhePheIlePheHisAlaLeuGlyValGluLeuPheGly 1748  
 Db 4964 TGCTGTGCATTTGCAAGAGCTGCTTCTTCAATCATGAGCATCGGACATGAGAGTGTGGG 5023  
 Qy 1749 AspLeuGluCysAspArgLuthHisPheProCysGluGlyLeuGlyValArgHisAlaThrPheArg 1768  
 Db 5024 AATATTCCTCCCTGATGATGAC-----ACCAGCATCAACCGCCCAACCACTCTCCG 5074  
 Qy 1769 AsnPheGlyMetAlaPheLeuThrLeuPheArgValIleSerThrGlyAspAsnTTPAsnGly 1788  
 Db 5075 ACGTTTTCGAAGGCTGATGCTCTTTCAGAGAGGCGCACGAGGAGAGGCTGCGACAGAG 5134  
 Qy 1789 IleMetLysAspThrLeuArgAsp-----CysAspGlnGlu-----SerThrCysArg 1804  
 Db 5135 ATCATGCTGTGCTGCTGAGAGACCAAGGCTGTGATGAGAGAGGCAATGCAACCGAGTGT 5194

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QY 1805 AsnThrValIleSerProIleTyrPheValSerPheValIleuThraIaGlnPheValIleu 1824
    ::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5195 GGAAGGACCTTTCCTCACTTCTGCTCTCTCACTCTCTGCTCTCTCTCTCTCTGAG 5254
QY 1825 ValAsnValIleIleValIleuMet 1833
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 5255 TTGAACCTCTTTGGCTGTGATCATGACAATTTTGAAGTACCTCAGCGGGACCTCTCC 5314
QY 1834 -----LysHisIleuGluGlu-SerAsnLysGluAlaLysGluGluIle 1849
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5315 ATCTTAGTCTTCACACCTTGATGAGTTCACTCCGGCTCTGGCTGAATACGACCGGCT 5374
QY 1849 uGuaIaGluLeuGluLeuGluMetLysThrIleu-SerProGlnProHisSerProLeuG 1869
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5375 GCGTGGGGCGCATCAGTTACATGACATGTTTGAATGCTGAACAACATGCTCCCGCT 5434
QY 1869 LysSerProPheLeuTyrProGlyValGluGlyProAspSerProAspSerProLysProG 1889
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5435 CTGGG-----GCTGGGGAGAAATGCGCTGCTGAGTTGCTTACAAAGCGCTG 5482
QY 1889 ValAlaLeuHisProAlaAlaHisAlaArgSerLaseHisSerHisLeuGluHisProt 1909
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5483 GTTCG---CATGAACATGCCCATCTCCACAGAGACATGATGTTCACTTCACGTCACG 5539
QY 1909 hrMetGlnProHisSerProThr-----GluLeuProGlyPro----- 1920
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5540 CTGATGGCCTCTCATCCGGACGCGCATGAGTACATCACTGGCCCCCAGCTGGACAAAGCAG 5599
QY 1921 -----AspLeuLeuThrValAlaArgLysSerGly----- 1929
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5600 CATCAGTGTGACGCGGAGTGTGAGAGAGATTTCCGTTGTGGCCCATGTGCCCG 5659
QY 1929 ----- 1929
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5660 AAGACTTTGACTTGTGTGTACCAACCCATAGCTGATGAGATGACAGTGGGAGGTT 5719
QY 1930 -----ValSerArgThrHisSerLeuProAsn 1939
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5720 TATGACGCTCTGATGATTTTGAATTTGACTTCTACAGCAACAACAAACACAGAGCCAGATG 5779
QY 1939 spSerTyrMetCysArg-----HisGlySerThrAlaGluGlyPro-----LeuG 1954
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5780 CAGCAGGCTCTGTGAGGCTCTCCAGATGGGCTGTGTCCTGTCTTCCACCTCTGAG 5839
QY 1954 LHis-----ArgGlyTyrProGlyLeuPro-LysAla 1963
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5840 GCCACCTTGAGACGACACACGCCGCTGTCTCCGAGGAGCCCGGGTTCCTTTCAGACG 5899
QY 1964 GlnSerGlySerValLeuSer-----ValHisSerGlnProAla----- 1976
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5900 AAGAGTTCCACCTCCCTCAGCAATGCGGGGCCATCAAAACCAAGAGTGGCATCAAA 5959
QY 1977 ---AspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnPro--- 1994
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Db 5960 GAGTGTGTCTCTGGGACCTCAAAAGAACCCAGAGTGCACCCCATGAGGCCAGGCCACCC 6019
QY 1995 -----HisSerAlaProThrTyrProGlyThrIleProLysLeuProProGly 2010
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Db 6020 CTGGAGCGTGGCCATCTCCAGAGATC-----CCTGTGGG 6055
QY 2011 ArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArg----- 2026
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Db 6056 CGGTCAAGAGCACTGGCTGTGAGCTTTCAGATGCACAGCATACCCGAGGGGCGCTGAT 6115
QY 2027 -----ThrAspSerLeuAspValGlnGlyLeuGlySerArgGlnAspLeuAla 2043
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Db 6116 GGGAGACCCCGAGCTGGCTGTGAGAGCCAGGAGTCAAGCCCTTCATGCCCCGCTTGG 6175
QY 2044 GluValSerGlyPro-----SerProProLeuAlaArgAlaLysSerThrProGly 2060
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Db 6176 GCCGAGACTCAAGCCCTTCACAGATGCCAGGCCCATCAAGGCGCTCAATC----- 6223
QY 2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet 2080

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Db 6224 -----TCCAGCGTGGCCCGACGCG---CCCCGTGGAC-TATCTTTGACAGCACACCCC 6273
QY 2081 ThrProProAlaProCysArgProGly-----ProGluProAsnTyrGlyLysGlyPro 2097
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Db 6274 GAGACCGCCACCCCTTACAGGCGCTGTGTCAGCACACCA-----CCA 6318
QY 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTyrIleSerGlyAspLeu 2117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6319 CCG-----CTG 6324
QY 2118 LeuProProGlyGlyGlnGlu---GluProProSerProArgAspLeuLysCysTyr 2136
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Db 6325 CCACCGCCGACAGGACAGAGAGCAGAGTCCCTGAGAAAGGGGCCAGCTGTCTGC--- 6381
QY 2137 SerValGluAlaGlnSerCysGlnArgArgProThrSerTyrIleAspGlnArgArg 2156
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6382 -----CGATATGATGGCGCACAGCAG----- 6405
QY 2157 HisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisIleuGlyThrAspPro 2176
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6406 -----TGCTGTGGGCGGGGCTGCCCTCCGAGAGAGGGGCTTA-CAG 6446
QY 2177 SerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLeuSer 2196
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6447 GCTGCGGGGAGAGAGAGCGCGGAGAGCGGGGCGGCTCCAGAGAGCGGAGCGAGC 6506
QY 2197 ProProSerIleThrIleAspProGluSerGln----- 2208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6507 CCT-----CATCTCTCTCTCGGACAGACAGCGCTTCACTCTCGAC 6551
QY 2209 -----GlyProArgThrProProSerProGlyIleCysLeuArgArg 2223
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Db 6552 GCTTGGGGGCGGTAGCGCCCGGAGCCAGAGCCCTCTCTCAGACAGCCACCAAGTGGC 6611
QY 2224 AlaProSerSerAspSerLysAspPro----- 2232
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6612 CAACAGCTGGCCAGAGCGCGGAGCCCAACAGAGGAGTGTCCGATGAGGAGCC 6671
QY 2233 -----LeuAlaSerGlyProProAspSerMetAlaIleSerProSerPro 2247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6672 CTTGCTGTCAATCTGTGTGTAGACCCCGCGCGGGGCGGAGGAGCAGCTCCCC 6731
QY 2248 LysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
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Db 6732 AGACGCGCTGACTC-----CCGCGCCAGCATCACT 6764

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RESULT 15  
 US-08-455-543A-7  
 / Sequence 7, Application us/08455543A  
 / Patent No. 5792846  
 / GENERAL INFORMATION:  
 / APPLICANT: Harpold, Michael  
 / APPLICANT: Ellis, Steven  
 / APPLICANT: Williams, Mark  
 / APPLICANT: Feldman, Daniel  
 / APPLICANT: McCue, Ann  
 / APPLICANT: Brenner, Robert  
 / TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
 / NUMBER OF SEQUENCES: 57  
 / METHODS  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Brown, Martin, Haller & McClain  
 / STREET: 1660 Union Street  
 / CITY: San Diego  
 / STATE: California  
 / COUNTRY: USA  
 / ZIP: 92101-2926  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Diskette  
 / COMPUTER: IBM Compatible  
 / OPERATING SYSTEM: DOS  
 / SOFTWARE: FastSeq Version 1.5

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/968,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6302-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..7163
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 7161..7362

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Alignment Scores:			
Pred. No.:	1,17e-100	Length:	7362
Score:	1784.50	Matches:	637
Percent Similarity:	38.87%	Conservative:	367
Best Local Similarity:	24.66%	Mismatches:	836
Query Match:	14.9%	Indels:	745
DB:	1	Gaps:	78

  

US-09-611-257A-37 (1-2266) x US-08-455-543A-7 (1-7362)	
QY 27 GLVALGLGLYARGPProGlyProGlySerAlaGluLYsaPProGlySerAlaPser 46	
Db 216 GGGGCGGGCGGGCGGGGGGCTCCGGGGGGCTGACAGCCCGGCGACGGGTCCTC 275	
QY 47 GLVALGLGLYLeuProTYrProAlaLeuAlaProValAlaPhe----- 61	
Db 276 TACAGCAATCGATCCGCCAGCGCGCGGACCAATCGGCGCTGTACAAACCCATCCCGTCC 335	
QY 62 -----PheTYrLeuSerGlnaPseraTYrPro 70	
Db 336 AAGCAGAACTGTTCACCGGTCAACCGCTCTTCCTTCGTTCCAGGAGACAAAGTGTC 395	

OY	71	ArgSerTrpCySleuAArgThnValCyAsnProTrpPheGluArgIleSerMetLeuVal	90
Db	396	CGCAAAATACGGGAAGCCGATCACCGAGTGGCTTCATTCAGAAATATGATCTGGCCAC	455
OY	91	IleLeuLeuSncysValThrLeuGlyMetPheArgProCysGluAspIleAlaCyAsp	110
Db	456	ATCATGCGCAACTCATCTGATCGTGGCCCTG-----GAGCAGCACTCCCTGAT	503
OY	111	SerGlnArgCySAspGllLeuGlnAlaPheAsp-----PheIlePheAlaPhe	127
Db	504	GGGGAACAACCGCCCATGTCGACCGGCTGACACACGAGGCCCTTATTCATCGGATC	563
OY	128	PheAlaValGluMetValIleValMetValAlaLeuGly--IlePheGlyValCys	146
Db	564	TTTTCGTTCCAGGAGGATCAAAATCATGCTCTGGGGCTTTGCTTCCACAAAGGCTCT	623
OY	147	TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu	166
Db	624	TACCTGCGGAACGGCTGGAACGTATGAGACTTCGTGCTGCCCTCCACAGGGATCCTGCC	683
OY	167	TySer-----LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArg	183
Db	684	ACGGCTGAACTGACTTCGACTTCGCA-----ACACTGAGGCGTGTGCT	728
OY	184	ValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeu	203
Db	729	GTGCTGAGGCCCCCTGAAGCTGCTGCTCGGATTCCAAGTTTGACAGGTGCTCAAGTCC	788
OY	204	LeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePhe	223
Db	789	ATCATGGAAGCCCATGTTCCACTCTCCAGATTTGGGCTTCTTCTTTCGCACTCTC	848
OY	224	IlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeu	243
Db	849	ATGTTTGGCATCATTTGGCTCGAATTTCTACATGGGCAAGTTCCACAAGCGCTGTTCC	905
OY	244	ProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsn	263
Db	906	-----CCCAACAGCACAGATCCGAG-----	926
OY	264	GluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArg	283
Db	926	-----	926
OY	284	SerValProThrLeuArgGlyAspGlyGlyGlyProCysGlyLeuAspTyrGlu	303
Db	927	-----CCCGG-----GGTACTTCCCTGTGTGGCAAGAGGCCCA	962
OY	304	AlaTyrAsnSerSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCys	323
Db	963	GGCCGGCTGTGCGAGGGGACACACGAGTGC-----CGGAGTACTCGGCCA-----	1007
OY	324	SerIleArgIleuHsAsnProPheLeuGlyAlaIleAsnPheAspAsnIleGlyTyrAla	343
Db	1008	-----GACCCCACTTTGGCATCCACCACTTTGACATATCTCTGTTGCC	1052
OY	344	TrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheVal	363
Db	1053	ATCTTGAAGCTTCCAGTGATCACCATGAGGGCTGACCTGACATCTCTATATATACA	1112
OY	364	MetAsp--AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGly	382
Db	1113	AACAGTGGCGGCGCAACCTGGAACGTGCTCATCTTCATCTCTCATATCATCTGGGC	1172
OY	383	SerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLys	402
Db	1173	TCTTCTTTCATGCTCAACCTGTGTCTGGCGGTGCTCCGGGAGATTGGCAAGAGCGCA	1232
OY	403	GlnArgGluSer-----GlnLeuMetArgGluGlnArgValArgPhe	416
Db	1233	GAGAGGGTGAAGAACCGCGCGCTTCTCTGAAGTGTGGCGCGGACAGCAATGACAG--	1289

QY 417 LeuSerAsnAlaSerThrIleuAlaSerPheSerGluProGlySerCysTrpGluIleu 436  
 Db 1290 -----CGAGAGCTC 1298  
 QY 437 LeuLysTrpIleuValTyrTrlIleuArgLysAlaAlaArgIleuAlaGlnValSerArg 456  
 Db 1299 AACGGGTACTGAGTGGATCTTCAAGCGGAGAGATGATCATGCTGCGCGAGGACAG 1358  
 QY 457 AlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlnGlnThr 476  
 Db 1359 AATGCA-----GAGGAGAG 1373  
 QY 477 GlnProSerSerSerCysSerArgSerHisArgArgLeuSerValHisIleuValHis 496  
 Db 1374 TCCCTTTGGACGTGCTGAAGAGAGCGGCCACCAAGAGAGCAAAATGACTGATCCAC 1433  
 QY 497 HisHisHisHisHisHisHisHisTyrHisIleuGlyAsnGlyThrLeuArgAlaProArg 516  
 Db 1433 ----- 1433  
 QY 517 AlaSerProGluIleGlnAspArgAlaAsnGlySerArgArgLeuMetLeuProPro 536  
 Db 1434 ---GCAGAGAGGAGAGAGCGCGTTCGACAT----- 1463  
 QY 537 ProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPhe 556  
 Db 1463 ----- 1463  
 QY 557 TyrHisAlaAspCysHisIleuGluProValArgCysGlnAlaProProProArgSerPro 576  
 Db 1463 ----- 1463  
 QY 577 SerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSer 596  
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 QY 617 ProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisIlyIleuLeu 636  
 Db 1463 ----- 1463  
 QY 637 GluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysIleuLys 656  
 Db 1464 -----CTCTGTGCTGTGGATCCCCCTTCGCCGCC 1493  
 QY 657 AlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGly 676  
 Db 1494 GCCAGCTCAAGAGCGGAGAGACAGAGAGCTGCTCATCTCCGAGAG----- 1541  
 QY 677 GluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPhe 696  
 Db 1542 -----AAGAGAGAAGATGTTCCGATT 1562  
 QY 697 ThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeu 716  
 Db 1562 ----- 1562  
 QY 717 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 736  
 Db 1563 -----TTTATC 1568  
 QY 737 ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn 756  
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 QY 757 ThrLeuSerMetClyIleGlyTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu 776  
 Db 1629 ACACGTGTGTGGCATGTGATCAACACAGCCCGCGCGCTTACCAAGACCTGTAT 1688  
 QY 777 IleSerAsnIleValPheThrSerLeuPheAlaLeuGlnMetLeuLysIleuVal 796

Db 1689 TTTGAGAGTTTGTCTTCTGAGTCTCTTCCACAGAGATGCTCCGAAGATGATGAC 1748  
 QY 797 TyrGlyProPheGlyTyrTrlIleuAsnProTyrAsnIlePheAspGlyValIleValAl 816  
 Db 1749 CTGGGGCCAGAGAGTACTTCGCGTCTTCCTCACTGCTTCGACTTGGGCTATCGTG 1808  
 QY 817 IleSerValITPGLuIleValGlyGln-----GlnGlyGlyLysLeuSer 831  
 Db 1809 GGGAGCGCTTGAAAGTGTCTGGCGGCATCAAGCCGGAGAGTCTTTGGATCACT 1868  
 QY 832 ValLeuArgThrPheArgLeuMetArgValLeuLysIleuValArgPheLeuProAlaLeu 851  
 Db 1869 GTGCGCGGGCCCTCGCTGTGAGATCTTCAAAAGTACAGAAATGACTGAGCTCCCTG 1928  
 QY 852 GlnArgGlnLeuValIleuMetCysThrMetAspAsnValAlaThrPheCysMetLeu 871  
 Db 1929 CGAAGCTGTGTGTCTCTGTAATCAATGAAGTCAATCATCAAGCTGCTCTTCTTG 1988  
 QY 872 LeuMetLeuPheIlePheSerIleLeuGlyMetHisIleuPheGlyCysLysPhe 891  
 Db 1989 CTCTTCCTGTATGTGTGTCTTCCCTGCTGGAGATGACACTTGTGGGGACACTTC 2048  
 QY 892 AlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrp 911  
 Db 2049 AACTCCAGAGATGAGACTCCACA-----ACCAACTTGACACTTCCTCCCTGCC 2096  
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 Db 2097 GCCATCTCACTGTCTTCCAGATCTTGACGGGAGGAGCTGGAAATGACATGATGATCAC 2156  
 QY 932 GlyMet-----AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAla 946  
 Db 2157 GGAATCGAATGCAAGAGCGGCGCTCAGCAAGCAATGTTCTGCTCTTTACTTCACTTGC 2216  
 QY 947 LeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGly 966  
 Db 2217 CTGACACTGTTCGAAACTACACTCTGCTGAATGCTTTCGCGCATGCTGTGACAAAC 2276  
 QY 967 Phe---GlnAlaGluGluIleSerLys-----ArgGluAspAlaSerGlyGln 981  
 Db 2277 CTGGCCAAAGCCCAAGAGCTGACCAAGATGAAGAGAGATGAGAAAGACACCAATCG 2336  
 QY 982 -----LeuSerCysIleGln 986  
 Db 2337 AAGCTTGCTCTGCAAAAGGCCAAAGAAGTGGTGAAGTCAAGCCCATGCTCCGCCGAC 2396  
 QY 987 LeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluProAspPhePhe 1006  
 Db 2397 ATCTCCATGCGCCGACAGGAGAGAACTCGGCCAAGCGCGCTCGGTGGGAGCAGCGG 2456  
 QY 1007 SerProSerLeuAspGlyAspGlyAspArgLysLysCysIleuAlaLeuValSerLeuGly 1026  
 Db 2457 GCCACGACGCTACGCGCTGAGAACTCGCGGCGCACTGCGAGCGCTGTACACAGATG 2516  
 QY 1027 Glu-----HisProGluLeuArgLys 1033  
 Db 2517 GACCCCGAGAGCGGCTGCGCTTCCGCACTACGCGCCACCTGCGGCCGACATGAAGAG 2576  
 QY 1034 SerLeuLeuProLeuIleIleHisThr-AlaAlaThrProMetSerLeuPro----- 1051  
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 QY 1052 -----LysSerThrSe 1055  
 Db 2637 GCGAAAGCCCGACTGAGGCTGCGGAGGCCCGGAGGCGTGCACCTCCGCGAGCAC 2696  
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 Db 2697 CACCGGACCGGAGCAAGACAAAGACCCCGGCGGGGGAGACAGAGCCGACAGAGGC 2756  
 QY 1072 -----SerGlySerAlaGluProGlyValAlaHisGluMetLysSerProPr 1087



Db 2757 CCGAAGCGGAGAGCGGGAGCCCGGTCGCGGAGAGAGCGCGCGCGGACCGGAC 2816  
 QY 1087 oSerAlaArg-----SerSerProHisSerProTyrSerAlaAlaSerSerTyrThrSe 1105  
 Db 2817 CACAGCAAGAGAGCGCGCGGCGCCCGGAGCGCGGAGCGAGCGCGGCGCGAGCGCCAGCG 2876  
 QY 1105 rArgHArgSerSerArgHisSerSerLeuGlyAlaProSerLeuAlaArgArgSerProSe 1125  
 Db 2877 CCGAGGCGCGCGCGCGCGGACCGCGCGCGGCTCC-----CGAGAGAGCGCGCGAG 2930  
 QY 1125 rGlyGlu----- 1127  
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 QY 1127 ----- 1127  
 Db 2991 GCCAAGGCGGAGCGCGCGCGGCGGACCGGCGGCGCCCGAGCGGCGCGCGGAGCGG 3050  
 QY 1128 -----ArgArgSerLeuLeuSe 1133  
 Db 3051 GAGAGCGGAGGAGCGCGCGCGGCGGACCGGCGCGGACCGGAGCGCGGCGGAGCGGCTGCTCAC 3110  
 QY 1133 r-GlyGluGluGln-GluserGlnAspGluGluSerSerGluGluGlnAlaSer 1152  
 Db 3111 GAGGCTGTGAGAGAGAGCCGAGAGAGAGGCGCAGAGAGAGGCGCTGAGATGTG 3170  
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 Db 3171 GAGGCCGACAGAGAGAAAGAGAGCTCCGAGACACAGCGCGGAGCGCACCTGAGACTG 3230  
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 QY 1349 LeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetVal---Ser 1367  
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 QY 1388 ProLeuArgValIleSerArgAlaGlnGlyLeuLyLeuValValGluThrLeuMetSer 1407  
 Db 3915 CCCCTCAAGACCATCAAAAGCGCTGCCAAGCTCAAGCGTGTGTGACATGCTGGTGAAC 3974  
 QY 1408 SerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGly 1427  
 Db 3975 TCCCTGAAGATGCTCTCAACATCTGATGTCTACATGCTCTTCACTGTTCAATATTGCC 4034  
 QY 1428 IleLeuGlyValGlnLeuPheLyGlyLysPhePheValCysGlnGlyGlu----- 1444  
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 Db 4095 CTGAGAGGAGACTGCGAGGGGTCAATTTGATTAAGAGAGAGAGAGAGAGAGAGAGAG 4154  
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 QY 1539 AsnPheHisLyCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGlyLys 1558  
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 Db 4431 -----TCAAGCTGAGAGAGAGAGAGAGGCTTTCGATGACTTCCGACATACCGCCAA 4484  
 QY 1574 ProTyr-----TyrSerAspTyrSerArg-----PheArgLeuLeuValHisLysLeu 1589  
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 18, 2005, 18:24:02 ; Search time 2770.66 Seconds  
(without alignments)  
5449.019 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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2	11815.5	99.3	7648	19	US-10-757-262-15	Sequence 15, Appl	
3	11815.5	99.3	7825	22	US-10-756-149-11	Sequence 31, Appl	
4	11815.5	99.3	7825	22	US-10-786-148-120	Sequence 120, Appl	
5	11353	95.4	8116	17	US-10-062-674-2011	Sequence 2011, Appl	
6	11111	93.3	7129	10	US-09-383-894-1	Sequence 1, Appl	
7	11111	93.3	7285	10	US-09-383-894-3	Sequence 3, Appl	
8	10945	91.9	6942	19	US-10-377-139-7	Sequence 7, Appl	
9	6315.5	53.1	3993	21	US-10-930-301-51	Sequence 51, Appl	
10	6216.5	52.2	7898	22	US-10-483-467-3	Sequence 3, Appl	
11	5495.5	46.2	6990	19	US-10-377-139-8	Sequence 8, Appl	
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## ALIGNMENTS

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; Publication No. US2004017561A1
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee Mackinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: Seq. Nos. 1-21 for 119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 10
; LENGTH: 7648
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-377-139-10

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Best Local Similarity: 95.25%  Mismatches: 1
Query Match:      99.26%      Indels:      111
DB:              19          Gaps:      2

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Qy 1121 ArgArgSerProSerG1yG1uAargSerLeuLeuSerG1yG1uG1yG1uG1uG1uG1u 1140  
Db 3361 CGGAGAAAGCCAAAGTGAAGAGCGGCGGTCCCTGTGTCGAGAAAGCCAGAGAGCCAG 3420  
Qy 1141 AspG1uG1uG1uSerSerG1uG1uAargA1aSerProA1aG1ySerAspH1eAargH1e 1160  
Db 3421 GATGAAGAGAGAGCTCAGAGAGAGAGCGGCGGACGCTTCGCGGAGTACCATTCGCCAC 3480  
Qy 1161 ArgG1ySerLeuG1uAarg1uA1ySerSerPheAspLeuProaspThrLeuG1uA1 1180  
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Qy 1181 ProG1yLeuH1eAargThrA1aSerG1yAarg1ySerA1aSerG1uH1eG1uAspCyAsp 1200  
Db 3541 CCAGGCTGATGATGCATGCGACATGGCCGAGGGGTGCTTCTGACAGCAGACTGCAAT 3600  
Qy 1201 G1yLySerA1aSerG1yAarg1uAargA1aLeuAargProaspAspPropoleuAsp 1220  
Db 3601 GGCAGATCGGCTTCAGAGGCGCTGCGCCGCGCTTCGCTGATACCCCTCAGTGAAT 3660  
Qy 1221 G1yAspAspA1aAspAspG1uG1yAsnLeuSer1yG1yG1uAargVal1AargA1aTrp1le 1240  
Db 3661 GGGAGATGACCGCATGACAGGGGCAACCTGAGCAAAAGGGAGCGGATCCGCGGTGATC 3720  
Qy 1241 ArgA1aAargLeuProA1aCyTyTrLeuG1uAargAspSerTrpSerA1aTyTr1lePhePro 1260  
Db 3721 CGAGCCGACTCCCTGCTGCTGCTGAGCGAGACTCCCTGATCAGCTTACATCTTCCCT 3780  
Qy 1261 ProG1uSerAargPheAargLeuLeuCyH1eAarg1le1eThrH1e1yMetPheAspH1e 1280  
Db 3781 CTTCACTGTCAGATTCGCGCTCTGTGTCACCGGATCATCACCAAGATGTTGACACAC 3840  
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Qy 1301 AspProH1eSerA1aG1uAarg1lePheLeuThrLeuSerAsnTyTr1lePheThrA1aVal 1320  
Db 3901 GACCCCAKAGCGCTGACCGCATCTTCTGACCTTCCAAATTAACATCTTCAACGAGTGC 3960  
Qy 1321 PheLeuA1aG1uMetThrVal1yVal1A1aLeuG1yTyTrCySPheG1yG1uG1uA1a 1340  
Db 3961 TTTCTGTGTAATATGACATGAGAGTGTGTGCACTGGGCTGTGTGTGGGAGAGAGGCG 4020  
Qy 1341 TyTrLeuAargSerSerTrpAanVal1leuAspG1yLeuLeuVal1leu1leSerVal1leAsp 1360  
Db 4021 TACCTGTGGAGAGTGTGAACGTGCTGAGAGGAGCTGTGTGCTCATCTCCGATCGAC 4080  
Qy 1361 1leuLeuVal1SerMetVal1SerAspSerG1yTyTr1y1leuG1yMetLeuAargVal1leu 1380  
Db 4081 ATTCTGTGTGCATGTGCTTCTGACAGGCGGACCAAGATCTGTGGGATGCTGAGAGGTGCTG 4140

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Db	4141	CGGGCTGCGCGAGACCCCTGGCCCGCTCGAGGTGTATCAGCCGGGCGAGGGGCTGAACGCTG	4200
QY	1401	ValValaGluThrLeuMetSerSerLeuYsProIleGlyAsnIleValIleCysCys	1420
Db	4201	GTGGGGAGACGGCTGATCTCTCACTGAAACCCATCGCAACATTGATGTCATCTGCTGT	4260
QY	1421	AlaPhePheIleIlePheGlyIleLeuGlyValaGlnLeuPheYsGlyYsPhePheVal	1440
Db	4261	GCGTTCTTCATCATATTTTTCGGCATCTTGGGGGTGGAGCGCTTCAAGAGGAATTTTTCGTG	4320
QY	1441	CysGInGlyIuAspThrArgAsnIleThrAsnYsSerAspCysValaGluAlaSerTyr	1460
Db	4321	TGCCAGGCGCAGGATACACAGAACTACCACTAAATTCGACTGTGGCCGAGGCGAGTTAC	4380
QY	1461	ArgTrpValaArgHisblyTyrAsnPheAsnIleuGlyGlnAlaMetSerLeuPhe	1480
Db	4361	CGGTGGCTCGCGCAACATTAACCTTGACAACTTGCCAGGGCTGATGTCCCTGTTC	4440
QY	1481	ValIleuAlaSerYsAspGlyTyrValAspIleMetTyrAspGlyLeuAspAlaValaGly	1500
Db	4441	GTTTTGGGCTCCAGAGATGGTTGGGTGACATCATGTCATGGGCTGGATGCTGTGGCC	4500
QY	1501	ValAspGInGInProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
Db	4501	GTGGACCGACAGCCCATCATGAACACACACCCCTGATGCTGTACTTCATCTCGTTC	4560
QY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValaGlyValaValaGluAsnPhe	1540
Db	4561	CTGCTCATTTGGGCTCTTGTTCCTGAACAGTTTGTGGGTGTGGTGTGAGAACCTTC	4620
QY	1541	HisYsCysArgGlnHisGInGluGluValaIaArgArgArgGluGluYsArgLeu	1560
Db	4621	CACAACTGTCCGACGACACACAGAGGAAGAAGAGCCCGCGCGAGAGAAACGCGCTA	4680
QY	1561	ArgArgLeuGluYsYsArgArg-----	1568
Db	4681	CGAAGACTGAGAAAGAAAGAAAGAACTAATGCTGACGATGATTAATGCTTCCGCGACG	4740
QY	1569	-----LysAlaGInCysYsProTyrTyrSerAspTyrSerArgPhe	1582
Db	4741	TCAGCCAGCGCTGCGCTCAGAAAGCCACGAGCAACCTTACTGCTCGACTCTCCGCTTC	4800
QY	1583	ArgLeuLeuValHisHisIleLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal	1602
Db	4801	CGGCTCTCTGTCACCACTTGTGACACGACCACTTCTGACACTCTTTCATCAKAGGTCTC	4860
QY	1603	IleGlyLeuAsnValValThrMetAlaMetGlnHisTyrGInGInProGInIleLeuAsp	1622
Db	4861	ATCCGGGCTGAAGCTGTGCACCATGGCCATGGAGCACTACAGACGCCCAATTCGGAT	4920
QY	1623	GluAlaLeuYsIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe	1642
Db	4921	GAGGCTCTGAAGATCTGCACACTTCTTCACTGTCATCTTGTCTTGAGTCAAGTTTC	4980
QY	1643	LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu	1662
Db	4961	AAACTTGTGGCCTTTGTGTTCCGTGCTTTCAGAGCAGAGTGAACCACTGGACCTG	5040
QY	1663	AlaIleValLeuLeuSerIleMetGlyIleThrLeuGInGluIleGluValAsnAlaSer	1682
Db	5041	GCCATTGTGCTGTCTCATCATGTGGGATCAAGCTGAGGAATCGAGTCAAGCGCTCG	5100
QY	1683	LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu	1702
Db	5101	CTGCCCATCAACCCACCATCATCTCGCATCTCAAGGGGTGCTGCCCATTTGCCGAGTCTGTG	5160
QY	1703	LysLeuLeuYsMetAlaValaGluMetArgAlaLeuLeuAspThrValMetGlnAlaLeu	1722
Db	5161	AAAGCTGCTGAAGATGCTGTGGGACATGGGGGGGCTGCTGACACGGGTATCAAGAGCCCTG	5220
QY	1723	ProGInValaGlyAsnLeuGlyLeuLeuPheMetLeuPhePheIlePheAlaAlaLeu	1742

Db	5221	CCCCAGTGGGAACTGGGACTCTCTTCAGTGTGTGTTCATCTTTTCAGCTTCG	5280
Oy	1743	GlValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly	1762
Db	5281	GGGTGGAGCTCTTTGGAGAACTGGAGGTGTACGAGACACCCCTGTGAGGGCTGGG	5340
Oy	1763	ArgHisAlaThrPheArgAspPheGlyMetAlaPheLeuThrLeuPheIleuValSerThr	1782
Db	5341	CGTCAATGCCACTTCTCGAACTTTGGCAATGGCTTCCTTAAACCTCTTCCGAGTCCACA	5400
Oy	1783	GlyAspAsnThrAspGlyIleMetCysAspThrLeuAspCysAspGlnGluSerThr	1802
Db	5401	GGGACAAATTGGAAATGGCAATTATGAAAGACACCTTCGGGAGCTGTGACAGGAACTCAC	5460
Oy	1803	CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe	1822
Db	5461	TGCTTAAACAACGGTCACTCTCGCTTACTTACTTTGTCTCTTCGTGTGACGGCCACTTC	5520
Oy	1823	ValIleuValAsnValValIleAlaValLeuMetCysHisLeuGlnGluSerAsnGlu	1842
Db	5521	GTGCTAGTCAACGTGTGTATCGCCGTGCTGATGAAAGCACCTGGAGGAGACAAAGAG	5580
Oy	1843	AlaIleGluGluAlaGluLeuGlnAlaGluLeuGluLeuGluMetCysThrLeuSerPro	1862
Db	5581	GCCAAAGAGAGGCGCAGCTTAGAGCTGAGCTGAGAGTGAAGAACCTTAGCCCC	5640
Oy	1863	GluProHisSerProLeuGlySerProPheLeuTyrProGlyValGluGlyProAspSer	1882
Db	5641	CAGCCCACTCCGCACCTGGGACAGCCCTTCTCTGTGGCTGGGGGTGAGGGCCGACAGC	5700
Oy	1883	ProAspSerProIleAspProGlyValAlaLeuHisAspProAlaAlaHisAlaArgSerAlaSerHis	1902
Db	5701	CCGACAGAGCCCAAGGCTGGGGCTGTGACACCAAGCGGCCACGGGAGATCAGCTCCAC	5760
Oy	1903	PheSerLeuGlnHisAspThr-----	1909
Db	5761	TTTTCCCTGGAGACCCACGACAGGACGCTGTTGACACCATATCCCTGCTGATCCAG	5820
Oy	1909	-----	1909
Db	5821	GGCTCCCTGGAGTGGGAGCTGAAGCTGATGACAGAGCTGGAGGCCCAAGGGGCGACCCC	5880
Oy	1909	-----	1909
Db	5881	TCTGCTTCCCTTCTGCCCCAGCCTGGGAGGCTCCGACCAAGATCCCTAGCTGAG	5940
Oy	1909	-----	1909
Db	5941	ATGAGAGCTCTGTCTGTGACGTGAGAGATTGTGTCTGAACCGTCTGTCTAGCTCTG	6000
Oy	1909	-----	1909
Db	6001	ACGGAATGACTCTTGCCCTGATGACATGCACACACTCTTAATTAGTGGCCCTGGAGACAA	6060
Oy	1910	MetGlnProHisAspProHisGluLeuProGlyProAspLeuLeuThrValArgLysSerGly	1929
Db	6061	ATGAGGCCCAACCCCAACGAGAGCTGGCAGGACCAAGCTTAAGTACGTGTGGAGATCTGGG	6120
Oy	1930	ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla	1949
Db	6121	GTCAGAGCGAAACGACACTCTGCCCCAATGACAGCTTCAATGTCTGGCAGTGGAGACATCGCC	6180
Oy	1950	GluGlyProLeuGlnHisArgIleTyrPglIleuProLysAlaGlnSerGlySerValLeu	1969
Db	6181	GAGGGGCCCTGGGAGACAGGGGCTGGGGGCTCCCAAAAGCTCAAGTCAAGGCTCCGCTTGG	6240
Oy	1970	SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro	1989
Db	6241	TTCGTTTCACTCCCAAGCAGACAGATTACAGTACATCTGACAGCTTCCCAAAAGTCAACT	6300
Oy	1990	HisLeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProLysLeuProProPro	2009

Db	6301	CATCGCTCACGCCCCACAGCGCCCCCACTCGGGGACCATCCCAACTGCCCCACCA	6360
Qy	2010	GLYATGSRPTROLEUALAGlnaRgProleuaRgaGlnAlaAlaIleArghrAaPser	2029
Db	6361	GGACGCTCCCTTGTGCTCAGAGCCACTCAGGCGCCAGGACCAATTAAGACTGACTCC	6420
Qy	2030	LeuAPValIGlnGlyLeuGlySerArGlnuAPLeuAlaGlnValSerGlyProSer	2049
Db	6421	TTGGACGTTCAAGGCTCTGGGACGCGGGAAGACCTGCTGCAAGAGTGTGTGGCCCTCC	6480
Qy	2050	ProPProleuAlaArGAlaTySerPheTpgLYGlnSerSerThrglnAlaGlnGlnHis	2069
Db	6481	CCGCCCTCGCCCCGGGCTACTCTTCTTGGGGCACTCAAGTACCAGGACAGCAGCAC	6540
Qy	2070	SerArGSerHisSerLYaIleSerLYHisMeThrProProAlaProCyPProGlyPro	2089
Db	6541	TCCGCGACGACAGCAAGATCTCCAAGCACTAAGACCCCGCAGCCCTTGTCCAGGCCCA	6600
Qy	2090	GLUPROAERTPGLYLYagLYProProGluThrArGSerSerLeuGluLeuAPThrgln	2109
Db	6601	GAAACCAACTGGGGGCAAGGCGCCTCCAGAGACCAAGACAGCTTAAAGTTGACACGAG	6660
Qy	2110	LeuSerTPPIleSerGlyYASpLeuLeuProProGlyGlyGlnGlnGluProProSerPro	2129
Db	6661	CTGACCTGATTTTCAGAGACCTCTCTGCCCCCTCGGGGCGCAGAGAGAGCCCATCCCA	6720
Qy	2130	ArgAPLeuLYaLYeCyArTYSerValGlnAlaGlnSerCYeGlnaRgaRgProThrSer	2149
Db	6721	CGGAGCCTGAAGAAGTCAACAGCGTGAAGGCCCAAGCTGCCAGCGCGGCTTAGCTCC	6780
Qy	2150	TrpLeuAPGluGlnaRgaRHisSerIleAlaValSerCYeLeuAPSPSerGlySerGln	2169
Db	6781	TGCGCTGATGAGCAGAGAGACACTCTATCGCGCTGACGCTGACGCGGCTCCCA	6840
Qy	2170	ProHISLeuGlyThrAPSPSerSerLeuGlyGlyGlnProleuGlyGlyProGlySer	2189
Db	6841	CCCCACCTGGGACAGACCCCTCTAACTTGGGGGCGAGCCTTTGGGGGCGCTGGGAGC	6900
Qy	2190	ArgProLYaLYeLeuSerProProSerIleThrIleAPProProGluSerGlnGly	2209
Db	6901	CGGCCCAAGAAAACCTCAGCCCGCTAGTATACCATAGACCCCCCGAGACCAAGT	6960
Qy	2210	ProArghrProProSerProGlyIleCYeLeuArGaRgaAlaProSerSerAPSPSer	2229
Db	6961	CCTCGGACCCCGCCGAGCCTGTATCTCTCCGAGGAGGGGCTCGTCCAGGACTCC	7020
Qy	2230	LYaAPProLeuAlaSerGlyProProAPSPSerMetAlaAlaSerProSerProLYaLYs	2249
Db	7021	AAGGATCCCTTGCGCTTGACCCCTCGACAGATGAGCTGCGCTCGCCCTCCCAAGAAA	7080
Qy	2250	APValIleuSerLeuSerGlyLeuSerSerAPProAlaAPLeuAPPro	2266
Db	7081	GATGCGTGAAGTCTCTCCGCTTATCTCTGACCCAGCAGACCTGAGCCCC	7131
RESULT 2			
US-10-757-262-15			
Sequence 15, Application US/10757262			
Publication No. US20040197825A1			
GENERAL INFORMATION:			
APPLICANT: Karicheti, Venkateswarlu			
APPLICANT: Eliabof, Scott D.			
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING			
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,			
TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,			
TITLE OF INVENTION: 33751, 52872, 14063, 20739, 35544, 43239, 44373, 51164,			
TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,			
TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,			
TITLE OF INVENTION: 32720, 4809, 15403, 16616, 17827, 32620, 577, 619, 1423,			
TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,			
TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR			
FILE REFERENCE: MP103-007PIRNONMIM			

	CURRENT APPLICATION NUMBER:	US-10/757,262
/	CURRENT FILING DATE:	2004-01-14
/	PRIOR APPLICATION NUMBER:	US 60/440,318
/	PRIOR FILING DATE:	2003-01-15
/	PRIOR APPLICATION NUMBER:	US 60/444,783
/	PRIOR FILING DATE:	2003-02-04
/	PRIOR APPLICATION NUMBER:	US 60/457,901
/	PRIOR FILING DATE:	2003-03-27
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/	PRIOR APPLICATION NUMBER:	US 60/471,614
/	PRIOR FILING DATE:	2003-05-19
/	PRIOR APPLICATION NUMBER:	US 60/478,742
/	PRIOR FILING DATE:	2003-06-16
/	PRIOR APPLICATION NUMBER:	US 60/488,529
/	PRIOR FILING DATE:	2003-07-18
/	PRIOR APPLICATION NUMBER:	US 60/491,156
/	PRIOR FILING DATE:	2003-07-30
/	PRIOR APPLICATION NUMBER:	US 60/499,594
/	PRIOR FILING DATE:	2003-09-02
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/	PRIOR FILING DATE:	2003-09-26
/	NUMBER OF SEQ ID NOS:	136
/	SOFTWARE:	FastSeq for Windows Version 4.0
/	SEQ ID NO:	15
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/	TYPE:	DNA
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/	NAME/KEY:	CDS
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Percent Similarity:	95.29%	Conservative: 1
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QY	41 ProGlySerAlaAspSerGlnAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
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QY	61 PhePheTyrlieuserglinspserrargproarsetrrpcyleuargThValCyasn	80
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Db	241 CCTGCTTTGAGGCATCGCATGTTGTGCATCTTCTCAACTGGGTACCTGGGACATG	300
QY	101 PheArgProCysegluAspIleAlaCyAspSerGlnArgCyAsrgIleleuglnAlaPhe	120
Db	301 TTCGGCGCATCGACGACATCGCTGTGACTCCGACGCCTCGCGGATCTTCAAGCCCTT	360
QY	121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
Db	361 GATGACTTCATCTTTGCTTTTCCCGGAGATGATGTGTGAAGATGTGTGGCTTGCGC	420
QY	141 IlePhgGlyValylselyertryrleuGlyAspThrTPpaAnaGlyLeuAspPhePheIleVal	160



Db 421 ATCTTTGGGAAAAAGTTACTGTGGAGACATTGGACCGGCTTGACTTTTCATCTGTC 480  
QY 161 ILEALIGLYMELUENGLUTYRSERLEUAPLEUGLNASNVALSERPHESESERALAVALARG 180  
Db 481 ATCGCAGGAGATGCTGAGTAAGTCTGTCGACCTGCACAAACGTCAAGCTTCTCAGCTGCAG 540  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 541 ACAGTCCGTGTGCTGGACCGCTCAGGGCCATTACCGGGTCCCGACGATGCGCATCTT 600  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGIYASNVALleuLeuLeuCysPhePhe 220  
Db 601 GTCACTGTGCTGTGATAGCTGCGCCATGCTGGCAAGCTCTGCTGCTCTGCTCTTCTTC 660  
QY 221 ValPhePheIlePheIleYIleValIGLYValIGLInLeuThrAlaGIYleuLeuArgAsnArg 240  
Db 661 GTCCTTTTCATCTTCGACATCGTGGCGTCCAGCTGTGGCAGGGTGTGCTTGGAAACCA 720  
QY 241 CysPheLeuProGIuAsnPheSerLeuProLeuSerValAspLeuGIuArgTYRTRYGIN 260  
Db 721 TGCTTCTTACTGAGAAATTTCAAGCTTCCCTGAGCTGACCTGGAGCGCTATTACAG 780  
QY 261 ThrGIuAsnGIuAspGIuSerProPheIleCysSerGIuProArgGIuAsnGIYMetArg 280  
Db 781 ACAGAGAACGAGGATGAGAGCCCTTCATCTGCTCCAGCAAGCGAGAACGGCATGCGG 840  
QY 281 SerCysArgSerValProThrLeuArgGIYAspGIYGIYGIYProProCysGIYleu 300  
Db 841 TCTGTGAGAAAGCTGTGCCAGCTGCGGGGAGCGGGGCGGTGGCCACCTTGGCGGTG 900  
QY 301 AspTYRGIuAlaTYRAsnSerSerAsnThrThrCysValAsnThrAsnGIYTRYR 320  
Db 901 GACTTAAGAGGCCCTTCAACAGCTCCACCAACACCACTGTGTCAACTGGAACAGTACTAC 960  
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QY 341 GIYTRYRAlaITRPIleAlaIlePheGIuValIleThrLeuGIuGIYTRYRAlaAspIleMet 360  
Db 1021 GGCTATGCTCGATGCCCATCTTCCAGGTATCATCAGTGAAGGGCTGTGGCATCATCAG 1080  
QY 361 TYRPhenAlaMetAspAlaHisSerPheTYRAsnPheIleTYRPhelIleLeuLeuIleIle 380  
Db 1081 TACTTTGTGATGATGATCTCATCTCTTCAACATTTTCATCTACTTCTCTCTCATCATC 1140  
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Db 1141 GTGGGCTCCTCTTTCATGATCAACCTGTGCTGTGTGATGTCACGCAAGTTCTCAGAG 1200  
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Db 1201 ACCAACACAGCGGAGAAAGCCAGCTGATGCGGAGACACCGTGTGGTTCCTGTCAACGCGC 1260  
QY 421 SerThrLeuAlaSerPheSerGIuProGIYSerCysTYRGIuGIuLeuLeuIleTYRleu 440  
Db 1261 AGCAACCTGCTGACTTCTCTGTAGCCCGGCAAGCTGTATGAGAGAGTCTCTCAAGTACTG 1320  
QY 441 ValTYRTrIleuArgIuAlaAlaArgArgLeuAlaGIuValSerArgAlaAlaGIYVal 460  
Db 1321 GTGTATCATCTCTGTAAAGGAGCCGCCAGGCTGAGGTCTCTGCGGACAGCAGGTGTG 1380  
QY 461 ArgValAlaIleuLeuSerSerProAlaProLeuGIYGIYGIuGIuThrGIuProSerSer 480  
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Db 1501 CATCAACCAACCACTGAGCAATGGGACGCTCAGGGGCCCGCCGAGCGAGCCGAG 1560

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QY 541 AlaLeuSerGIYAlaProProGIYGIYValaIleuSerValHisSerPheTYRHisAlaAsp 560  
Db 1621 GCCCTCTCCGGGGGCCCTCTGTGTGGCAGAGTGTGTGACAGGCTTCTTACCATGCGCAC 1680  
QY 561 CysHisIleuGIuProValArgCysGIuAlaProProProAlaArgSerProSerGIuAlaSer 580  
Db 1681 TGCCATTAGAGCCAGTCCGCTGCGCAGGCGGCCCTCCAGAGTCCCATCTGAGGCAATCC 1740  
QY 581 GIYArgThrValIGLYSerGIYLYSerValTYRProThrValHisThrSerProProGIu 600  
Db 1741 GCGAGAGCTGTGGGAGCGGGAGAGTGTATCCACCGTGCACACCAAGCCTTCCACCGAG 1800  
QY 601 ThrLeuIYSGIuIYAsIleuValIGIuValAlaAlaSerSerGIYProProThrLeuThr 620  
Db 1801 AGCTGAAGAGAAAGCACTAGTAGAGGTGGCTGCAGCTCTGGGCCCCCAACCTTCAAC 1860  
QY 621 SerLeuAsnIleProProGIYProTYRSerSerMetHisIYIleuLeuGIuThrGIuSer 640  
Db 1861 AGCTTCAACATCCACCCGGGCCCTTACAGCTTCCATGCACAAAGCTGTGGAGACAGAGT 1920  
QY 641 ThrGIYAlaCysGIuSerSerCysIYsIleSerSerProCysIleuIYAsIleAspSerGIY 660  
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; Publication No. US20050191634A1  
; GENERAL INFORMATION:  
; APPLICANT: WANG, JIAN-YUAN  
; APPLICANT: LIN, SHIU-RU  
; TITLE OF INVENTION: GENES FOR DIAGNOSING COLORECTAL CANCER  
; FILE REFERENCE: BHT/3230-85  
; CURRENT APPLICATION NUMBER: US/10/786,148  
; CURRENT FILING DATE: 2004-02-26  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 120  
; LENGTH: 7825  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
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QY	1001	SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu	1020
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QY	1041	IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlu	1060
Db	3493	ATCCACACAGGCGCCACACCCATGTCGTGCCAAGACACACAGAGCGGCTGGGGAG	3552
QY	1061	AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla	1080
Db	3553	GCGCTGGGCGCTGCTCCGCGCGCACACGACAGCGGCTGGGAGAGCTCGGGCGGCGC	3612
QY	1081	HisGluMetLysSerProProSerAlaArgSerProHisSerProTrpSerAla	1100
Db	3613	CACGAGATGAAGTACCGCCCAAGCGCCCGCAGCTTCGCAACAGCCCTGGAGGCGCTGCA	3672
QY	1101	SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys	1120
Db	3673	AGCACTGAGCACAGCAGGCGCTCCAGCCGGAACAGCTCGGCCGTGACCCAGCTGAG	3732
QY	1121	ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnSerGln	1140
Db	3733	CGGAAMACCCAGAGTGAAGACCGCGGCTCCTGTGTGCGGAGGAAGCCAGAGAAGCGAG	3792
QY	1141	AspGluGluGluSerSerSerGluGluGluArgLysAspProAlaGlySerAspHisArgHis	1160
Db	3793	GATGAAGAGAGAGCTTCGAAGAAGAGCGGGCCACCTCGCGGCAATGACATCGCCAC	3852
QY	1161	ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
Db	3853	AGGGGGTCCCTGGAGCGGAGGCCAAGAAGTCTCTTGACCTGCCACACACTCAGAGTG	3912
QY	1181	ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn	1200
Db	3913	CCAGGGCTGCATCGCACTGCACATGGCCGAGAGGCTGCTTCTTGAGCACACAGACTGCAT	3972
QY	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
Db	3973	GGCAGTGGCTTCAGGGCGCTTGCGCCCGGGCCCTGCGGCTGATGACCCCCACTGGAT	4032
QY	1221	GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyLysValArgAlaTrpIle	1240
Db	4033	GGGAGTGAAGCCGATGACGAGGGCAACTGAGCAAAAGGGAAACGGGTCCGCGGTGGATC	4092
QY	1241	ArgAlaArgLeuProAlaCysTYrLeuGluArgAspSerTrpSerAlaTYrIlePhePro	1260
Db	4093	CGAGGCCACACTCCCTGCTGTGCTTCAGAGGAGCTCTGTGATCAGCTCAATCTTCCT	4152
QY	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280
Db	4153	CCTCAGTCAAGTTCGCTCTCTGTGTATCCGGATCATCACCCACAGATGTTGACCAAC	4212
QY	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300
Db	4213	GTTGGCTTTCATCATCATCTCTTAACTGCATCACCATCGCATGAGAGCGCCCAAAATT	4272

OY	1301	AspProHisSerAlaGluAlaGllIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal	1320
Db	4273	GAACCCCAACAGCGGTGAACGCATCTTCCGAGACCTTCCACATTACATCTTACCGGAGTC	4332
OY	1321	PheLeuAlaGluLeuCThrValIlyValValAlaLeuGlyYTrpCysPheGlyGluGlnAla	1340
Db	4333	TTTTCTGGCTGAATGACAGTGAAGTGGTGGCACTGGGGCTGGTGGCTTCCGGAGACAGGCG	4392
OY	1341	TyrLeuArgSerSerTyrPheAsnValLeuAspGlyLeuLeuValIleuIleSerValIleAsp	1360
Db	4393	TACCTGGCGAGACAGTTGGAACGTGTGTCGACGGGGCTGTGGTGTCTCATCTCCGTCAACGAC	4452
OY	1361	IleLeuValIleSerMetValIleSerAspSerGlyYThrIlySileuGlyIleuGlyIleuMetLeuArgValIleu	1380
Db	4453	ATTCTGGTGTCCATGTGCTCTGTGACAGGGGACCAAGATCTCTGGGACATGTGAGAGGGTGTG	4512
OY	1381	ArgLeuLeuArgThrThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuIlySleu	1400
Db	4513	CGGCTGGCTGGAGACCTGGCCCCGCTCAGGGTATACAGCCGGGCGACAGGGGCTGAAAGCTG	4572
OY	1401	ValValGluThrLeuMetSerSerLeuIlyProIleGlyAsnIleValValIleCysCys	1420
Db	4573	GTGGTGGAGAGCGGTAGTGTCTCTACGTGAACCCATCGGACAACATTGTGATCATCTGTGT	4632
OY	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheIlySglyIlySlyPhePheVal	1440
Db	4633	GCCCTTCTTCATCATTTTCGGCATCTTGGGGGTGACGCTTCTTCAAGAGGAATTTTCGTG	4692
OY	1441	CysGlnIlyGluAspThrArgAsnIleThrAsnIlySerAspCysAlaGluIleAspTyr	1460
Db	4693	TGCCAGGCGCAGATACCAAGAACATACCAAAATTAATCGAGCTGTGCGAGGCCAAGTTAC	4752
OY	1461	ArgTyrValAlaArgHisIlySlyTyrAsnPheAspAsnIleuGlyGlnAlaLeuMetSerLeuPhe	1480
Db	4753	CGGTGGGTCCGGCACAAGTACACTTTGACAACTTGGCCAGGCCCTGATGTCCCTGTTC	4812
OY	1481	ValLeuAlaSerIlyAspGlyYTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
Db	4813	GTTTTGGCTTCCAAAGATGGTGGGTGGACATGATACATGAGGGCTGATGTGTGTGGGC	4872
OY	1501	ValAspGlnGlnProIleMetAsnHisAsnProTyrMetLeuLeuTyrPheIleSerPhe	1520
Db	4873	GTGACACGACGCCATCATGAAACACACACCCTCGATGCTGCTGATCTTCACTCTGTTCC	4932
OY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540
Db	4933	CTGTCTCATTTGGGCTTCTTGTTCCTGAAACATGTTTGGTGGTGGGTGGTGGAGAACTTCC	4992
OY	1541	HisIlyCysArgGlnHisGlnGluGluGluAlaArgArgArgGluIlyIlyValGleu	1560
Db	4993	CACAAAGTGTGGCGACGCCACGAGAGAAAGAGAGGCCCGCGCGGAGAGAGAGCGCTTA	5052
OY	1561	ArgArgLeuGlnIlyIlySlySArgArg-----	1568
Db	5053	CGAAGACTGGAGAAAAAGAAAGAAATCTAATCTGGACGATGTAAATTGCTTCCGGCAGC	5112
OY	1569	-----LysAlaGlnCysIlyProTyrTyrSerAspTyrSerArgPhe	1582
Db	5113	TCAGCCAGCGCTGGGTGAGAAAGCCAGTGCMAACCTTACTACTCCAGTACTCCCGCTTC	5172
OY	1583	ArgLeuLeuValHisHisIleuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal	1602
Db	5173	CGGCTCTCGTCCACCACTGTGTGACACAGCACTAATCTGGACCTTTCATCACAGGATGTC	5232
OY	1603	IleGlyLeuAsnValValIThrMetAlaMetGlnHisTyrGlnIlnProGlnIleLeuAsp	1622
Db	5233	ATCCGGGTGGAACGTGTACACCAATAGCCATGTAGACACTACACAGAGGCCACGATTCGGAT	5292
OY	1623	GluAlaLeuIlySileCysAsnTyrIlePheThrValIlePheValIleuGluSerValPhe	1642
Db	5293	GAGGCTCTGAAGATCTGCACATCATCTTACACTGTCTCTTGTCTTGGAGTACAGTTTTC	5352
OY	1643	LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTyrTrpAsnGlnLeuAspLeu	1662

Db 5353 AAACCTGTGGCTTTGGTTCCTCGGTCTTCCAGACAGGTGAACCCAGCTGGACTG 5412  
Qy 1663 AAlIeValIleuSerIleMetGlyIleThrIeuGluIleGluValIleAlaIleSer 1682  
Db 5413 GCCATTGTGCTGTCTTCATCATGAGCATCAAGCTGAGAGAAATCGAGGTCAACGCTCG 5472  
Qy 1683 LeuProIleAnProThriIleIleArgIleMetArgValIleuArgIleValIleu 1702  
Db 5473 CTGCCCATCAACCCACCATCATCCGCATCATGAGGTGCTGCGCATTTGCCAGAGTCTG 5532  
Qy 1703 LysLeuLeuLysMetAlaValIleMetArgAlaLeuLeuAspThrValIleMetGluAlaLeu 1722  
Db 5533 AACCTGTGAAGATGTGCTGTGGGATCGCGGCTGTGTGACACAGGTGATGACAGGCTTG 5592  
Qy 1723 ProGluValIleValIleuLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaIleLeu 1742  
Db 5593 CCCAGGTGGAGAACCTGGGACTTCTTCAATGTGTGTGTTTTCATCTTTCAGACTCTG 5652  
Qy 1743 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762  
Db 5653 GGGGTGAGGCTCTTGGACAGCTGAGGTGACGAGACACACCCCTGTGAGGGCTGGG 5712  
Qy 1763 ArgHisAlaThrPheArgPheArgPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782  
Db 5713 CGTCATCCCACTTTCGGAACCTTGGCATGCGCTTCTTAACCTTCTCCAGATCTCCACA 5772  
Qy 1783 GlyAspAnThrPheAnGlyIleMetLysAspThrLeuArgAspCysAspGluLeuSerThr 1802  
Db 5773 GGTACAAATTTGAATGGCATTTATAGAGACACCTCCGGGACTGTGACAGAGTCCACC 5832  
Qy 1803 CysElyrAsnThrValIleSerProIleTyPheValSerPheValLeuThrAlaGluPhe 1822  
Db 5833 TGCTACAAACAGGTCATCTGCTCATCTGCTTGTGTCTTCGTGTCGACGGCCAGATTG 5892  
Qy 1823 ValIleuValIleuValIleValIleValIleuMetLysHisIleuGluGluSerAsnLysGlu 1842  
Db 5893 GTGCTAGTCAACGTGTGATGCGCGTGTGTGAAGACCTGGAGAGAGCAACAGAG 5952  
Qy 1843 AlaIysGluGluValIleGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro 1862  
Db 5953 GCCAAGAGAGGCGGAGCTAGAGCTGAGCTGAGCTGAGATGAAAGACCTTACGCC 6012  
Qy 1863 GluAnProIleSerProLeuGlySerProPheLeuThrProGlyValIleGlyProAspSer 1882  
Db 6013 CAGGCCCACTGCACTGGGACGCCCTTCTGCTGGCTGGGGTCAAGGGCCCCGACAGC 6072  
Qy 1883 ProAspSerProLysProGlyValIleuHisProAlaAlaHisAlaArgSerAlaSerHis 1902  
Db 6073 CCCGACAGCCCAAGCCTGGGGCTCTGCACCAGCGGCCCAAGGATCAGCTCCAC 6132  
Qy 1903 PheSerLeuGluHisProThr----- 1909  
Db 6133 TTTTCCCTGGAGCACCCACGACAGCAGCTGTTTGAACCAATATCTCTGATCCAG 6192  
Qy 1909 ----- 1909  
Db 6193 GGCTCCCTGAGTGGAGCTGAAGCTGATGACGAGCTGGAGGCCAGGGGCGACGCC 6252  
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Db 6253 TCTGCTTCCCTTGCAGCCCAAGCTGGGAGCTCCGACCAAGANTCCTTAGAGTGAG 6312  
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Db 6313 ATGAGAGCTCTGTCTCTGACGTCAAGATTTGTGTCTGAACCGTCTCTTAGCTTG 6372  
Qy 1909 ----- 1909  
Db 6373 ACGATGACTCTTTCCTGATGACATGACACACTTACTTAAGTCCCTGAGAGCAAT 6432  
Qy 1910 MetGluProHisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly 1929

Db 6433 ATGCAACCCCAACCCCAAGAGCTGCCAGGACCACTTACTGACTGTGCGAAGTCTGG 6492  
Qy 1930 ValSerArgThrHisSerLeuProAsnAspSerTyPheCysArgHisGlySerThrAla 1949  
Db 6493 GTCAAGCCAAACGACTCTGCGCCAATGACAGTCAATGTGTGCGATGGAGCACTGCG 6552  
Qy 1950 GluGlyProLeuGlyHisArgGlyTyPheGlyLeuProLysAlaGluSerGlySerValIleu 1969  
Db 6553 GAGGGGCCCCGTGGACACAGGGGCTGGGGCTCCCAAGAGCTCAGTCAAGCTCCGCTTG 6612  
Qy 1970 SerValHisSerGluProAlaAspThrSerTyIleLeuGluLeuProLysAspAlaPro 1989  
Db 6613 TCCGTTCACTCCACGACACAGATACCACTCATCTCTCAGGTTCCAAAGATGCACCT 6672  
Qy 1990 HisLeuLeuGluAnProHisSerAlaProThrTyPheIleThrIleProLysLeuProPro 2009  
Db 6673 CATCTGCTCCAGCCCAAGCGCCCAACCTGGGGACCATCCCAAACTGCCCCACCA 6732  
Qy 2010 GlyArgSerProLeuAlaGluArgProLeuArgArgGluAlaAlaIleArgThrAspSer 2029  
Db 6733 GAGCGCTCCCTTGTGCTCAGAGGCCACTCAGGCGCCAGGACCAATAGACTGACTCC 6792  
Qy 2030 LeuAspValGluGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer 2049  
Db 6793 TTGGAGCTTCAAGGCTCTGGGACCGGGAAGACTGCTGGACAGATGAGTGGGCCCTCC 6852  
Qy 2050 ProProLeuAlaArgAlaTyPheThrPheTyPheGluHisSerSerThrGluAlaGluHis 2069  
Db 6853 CCGCCCTGGCCCGGAGCTTACTCTTCTGGGGCAGTCAAGTACCCAGGACAGGACAC 6912  
Qy 2070 SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089  
Db 6913 TCCCGACGCCACAGCAAGATCTCAAGACATACCCCGACCCCTTGGCCAGGCCCA 6972  
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Db 6973 GAACCCAACTGGGGCAAGGGCCCTCCAGAGACCAAGAGAGCTTAGATTTGACAGGAG 7032  
Qy 2110 LeuSerThrIleSerGlyAspLeuLeuProProGlyGlyGluGluGluProProSerPro 2129  
Db 7033 CTGAGCTGATTTCAAGAGACTCTGCGCCCTGGGGCGGCGAGAGGAGGCCCATCCCA 7092  
Qy 2130 ArgAspLeuLysLysCysTyPheSerValIleAlaGluSerCysGluAnArgProThrSer 2149  
Db 7093 CGGACCTTGAAAGAGGCTACAGCTGAGGCGCCAGAGCTCCAGCGCGCCCTACGTC 7152  
Qy 2150 TrpLeuAspGluGluAnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlu 2169  
Db 7153 TGGCTGATAGAGAGAGAGACACTCATGCGGTCAAGCTGCTGACAGCGGCTCCCA 7212  
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Db 7213 CCCCACTGGGACACAGCCCTCTAACCTTGGGGGCGACGCTCTTGGGGGGCTGGGAGC 7272  
Qy 2190 ArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGluGly 2209  
Db 7273 CGGCCCAAGAAAAACACAGCCCGCTAGATACCACTAACCCCTCCGAGAGCAAGGT 7332  
Qy 2210 ProArgThrProProSerProGlyIleCysLeuArgArgArgAlaProSerSerAspSer 2229  
Db 7333 CTTGAGACCCCGCCAGCCTTGATGTGCTCCGAGAGAGGCTCCGTCAAGGACTCC 7392  
Qy 2230 LysAspProLeuAlaSerGlyProProAspSerMetAlaIleSerProSerProLysLys 2249  
Db 7293 AAGGATCCCTTGGCTGCTGCGCCCTGACAGATGCTCTCGCCCTCCCAAGAAAA 7452  
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RESULT 5  
US-10-062-674-2011  
; Sequence 2011, Application US/10062674

Publication No. US2004000559A1  
GENERAL INFORMATION:  
APPLICANT: Lotting, Jeanne F.; Kaser, Matthew R.  
TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS  
FILE REFERENCE: PA-0026-1 CIP  
CURRENT APPLICATION NUMBER: US/10/062,674  
CURRENT FILING DATE: 2002-01-30  
PRIOR APPLICATION NUMBER: US 09/625,102  
PRIOR FILING DATE: 2000-07-24  
NUMBER OF SEQ ID NOS: 2217  
SOFTWARE: PERL Program  
SEQ ID NO 2011  
LENGTH: 8116  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No. US2004000559A1 404183.1  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1) ... (8116)  
OTHER INFORMATION: a, t, c, g, or other  
US-10-062-674-2011  
  
Alignment Scores:  
Pred. No.: 0 Length: 8116  
Score: 11353.00 Matches: 2204  
Percent Similarity: 93.48% Conservative: 19  
Best Local Similarity: 92.68% Mismatches: 20  
Query Match: 95.37% Indels: 135  
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QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGlyLysAsp 40  
DB 473 CGGCTCAACGACCTGTCGGGGGCGGGGGCGGGCGGGGCTCAACAGAAAGGAC 532  
QY 41 ProGlySerAlaAspSerGlyAlaGlyLysProGlyProAlaLeuAlaProValVal 60  
DB 533 CCGGCGACCGCGGACCTCCAGGCGGAGGGCTCCGATCCCGCGCTGGCCCGGATGTT 592  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80  
DB 593 TTCTTCTACTTGAAGCCAGGACAGCCCGCGGAGCTGGTGTCTCCGACGGTCTGTAAC 652  
QY 81 ProTyrPheGluLysArgLysSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
DB 653 CCTGTGTTGAGGCGATCAGCATGTGTGTCATCTTCAACTGCGTAGACCTCGGCGATG 712  
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
DB 713 TTCGGGCATGCAAGACATCGCTGTGACTCCCAAGCGCTCGCGGATCTCGCAGGCTTT 772  
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValIlyMetValAlaLeuGly 140  
DB 773 GATGACTTTCATCTTTCGCTTCTTTCGCGTAGATGTGTGAAGATGTGTGGCTTGAGC 832  
QY 141 IlePheGlyLysArgCysTyrLeuGlyAspThrThrAsnArgLeuAsnPhePheIleVal 160  
DB 833 ATCTTTGGGAAAAAGTTAAGCTGGAGACACTTGGAAACCGGCTTACCTTTTCATCGTC 892  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
DB 893 ATGCGAGGATGCTGGAGTACTCGCTGGACCTCGAAGACGTCAAGCTTTCAGCTGTCAAG 952  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
DB 953 ACAAGTCGATGTGTGGACCGGTCAAGGCGCATTAACCGGGGTGCCAGCATGCGCATCTTT 1012

QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValIleLeuLeuCysPhePhe 220  
DB 1013 GTCAGGTGCTGCTGATACGCTGCTCAATGCTGGGCAAGTCTGCTGCTTCTTC 1072  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240  
DB 1073 GCTTCTTCATCTTGGGATCGTGGCGTCCAGCTGTGGGAGGGCTGCTCGAAGCGA 1132  
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
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QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGlyAsnGlyMetArg 280  
DB 1193 ACAAGAACAGAGATGAGAGCCCTTCACTTGTCTCCAGCCAGCGAAGACGCTGCGG 1252  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
DB 1253 TCTTCAGAGAGCTGCCACGCTGCGGGGAGCGGGGCGGTGGCCACCTTGCGGTCTG 1312  
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyr 320  
DB 1313 GACTATGAGGCTTACACAGCTCCAGCAACACCACTGTGTCACTGAAACGATATAC 1372  
QY 321 ThrAsnCysSerAlaGlyGlyLysAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340  
DB 1373 ACCAATGCTTCCGCGGGGAGACAAACCTTCAAGGCGCGCATCACTTGACAACTT 1432  
QY 341 GlyTyrAlaTyrIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360  
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DB 1493 TACTTGTGATGATGATGCTCATCTTCAATTCATCTTCAATTCATCTTCAATCTC 1552  
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
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QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420  
DB 1613 ACCAAGACGCGGAAAGCAGCTGATGGGAGGACGCGTGCCTGTCGCAAGCGCC 1672  
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440  
DB 1673 ACCACCTGCTGATGCTTCTGTAGGCCGCGCAGCTCTATGAGAGCTGCTCAAGTAC 1732  
QY 441 ValTyrIleLeuArgLysAlaIleArgArgLeuAlaGlnValSerArgAlaIleGlyVal 460  
DB 1733 GTGTATCTCTTCGTAAAGGACCCGCGAGCTGCTCAGGTCTTCGCGGACAGGTGTG 1792  
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480  
DB 1793 CGGATGGGCTGCTCAGACAGCCACACCCCTCGGGGCGCAGAGAACCCAGCCAGCAGC 1852  
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisIleHisIleHis 500  
DB 1853 AACTGCTCGCTCCACCGCGCTATCCGTCCACCACTGTGTNNNNNNNNNNNNNNNN 1912  
QY 501 HisIleHisIleTyrHisIleLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520  
DB 1913 NNNNNNNNNNNNTACCACTGGGCAATGGAGAGCTCAAGGCCCCCGGCGCAGCCGAGG 1972  
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540  
DB 1973 ATCCAGGACAGGAGTGCATATGGTCCCGCGGCTCATGCTCCACCAACCTCGACGCT 2032  
QY 541 AlaLeuSerGlyAlaProProGlyGlyValArgLysSerValHisSerPheTyrHisIleAsp 560  
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Db 4184 CGTGGTCCTTGTCATCATCTTCCTTAACGTGCATGCACCATGCCATGGAGGCCCCAAAT 4243  
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Db 4244 TGACCCCCACAGCGCTGAACGCGATCTTCCTGACCCCTCCAAATTACATCTTCACCCCAAT 4303  
QY 1320 lPheLeuAlaGluMetThrValLeuValAlaAlaLeuGlyTyrCysPheGlyGluGlnAl 1340  
Db 4304 CTTTCTGGCTGGAATATACAGTGAAGGTGGTGGCATCTGGGTGGCTTGGGGAGCAGGC 4363  
QY 1340 aTyrLeuArgSerSerTyrAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360  
Db 4364 GTACCTGGCGAGCAGTTGGACGTGCTGGACGGGGCTGTGGTCTCATCTCCGTCATCA 4423  
QY 1360 pIleLeuValSerMetValSerAspSerGlyThrIleValIleLeuGlyMetLeuArgValIe 1380  
Db 4424 CATTCGGGTGTCATGGTCTCTGACAGCGCACCAAGATCCTGGGATGCTGGGGTGTGT 4483  
QY 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuIleVal 1400  
Db 4484 GCGGCTGGCTGGACCCCTGGCCGCTCAGGGTATCAGCGGGCCAGGGGCTGAAGCT 4543  
QY 1400 uValValGluThrLeuMetSerSerLeuIleGlyAsnIleValValIleCysCy 1420  
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Db 4604 TGGCTTCTTCATCATATTTCGGCATCTTGGGGGTGAGCTCTTCMAAGGAAAGTTTTCGT 4663  
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Db 4664 GTGCCAGGGGAGAGATACAGAAATCACCANTAAATCGAGCTGGCCAGGCCAGTTA 4723  
QY 1460 rArgTyrValArgHisLeuTyrTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeu 1480  
Db 4724 CCGGTGGGTCCGGCACAGTAACTTTGACAACCTTGGCCAGGCCCTGATGTCCTGTT 4783  
QY 1480 eValLeuAlaSerIleAspGlyTyrTrpValAspIleMetTyrAspGlyLeuAspAlaVal 1500  
Db 4784 CGTTTGGCTCCAAAGATGTGGTGGTGAACATCATGTACGATGGGCTGGATCTGTGG 4843  
QY 1500 yValAspGlnGlnProIleMetAsnHisAsnProTyrMetLeuLeuTyrPheIleSerP 1520  
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Db 4904 CCGCTCATGTTGGCTTCTTGTCTGGAACATGTTGTGGGTGTGGTGGAGAACTT 4963  
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QY 1593 lAsTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValIleThrMetAlaMet 1613  
Db 5144 ACTAAGCTGACCTTTCATCACAGGTGTATCGGGCTGAACGTGGTACACATGGCCATGG 5203  
QY 1613 lHisTyrGlnGlnProGlnIleLeuAspGlnAlaLeuIleCysAsnTyrIlePhe 1633  
Db 5204 AGACACTACAGAGAGCCCGAATTTCTGAGTGAAGGCTTGAAGATCTGCACACTACATCTTCA 5263  
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Db 5264 CTGTCACTTGTGCTTGAAGTCAAGTTTCAAACTTGTGGCTTGTGTTCCGTCGGTTC 5323

QY 1653 heGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleT 1673  
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QY 1673 hTyrLeuGluGlnIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIle 1693  
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QY 1693 eArgValLeuArgIleAlaArgValLeuLeuLeuMetAlaValGlyMetArg 1713  
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Db 5624 ACGAGACACACCCCTGTAGGGGCTGGGCGCTCATGCCACCTTTCGAACTTGGCATGG 5683  
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QY 1997 AlaProThrTrpGlyTrpTrpIleProLysLeuProProGlyArgSerProLeuAlaGln 2016  
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QY 2235 rGlyProPro-AspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeu 2254  
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RESULT 6

US-09-383-894-1  
; Sequence 1, Application US/09383894  
; Publication No. US20030125269A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Ming  
; TITLE OF INVENTION: T-Type Calcium Channel  
; FILE REFERENCE: 004, 00191  
; CURRENT APPLICATION NUMBER: US/09/383, 894  
; CURRENT FILING DATE: 1999-08-26  
; EARLIER APPLICATION NUMBER: US 60/098, 004  
; EARLIER FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: US 60/117, 399  
; EARLIER FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 7129  
; TYPE: DNA  
; ORGANISM: Rattus sp.  
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Alignment Scores:  
Pred. No.: 0 Length: 7129  
Score: 1111.00 Matches: 2135  
Percent Similarity: 94.80% Conservative: 35  
Best Local Similarity: 93.27% Mismatches: 95  
Query Match: 93.34% Indels: 24  
DB: Gaps: 5  
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DB 61 CAGCTCAACGACCTGTTCGGGGGCGGGGCGGCGAGGGCGGGGTGACAGGAAAGAGC 120  
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProVal 60  
DB 121 CCGGAGCGCGGAGCTCCAGGCGGAGGGGCTCCGTAACCGGCGCTAGCCCGGTGTT 180  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80  
DB 181 TTCTTCACTTGAAGCCAGAGCAGCCCGCGGAGCTGTGTCTCCGACAGGTCTTAAC 240  
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
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DB 301 TTCAAGCGCGTGTAGAGACATTTGCTGTGACTCCAGAGGCTCGCGATCTCGAGGCTTC 360  
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValLysMetValAlaLeuGly 140  
DB 361 GATGACCTTCATCTTGTGCTTCTTGTGTAATGTGTGAAGATGGGCTTGCGC 420  
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160  
DB 421 ATCTTGGAGAAAGATGTACCTGGAGACACTTGGACACCGGCTTGACTTTTCATTGTCTC 480  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
DB 481 ATTGACAGAGATGCTGAGATTTGCTGGACTCGAGAACTGACGTTCTCCGACGTGAG 540  
QY 181 ThrValArgValLeuArgProLeuAlaIleAsnArgValProSerMetArgIleLeu 200  
DB 541 ACAGTCCGTGTGTGACACCGCTCAAGGCATTAAACCGGGTGGCCAGCATGCGCATTTCTC 600  
QY 201 ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220



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QY 481 SerCysSerArgSerHisArgArgLeuSerValHisIleValHisIleHisIleHis 500  
Db 1441 AGCTGACCTGCTCAACCTGCTGTGTCTGTCTCAACCACTGCTTCAACCACTCAAC 1500  
QY 501 HisHisIleHisIleTyrHisIleGlnGlyAsnGlyThrLeuArgAlaProArgAlaSerProGln 520  
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Db 1801 ATATCGAAGATTAAGCACTAGTGGAGGTGGCCCCCAAGCCCTGGGCCCCCACTCAC 1860  
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGlnThrGlnSer 640  
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QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerProCysLeuValAlaAspSerGly 660  
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QY 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839  
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Db 4261 TGCTGTGCTCTTCTTCACTTTTGGAAATTTCTGGGGTGCAGCTCTTCAAGGGAAGTTC 4320
QY 1439 PheValCysGlnIyGluAspThrArgAsnIleThrAsnIysSerAspCysAlaGluAla 1458
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Db 4321 TTGCTGTGTGAGGTGAGGACACAGGAACATCATCAAAATCCAGTGGCTGAGGCC 4380
QY 1459 SerTyrArgTrpValArgHisIleIysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
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Db 4381 AGCTACGATGGGTCCGCGACAAAGTCAACTTGAACAACCTGGGCGAGGCTGAGTGTCC 4440
QY 1479 LeuPheValLeuAlaSerIysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498
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Db 4441 CTGTTGTGTGCTGCTCCAGAGATGGTGGTTGATCATCATGATATGATGGCTGATGCT 4500
QY 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
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Db 4501 GTGGGTGTGATACAGACAGCCCATGATGAACCAACCCCTGATGCTGATTAATCTCATC 4560
QY 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValIleGlu 1538
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Db 4561 TCTTCTCTCTCATCTGTGGCTTCTTGTCTCTGAACATGTTTGTGGCGGTGTGGAG 4620
QY 1539 AsnPheHisIysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluIys 1558
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QY 1559 ArgLeuArgArgLeuGluIysIysArgArg----- 1568
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Db 4681 CCACTACGAGGCTGTGAGAAAGAGAGAGATCTAATGTGACGATGTAATTTGCTTCC 4740
QY 1569 -----LysAlaGlnCysIysProTyrTyrSerAspTyrSer 1580
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Db 4741 GGCAGCTCAACCAAGCGCTGCGTCAGAAAGCCCACTGCAAGCCCTCACTGACTGCTCG 4800
QY 1581 ArgPheArgLeuLeuValHisHisIleLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1600
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Db 4801 AGATTTCGGGCTCTTGTCCACCACTGTGTACCAAGCCACTACTGACCTTTCATCACT 4860
QY 1601 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1620
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Db 4861 GGTGTATCGGGCTGAGACGTGTGTCATCATGATGGAATTAACGAGCGCCAGATC 4920
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Db 4921 CTGACGAGGCTGTGAAGATCTGCAATTCATCTTTAACCTCACTCTTGTGTGAGTCA 4980
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Qy 1681 AAserLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1700  
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Qy 1701 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln 1720  
Db 5161 GTTCTGAAGCTGTTGAAGATGGCTGGGATCGGACCTGGACCTGGACACGGGATGACAG 5220  
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Qy 1998 ProThrTrpGlyThrIleProLysLeuProProGlyValArgSerProLeuAlaGlnArg 2017  
Db 6061 CCCACCTGGGGGCCATCCCTAAATACCCCACTGGCGCTGCCCTGTGCTCAGAGG 6120

Qy 2018 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2037  
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Qy 2058 PheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSer 2077  
Db 6241 TTCTGGGGCGGGTCAAGATCCAGGTGACAGAGCCCTTCCGCGATCCAGAGCAAAATCTCC 6300  
Qy 2078 LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro 2097  
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Qy 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117  
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Qy 2118 LeuProProGlyGlyGluGluGluProProSerProArgAspLeuLysCysTySer 2137  
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Qy 2138 ValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHis 2157  
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Qy 2178 AsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysValLysLeuSerPro 2197  
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Qy 2218 IleCysLeuArgArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyPro 2237  
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Qy 2238 ProAspSerMetAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeu 2257  
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Db 6838 TCTTTCGACCCAAACAGACATGAGACCC 6864

RESULT 7  
US-09-383-894-3  
; Sequence 3, Application US/09383894  
; Publication No. US20030125269A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Ming  
; TITLE OF INVENTION: T-Type Calcium Channel  
; FILE REFERENCE: 004,00191  
; CURRENT APPLICATION NUMBER: US/09/383,894  
; EARLIER FILING DATE: 1999-08-26  
; EARLIER APPLICATION NUMBER: US 60/098,004  
; EARLIER FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: US 60/117,399  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 3  
; LENGTH: 7285  
; TYPE: DNA  
; ORGANISM: Rattus sp.

US-09-383-894-3

## Alignment Scores:

Pred. No.:	0	Length:	7285
Score:	1111.00	Matches:	2135
Percent Similarity:	94.80%	Conservative:	35
Best Local Similarity:	93.27%	Mismatches:	95
Query Match:	93.34%	Indels:	24
DB:	10	Gaps:	5

US-09-611-257a-37 (1-2266) x US-09-383-894-3 (1-7285)

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QY      21 ArgLeuAsnAspLeuSerGlyAlaGlyAlaArgProGlyProGlySerAlaGlyLeuAsp 40
DB      217 CACCTTCAACCACTGTCCTGGGGCCGGGGCCGGCAGGGGGTCTGACGGAAAGAGAC 276

QY      41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProVal 60
DB      277 CCGGGCAGCCCGGACTCCAGCGGAGGGGCTGCCGTACCCGGGGCTAAGCCCGGTGCTT 336

QY      61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
DB      337 TTTCTTACTTGAACCGACAGCCGCCCGCGAGCTGTGTCTCCGACGGTCTGTMAC 396

QY      81 ProThrPheGluArgTyrIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
DB      397 CCGTGTGTCAGGAGACAGTATGCTGTGTCTTCAACTGTGTGACTCTGGGTATG 456

QY      101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
DB      457 TTCAGGCGCGTGTAGAGACATTGGCTGTGACTCCAGCGCTGCCGAGATCTGGAGCCTTC 516

QY      121 AspAspPheIlePheAlaPhePheAlaValGluMetValAllyMetValAlaLeuGly 140
DB      517 GATGACTTCATCTTTCCTTCTTGTGCTGTGAAATGTGTGAAAGTGTGGCTTGGCG 576

QY      141 IlePheGlyValValCysGlyTyrLeuGlyAspThrThrAsnArgLeuAspPheIleVal 160
DB      577 ATCTTGGGAAAGAAATGTACCTGGAGACATTGGAAACCGGCTTGTGACTTTTCATTGTC 636

QY      161 IleAlaGlyMetLeuGlnTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
DB      637 ATTGCGAGGAGATGCTCGAGATTCCTGCTGACTCGACGAACCTCAGCTTCGCGAGTACG 696

QY      181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
DB      697 ACAAGTCCGTGTGTCGACACCGCTCAGGGGCATTAAACGGGGTGCACACATGCGCATTC 756

QY      201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyValAsnValLeuLeuLeuCysPhePhe 220
DB      757 GTACACATTACTGTGACACCTTGCCTATGCTGGGCAACGCTCGTGTCTCTGTTTCTTC 816

QY      221 ValPhePheIlePheGlyIleValGlyValGlnLeuThrAlaGlyLeuLeuArgAsnArg 240
DB      817 GTCTTTTTCATCTTTGGCATCGTGGGCTCAGCTGTGGGCAAGCATGCTTCGAAACGA 876

QY      241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
DB      877 TGCTTCTCCCGGAGACTTCAGCCCTCCCTGAGCTGGACCTCGAGAGCTTATTATTCAG 936

QY      261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGlyAsnGlyMetArg 280
DB      937 ACAAGAGATAGAGAGAGAGCCCTTCAATGCTCTCAAGCTCGGAGAAATGGATAGAGA 996

QY      281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
DB      997 TCTCGAGAGAGTGTGCCACACTGCTGTGGGAAAGCGGTGTGGCCACCTCGTAGCTG 1056

QY      301 AspTyrGluAlaTyrAsnSerSerAsnThrCysValAsnThrPasnGlnTyrTyr 320
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DB      1057 GACTATGAGACTTATACAGTTCACAGAACACCACTGTGTCACTGAGAACAGTACTAT 1116

QY      321 ThrAsnCysSerAlaGlyGlyIleAsnProPheLeuGlyAlaIleAsnPheAspAsnIle 340
DB      1117 ACCAATGCTGTGTGGGGCGAGACCAACCCCTTCAAGAGCGCCATCAACTTGTGCAACATT 1176

QY      341 GlyTyrAlaThrIleAlaIlePheGlnValIleThrLeuGlyTyrThrValAspIleMet 360
DB      1177 GGCTATGCTGTGATCCCATCTTCCAGTTCATCACTGAGAGGCTGTGGTTCGACATCAATG 1236

QY      361 TyrPheValMetAspAlaIleSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
DB      1237 TACTTGTAAATGAGACGCTCACTCTTCTTCAACTTATCTACTTCTTCTTCACTATC 1296

QY      381 ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGln 400
DB      1297 GTGGGCTCTCTTTCATGATCAACCTGTGCTGTGTGTATGTCACAGGATTCCTCGAG 1356

QY      401 ThrLeuGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
DB      1357 ACCAAACAGCGGAGAGATCAGCTGATGCGGAGACCGGTACGATTCTGTCCAATGCT 1416

QY      421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuTyrLeu 440
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QY      461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
DB      1537 CCGGCTGGGCTGTCTGACAGCCAGTGGCCCGTATGAGGAGGAGAGGCCAGGCCAAGTGC 1596

QY      481 SerCysSerArgSerSerIleArgArgLeuSerValIleIleIleValIleIleIleIleIle 500
DB      1597 AGCTGACCTGTGACACCGTGTGTGTGTCTGTCTTACCACTGTATCCACCACTACACAC 1556

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DB      1657 CACCATCACACATCACACACCGGTATATGGAGCGCTCAGAGTTCCCGGGCCACCCAGAG 1716

QY      521 IleGlnAspArgAspAlaIleGlySerArgArgLeuMetLeuProProSerThrPro 540
DB      1717 ATCCAGAGACAGGAGATCCAAATGCTGTCCCGGCTCATGTACACACACCTCTTACACC 1776

QY      541 AlaLeuSerGlyValaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
DB      1777 ACTCCCTCTGGGGGCCCTCCGAGGGGTGGAGTCTGTACACAGCTTCTTACCATGTGTAC 1836

QY      561 CysHisIleGluGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
DB      1837 TGCCACTTGGAGGCAAGTCCCTTGCAGGCAACCCCTTCCAGAGGCCCATGAGGAGCATCT 1896

QY      581 GlyArgThrValGlySerGlyValTyrProThrValHisThrSerProProProGlu 600
DB      1897 GTTAGAGCTGTGGTGTGGGAAAGTGTACCCCACTGTGATACAGAGCCCTCCACACAGAG 1956

QY      601 ThrLeuLeuGlyValaIleuValIleuValAlaIleSerSerGlyProProThrLeuThr 620
DB      1957 ATACTAGAGATTAACACATAGTGGAGGTGGCCCAAGCCCTGTGGGCCCTCACCTTACC 2016

QY      621 SerLeuAsnIleProProGlyProTyrSerSerMetHisIleCysLeuLeuGluThrGlnSer 640
DB      2017 AGCTTCAACATCCCACTGGGCCCTTCAAGTCTCATCAACAAGCTCTCGAGACACAGAGT 2076

QY      641 ThrGlyAlaCysGlnSerSerCysIleIleSerSerProCysLeuValaAspSerGly 660
DB      2077 ACCGAGAGCTGCAATGCTCTGCAAAATCTCCAGCCCTTGTCCCAAGGAGACAGTGTGA 2136

QY      661 AlaCysGlyProAspSerCysProTyrCysValaArgAlaGlyAlaGlyValaGluLeu 680
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Qy 701 GlnHisSerASPleuArgASPProHisSer---ArgArgGluArgSerLeuGlyProASP 719  
Db 2257 CAGCAGACGTGACTCCGGGATCCCAACAGCCGGCCGACAGCGAGCTGGGCCCAAGT 2316  
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Db 3997 GACCATGTGTCTGTATCATCTTCTCAACTATACCATGCTATGAGAGGCCCC 4056  
Qy 1299 LyS1leASPProHisSerA1aGluArg1lePheLeuThrLeuSerASP1y1lePheThr 1318  
Db 4057 AAAATTTGACCCCAAGCGGTGAGGATCTTCCGACCCCTCTCCAACTACATCTTACAG 4116  
Qy 1319 A1aValPheLeuA1aGluMetThrValLySPVal1aA1aLeuGlyTrrCysPheGlyGlu 1338  
Db 4117 GCAGTCTTTCAGCTGAATGACGTGAAGGTGGGACGTGGGTGTGTGGGAG 4176  
Qy 1339 GlnA1aTyrLeuArgSerSerTrpASP1yLeuASP1yLeuLeuVal1leSerVal 1358  
Db 4177 CAGGCTTACTTCCGACAGAGCTGGAATGTGCTGACAGGCTTGTGTCTACTCCGTC 4236  
Qy 1359 1leASP1leuVal1SerMetValSerASPserGlyThrLyS1leLeuGlyMetLeuArg 1378  
Db 4237 ATCGACATCTGTGTCTCATGGTCTCCGACAGCGGACCAAGATCTTGGCATGCTGAGG 4296  
Qy 1379 Val1leuArgLeuArgThrleuArgProleuArgVal1leSerArgA1aGluGlyLeu 1398  
Db 4297 GTGTCGGGTGTGCGGACCTGTGCTCACTCAAGGTATCATGACGCGGAGCCCAAGGAGACTG 4356

Qy	1399	LyseLeuValValGluThrLeuMetSerSerLeuLeuProIleGlyAsnIleValValIle	1418
Db	4357	AAAGCTGGGTAGAGACTGATGATCATCCCTCAAAACCCATGGCAACATTTGGTCATT	4416
Qy	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheGlyLysPhe	1438
Db	4417	TGCTGTGCTCTTCTTCATCATTTTGGAAATCTCGGGGTGAGCTCTTCAAGGGAAGTTC	4476
Qy	1439	PheValCysGlnGlyGlnAspThrArgAsnIleThrAsnLysSerAspCysAlaGlnAla	1458
Db	4477	TTCTGTGTCAAGGTAGAGACACCAAGAACATCATTAACAATCCAGCTGGCTGAGGCC	4536
Qy	1459	SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478
Db	4537	AGCTACGATGGGTCCGGCACAAGTCAACTTGGACAACTGGGCGCAGCTCGATGTCC	4596
Qy	1479	LeuPheValLeuAspLysSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla	1498
Db	4597	CTGTGTGTCTGGCTTCCAAAGATGTTGGGTGACATCATGTATGATGGGCTGGATGCT	4656
Qy	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuTyrPheIle	1518
Db	4657	GTGGGTGTGATCAGACGCCCATCATTAACCAACCCCTGGATGCTGATATCTTATC	4716
Qy	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu	1538
Db	4717	TCCTTCCTCTCATCCGTGGCTTCTTTGTCTGCTGAACATGTTGTGGCGGTGGTGGAG	4776
Qy	1539	AsnPheHisLysCysArgGlnHisGlnGlnGlnGlnAlaArgAspArgGlnGlnLys	1558
Db	4777	AACCTTCATTAAGTGCACACACACACAGAGAGAGAGCGGCGGTGAGAGAG	4836
Qy	1559	ArgLeuArgArgLeuGlnLysLysArgArg	1568
Db	4837	CGACTACGAGGCTCGAGAAAGAAAGAAAGAAATTAATGTCAGATGTAATTGCTCC	4896
Qy	1569	-----LysAlaGlnCysLysProTyrTyrSerAspTyrSer	1580
Db	4897	GGCAGCTCAGCCAGCGCTGCCTGCAAGACCAGTGCAGGCCCTTACTCTGACTATCG	4956
Qy	1581	ArgPheArgLeuLeuValHisIleLeuCysThrSerHisTyrLeuAspLeuPheIleThr	1600
Db	4957	AGATTCGGGTCTCTTGTCCACCACTGTGTACCAAGCACTACGAGCTCTTCATCATCT	5016
Qy	1601	GlyValIleGlyLeuAsnValIleThrMetAlaMetGlnHisTyrGlnGlnProGlnIle	1620
Db	5017	GGTGTCTATCGGGCTGAACGTGTGATCATATGGCCATGGAACATTACCAAGCCCCAATC	5076
Qy	1621	LeuAspGlnAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGlnSer	1640
Db	5077	CTGGACAGAGCTCGAAGATCTGCATTACATCTTACCGTCATCTTGTGTTGATGTC	5136
Qy	1641	ValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeu	1660
Db	5137	GTTTCAAACTTGTGGCTTGTGGCTTCCGCGTTCCTCCAGGACAGGTGAACCACTG	5196
Qy	1661	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGlnIleGlyValAsn	1680
Db	5197	GACCTGCTATTGTGCTTCTGTCTCATATGGGCATCACTGAGAGAGATTGAGTCAAT	5256
Qy	1681	AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	1700
Db	5257	GCTTCGCTGCCATCAACCCACCATCATCCGTATCATAGGGGTGCTCCGATGTCTCG	5316
Qy	1701	ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln	1720
Db	5317	GTTCTGAAGCTGTTGAAGATGCTGTGGGCATGCGGCATGCTGGAACAGGTATGAC	5376
Qy	1721	AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla	1740
Db	5377	GCCCTGCCCAAGGTGGGAACTGGGACTTCTTTCATGTTATTTTTCATCTTTTGA	5436
Qy	1741	AlaLeuGlyValGluLeuPheGlyAspLeuGlnCysAspGlnThrHisProCysGlnGly	1760
Db	5437	GCTTCGGGCTGAGACTCTTTGGAGACTGAGTGAAGACACACCTTGTAGAGGC	5496
Qy	1761	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1780
Db	5497	TTGGGTGGGATGCCACTTTTAGAACTTTGGATAGGCTTTCTGTACCTCTTCCAGTTC	5556
Qy	1781	SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGln	1800
Db	5557	TCCACTGTGACAACTGGAATGATTAATGAAGAACACCTCCGGAGCTGTACAGAGAG	5616
Qy	1801	SerThrCysThrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla	1820
Db	5617	TCCACTGTGACAACTGATCATCTTCCCTTAATCTTTGTGTCTTCTGTGACAGGCC	5676
Qy	1821	GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlnGlnSerAsn	1840
Db	5677	CAGTTGTCTGTGTCACAGGTGTCATAGCTGTGTGATGATGAAGACCTGGAAAGAACAA	5736
Qy	1841	LysGlnAlaLysGlnGlnAlaGlnLeuGlnAlaGlnLeuGlnGlnLeuLysThrLeu	1860
Db	5737	AAAGAGCCAAAGAGAGAGCCGAGCTCAGAGCCGAGCTGAGCTGAGATGAAGAGCTTC	5796
Qy	1861	SerProGlnProHisSerProLeuGlnLysSerProPheLeuTrpProGlyValGlnGlyPro	1880
Db	5797	AGCCCGAGCCCACTCCCGCTGGGCAAGCCCTTCTTGGCCCGGGGTGAGAGGTTC	5856
Qy	1881	AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla	1900
Db	5857	AACAGTCTGACAGCCCTTAAGCTGGGGCTCCACACCACTGCCCCCATTTGAGAGACC	5916
Qy	1901	SerHisPheSerLeuGlnHisProThrMetGlnProHisProThrGlnLeuPro-----	1918
Db	5917	TCGGGCTTCTCCCTTGAAGACCCCAAGATGTATCCCAACCCCAAGAGGTGCCAGTCCC	5976
Qy	1919	---GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro	1937
Db	5977	CTAGAACCAAGCTGTGATGTGAAGAAAGTCTGGGTGACAGCCGACGACTTCTGCCC	6036
Qy	1938	AsnAspSerTyrMetCysArgHisGlySerThrAlaGlnGlyProLeuGlnHisArgGly	1957
Db	6037	AATGACAGCTACATGTGTCCGCAATGGAGACATGCTGAGAGATCCCTTAGGACACAGGGC	6096
Qy	1958	TyrGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAsp	1977
Db	6097	TGGGGGCTCCCAAAACCCAGTCAAGCTCATCTTGTCCGTCTACTCCCAACAGCAGAC	6156
Qy	1978	ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAla	1997
Db	6157	ACCAAGCTGATCTTACAGCTTCCCAAGATGTCACTATCTGCTCAAGCTCATGGGGCC	6216
Qy	1998	ProThrTrpGlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArg	2017
Db	6217	CCCACTGGGGGCCCATCTCCCTTAATCAACCCACCTGGCGGCTCCCTGTGCTCAGAGG	6276
Qy	2018	ProLeuArgArgGlnAlaAlaAlaIleArgThrAspSerLeuAspValGlnGlyLysSer	2037
Db	6277	CTCTCAGAGGCGCAGCAGCAATAGAGACTGACTCTCCGTGATGTGAGGGCTGGGTAGC	6336
Qy	2038	ArgGlnAspLeuLeuAlaGlnValSerGlyProSerProProLeuAlaArgAlaTyrSer	2057
Db	6337	CGGGAAGACTGTTGTACAGGTGAAGTGGGCTCTGCTGCTTGAACCGGTCTCATTC	6396
Qy	2058	PheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSer	2077
Db	6397	TTCTGGGGCGGGTTCAGACATCCAGGTGACAGACGTTCCGGCATCCAGAACAAAGTCC	6456
Qy	2078	LysHisMetThrProProAlaProCysArgProGlyProGlnProAsnTrpGlyLysGlyPro	2097
Db	6457	AAGCACATCCGCTGCGAGCCCTTGCACAGGCTGGAACCCAGCTGGGCGCAAGACCTT	6516
Qy	2098	ProGlnThrArgSerSerLeuGlnLeuAspThrGlnLeuSerTrpIleSerGlyAspLeu	2117

Db 6517 CCAGAGACCCAGAGACGTTAGAGCTGACACAGAGCTGAGTTCAGAGACCTC 6576  
QY 2118 LeuProProGlyGlyGlnGlnGluProProSerProArgAspLeuLysLysCysTyrSer 2137  
Db 6577 CTT---CCGAGAGACCCAGAGAACCCCTGTCCCAACCGGACCTGAGAAAGTGTACAGT 6633  
QY 2138 ValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHis 2157  
Db 6634 GTAGAGACCCAGAGACTGACAGGGCGGAGGCTGGGTCTGGCTAGATGAAACAGCGAGACAC 6693  
QY 2158 SerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSer 2177  
Db 6694 TCCATTGCTGTGAGGCTGTGTGAGCAGCGGCTCCCAACCCCGCTATGTCCAAGCCCTCA 6753  
QY 2178 AsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysAlaLysLeuSerPro 2197  
Db 6754 AACCTCGGGGGCCAACTCTTGGGGGTCTGGGAGCGGCGCTTAAGAAAACCTCAGCCCA 6813  
QY 2198 ProSerIleThrIleAspProProGlnSerGlnGlyProArgThrProProSerProGly 2217  
Db 6814 CCGAGTATCTCTATGACACCCCGAGAGCCAGGGCTCTCGGCCCAATGCAGTCTGTGT 6873  
QY 2218 IleCysLeuArgArgArgIleProSerSerAspSerLysAspProLeuAlaSerGlyPro 2237  
Db 6874 GTCTGCTCAGAGAGAGGGCGCGGCGAGTGACTTAAGGATCCCTCGGTCTCAGACCCC 6933  
QY 2238 ProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeu 2257  
Db 6934 CTTGACAGACGCGCTGCTCACCCTCCCAAGAAAGACACCGTGAAGTCTCTGTGTTTG 6993  
QY 2258 SerSerAspProAlaAspLeuAspPro 2266  
Db 6994 TCTTCTGACCCACAGACATGAGACCCC 7020

RESULT 8  
US-10-377-139-7  
; Sequence 7, Application US/10377139  
; Publication No. US20040175761A1  
; GENERAL INFORMATION:  
; APPLICANT: Mackinnon, Roderick  
; APPLICANT: Jiang, Youkang  
; APPLICANT: Lee Mackinnon, Alice  
; APPLICANT: Ruta, Vanessa  
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins  
; TITLE OF INVENTION: Uses thereof  
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9  
; CURRENT APPLICATION NUMBER: US/10/377,139  
; CURRENT FILING DATE: 2003-03-01  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 6942  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-377-139-7  
Alignment Scores:  
Pred. No.: 0 Length: 6942  
Score: 10945.00 Matches: 2107  
Percent Similarity: 93.99% Conservative: 34  
Best Local Similarity: 92.49% Mismatches: 101  
Query Match: 91.94% Indels: 36  
DB: 19 Gaps: 6  
US-09-611-257a-37 (1-2266) x US-10-377-139-7 (1-6942)

QY 1 MetAspGluGlnGluAspGlyAlaGlyAlaGlnGlnSerGlyGlnProArgSerPheMet 20  
Db 114 ATGGAGAGAGAGAGATGAGCGGGCGCCGAGAGATCGGAGACCCCTGACTTCACAG 173  
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp 40  
Db 174 CAGCTCAACGACTGTGCGGGGGCGGGGGCGGCGAGGGCGGGGATCGACGGAAGAGAC 233

QY 41 ProGlySerAlaAspSerGluAlaGlnGlyLeuProTyrProAlaLeuAlaProValVal 60  
Db 224 CCGGGAGCGGAGATCCGAGCGGAGGGGCTGCCGTACCCGGCCCTGAGCCCGGTGTT 293  
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80  
Db 224 TTTCTTCTATGAGCAGAGACAGCGCCGCGGAGCTGTGTCTCCGACGGTCTGTAAAC 353  
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100  
Db 354 CCGGTGTCGAGCGAGTACATGCTGTCAATTCCTTCAACTGTGTACCTGTGGGTATG 413  
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120  
Db 414 TTCAGGCGGTGAGAGACATTTGCTGTACCTCCAGCCCTGCCGATCTCAGAGCCCTTC 473  
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140  
Db 474 GATGACTTCATCTTTGCTTTGCTGTGGAAATGATGTGAAGATGTGGCTTGGGC 533  
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160  
Db 534 ATCTTGGGAAAGAAATGTTACCTGGAGACACTTGGAACCGGCTTGACTTTTCAATTGC 593  
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180  
Db 594 ATTTGAGGAGATGCTGAATATTCCTGACCTTGCAACATGCACTTCTCCGAGATCAGG 653  
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200  
Db 654 ACAATCCGATGCTGCGACCGGCTCAGGCGCATTTACCGGGATGCCAGATGGCATTCCTC 713  
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220  
Db 714 GTCACTTATCTGCTGAGACACTTGTGCTGAGGCAACGTCCTGCTCTCTGTTTCTTC 773  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240  
Db 774 GTCTTTTCATTTTGGCATGTGGGCGTCCAGCTGTGGGAGACATGCTTCGCAACCG 833  
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260  
Db 834 TGTCTTCTCCCGAGAACCTTCAAGCTCCCGTGAAGCTGAGCTGAGACCTTATTAACAG 893  
QY 261 ThrGluAsnGluAspGlnSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280  
Db 894 ACAGAGAAATGAGAGAGAGAGCCCTTCAATCTGCTCAGCCTCGGAGAAATGGCATGAGA 953  
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300  
Db 954 TCTTCGAGAGATGTGCCACACTGCTGGGAGAGCGGTGTGGCCACCTCGCAGTCTG 1013  
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrTyrCysValAsnTrpAsnGlnTyrTyr 320  
Db 1014 GACTATGAGACTTATTAACATTCAGCAACACCACTGTGTCACTGGAACCAAGATCATAT 1073  
QY 321 ThrAsnCysSerAlaGlyGlnHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340  
Db 1074 ACCAATGCTGTGCGGGGAGAGACAAACCTTCAAAAGGCGGCATCAACCTTGACAAACAT 1133  
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlnGlyTyrValAspIleMet 360  
Db 1134 GGCTATGCTGTGATGCAATCTTCCAGGTATCATCACTGAGAGGCTGGGTGCACATCATG 1193  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380  
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QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400  
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QY 401 ThrLysGlnArgGlnSerGlnLeuMetArgGlnGlnArgValArgPheLeuSerAsnAla 420  
 DB 1314 ACCAAACAGCGGGAGATGACGTGATGCGGGAGACAGGTGTACGATTCCTGTCCTCAATGCT 1373  
 QY 421 SerThrLeuAlaSerPheSerGlnProGlnGlnSerCysThrGlnGlnLeuLeuLeuLeuLeu 440  
 DB 1374 AGCACCTTGCAAGCTTCTCTGAGCCAGCGAGCTGTATGAGAGGACTCAATCAAGTACTG 1433  
 QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlnVal 460  
 DB 1434 GTGTACATCTCCGAAAGACGCCAGAGGCTGCGCAGGCTCTTAAAGGCTATAGGGGTG 1493  
 QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlnGlnGlnGlnGlnGlnGlnGlnGln 480  
 DB 1494 CGGGCTGGGCTGCTCAGACACCCAGTGGCCGTAAGTGGGAGAGGAGCCAGCCAGTGGC 1553  
 QY 481 SerCysSerArgSerSerAlaArgArgLeuSerValHisHisLeuValHisHisHisHis 500  
 DB 1554 AGCTGACCTGCTCAGACACCCGTCGTCTGTCTGTCCACCACTGGTCCACCACTACAC 1613  
 QY 501 His 520  
 DB 1614 CACCATCACCACTACCACTGGGTAATGGACCTCAGAGTTCCTCCGGGCGCACGCCAG 1673  
 QY 521 IleGlnAspArgAspAlaAsnGlnSerArgArgLeuMetLeuProProProSerThrPro 540  
 DB 1674 ATCCAGGACAGGAGTGCATAGGGTCTCGCGGCTCATGCTACCAACCACTCTACAC 1733  
 QY 541 AlaLeuSerGlnValProProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 560  
 DB 1734 ACTCCCTCTGGGGGCTCCGAGGGGCGGAGCTGTACACAGCTTCTACAGTGTGAC 1793  
 QY 561 CysHisLeuGlnProValArgCysGlnAlaProProProArgSerProSerGlnAlaSer 580  
 DB 1794 TGCACCTTGAGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1853  
 QY 581 GlnArgThrValGlnSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 600  
 DB 1854 GGTAGAGCTGTGGGTAGTGGGAAAGGTGTACCCCACTGTGATACCAAGCCCTCCAC 1913  
 QY 601 ThrLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 620  
 DB 1914 ATACTGAAGATTAAGACATAGTGAAGTGGGCGCCCGCCCTGGGCGCCCGCCCTTAC 1973  
 QY 621 SerLeuAsnIleProProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 640  
 DB 1974 AGCTTCAACATCCCACTGGGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCT 2033  
 QY 641 ThrGlnValArgGlnSerSerCysValIleSerSerProCysLeuValAlaAspSerGln 660  
 DB 2034 ACCGAGACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2093  
 QY 661 AlaCysGlnProAspSerCysProTyrCysAlaArgAlaGlnGlnGlnGlnGlnGlnGln 680  
 DB 2094 GCCGCGCGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2153  
 QY 681 AlaAspArgGlnMetProAspSerAspSerGlnAlaValTyrGlnPheThrGlnAspAla 700  
 DB 2154 GCTGACCATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2213  
 QY 701 GlnHisSerAspLeuArgAspProHisSer---ArgArgGlnArgSerLeuGlnProAsp 719  
 DB 2214 CAGACAGTGACCTCCGGGATCCCAACAGCGCGCGGAGAGCGAGCTGCGGCCAGAT 2273  
 QY 720 AlaGlnProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPheArgLysIle 739  
 DB 2274 GCAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2333  
 QY 740 ValAspSerLysTyrPheGlnArgGlnIleMetIleAlaIleLeuValAsnThrLeuSer 759  
 DB 2334 GTAAATGCAAAATCTTTGGCGGGGAAATCATGATCCGATCTGGGTCAATACACTGAC 2393  
 QY 760 MetGlnIleGlnTyrHisGlnGlnProGlnGlnLeuThrAsnAlaLeuGlnIleSerAsn 779

DB 2394 ATGGGCATGATGATCCACAGACAGCCCGAGAGCTTACCAAGCCCTGGAATACAGAAC 2453  
 QY 780 IleValPheThrSerLeuPheAlaLeuGlnMetLeuLeuValIleValIleValIleVal 799  
 DB 2454 ATGCTTTCACCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2513  
 QY 800 PheGlnTyrIleValAsnProTyrAsnIlePheAspGlnValIleValValIleSerVal 819  
 DB 2514 TTTGGCTACATTAAAGATCCCTAACACATCTTGATGGTGTATGATGATGATGATGAT 2573  
 QY 820 TrpGlnIleValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 839  
 DB 2574 TGGGAATTTGGCCAGACAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2633  
 QY 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859  
 DB 2634 CGGGTCTGAGAGCTGGTGGCTTCTGCGCGCCCTGACAGCCAGCTCGTGGTGTCTCAT 2693  
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 QY 980 GlnGlnLeuSerCysIleGlnLeuProValAspSerGlnGlnGlnValAspAlaAsnLysSer 999  
 DB 3027 -----GGAATGCCACCAAGTCT 3044  
 QY 1000 GlnSerGlnProAspPhePheSerProSerLeuAspGlnValAspArgLysLysCys 1019  
 DB 3045 GAGTCAAGAGCTGATTTTCTTTCGCCAGATGATGATGATGATGATGATGATGATGATGAT 3104  
 QY 1020 LeuAlaLeuValSerLeuGlnGlnIleAspProGlnLeuArgLysSerLeuLeuProLeu 1039  
 DB 3105 TTGGCCTGCTGCTTGGGAGAAACAGCGGAACTGGAAGAAGCTTTTGGCAACCCCTC 3164  
 QY 1040 IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlnLeuGln 1059  
 DB 3165 ATCATCATACGCTGCGACACCAATGTACACCCCAAGAGCTCCAGACAGGATGAGGG 3224  
 QY 1060 GlnAlaLeuGlnProAlaSerArgArgThrSerSerSerGlnLysSerIleGlnProGlnAla 1079  
 DB 3225 GAAGCACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3284  
 QY 1080 Ala---HisGlnMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098  
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 QY 1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlnValArgAlaProSer 1118  
 DB 3345 GCGGCAAGCAGCTGACACAGAGGAGGCTCCAGCAGAGAAACAGCTGCGGCGCGGCCAGC 3404  
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Db 3405 CTAAGCGAGAGAGCGCCGAGCGGAGGCTCCCTGCTGTCGAGAGGGCCAGAG 3464  
QY 1139 SerGIAspGluGluGluSerSerGIuGIuArgAlaSerProAlaGlySerAspHis 1158  
Db 3465 AGTCAGAGATGAGAGGAAAGTTTCAGAAAGAGACCGGCGCCAGCCAGCAGCTGATCCAT 3524  
QY 1159 ArgHisArgGlySerLeuGIuArgGIuAlaLysSerSerPheAspLeuProAspThrLeu 1178  
Db 3525 CGCCACAGGGGATTCCTTGACGTCGAGGCCAAGATTCCTTGACCTGCCCTGACATCTTCG 3584  
QY 1179 GlnValProGlyLeuHisArgThrAlaSerGIyArgGlySerAlaSerGIuHisGlnAsp 1198  
Db 3585 CAGGTCGCGGGGCTGCACCGCAGCAGCGGCGCGAGCTGCTGCTGAGCAGCAAGAC 3644  
QY 1199 CysAsnGlyLysSerAlaSerGIyArgLeuAlaArgAlaLeuArgProAspAspProPro 1218  
Db 3645 TGTAAATGGCAAGTCGCTTCAGGGCGTTGGCCCGCAGCTGAGACTATGACCCCA 3704  
QY 1219 LeuAspGlyAspAspAlaAspAspGIuGIyAsnLeuSerLysGlyGluArgValArgAla 1238  
Db 3705 CTGGATGGGGATGATACATGATGAGGAAATCTGAGCAAGGGAAAGCATACAGCC 3764  
QY 1239 TrpIleArgAlaArgLeuProAlaCysTyrlLeuGIuArgAspSerTrpSerAlaTyrlle 1258  
Db 3765 TGGGTCAGATCCCGGCTTCCTGCTGCTGCGCAGACGAGATTCTGTGTCCGGCTATATC 3824  
QY 1259 PheProProGluSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278  
Db 3825 TTTCCCTCCAGTCAGAGGTTTCGTCTCCGTGTCCACCGATCATCCACCAAGAGATT 3884  
QY 1279 AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGIuArgPro 1298  
Db 3885 GACCATGTGCTCTGCTCATCTCTCTCACTGATCATCACTCCCTATGAGCCGCC 3944  
QY 1299 LysIleAspProHisSerAlaGIuArgIlePheLeuThrLysSerAsnTyrllePheThr 1318  
Db 3945 AAATATGACCCCAAGCGGTGAGCCATCTCTGACCTTCAGCTTCACATCATCTTCAGC 4004  
QY 1319 AlaValPheLeuAlaGluMetThrValLysValAlaAlaLeuGIyTrpCysPheGlyGlu 1338  
Db 4005 GCAGTCTTCTACGCTAAATGACAGTGAAGGTGGTGGCACTGGGCTGTGGCTTGGGAG 4064  
QY 1339 GlnAlaTyrlLeuArgSerSerTrpAsnValLeuAspGIyLeuLeuValLeuIleSerVal 1358  
Db 4065 CAGGCTTACCTGCGACAGCTGGAATGTGCTGAGCGGCTGTGTGCTCATCTCCGTC 4124  
QY 1359 IleAspIleLeuValSerMetValSerAspSerGIyThrLysIleLeuGIyMetLeuArg 1378  
Db 4125 ATGCATATCTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCTTGGCATGTGAGG 4184  
QY 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398  
Db 4185 GTGCTCGGCTGTGGGACCCCTGCTCCACTCAGGGTCACTGCGGGCCCAAGGAACTG 4244  
QY 1399 LysLeuValValGIuThrLeuMetSerSerLeuLysProIleGIyAsnIleValIle 1418  
Db 4245 AAGCTGGTGGTAGAGCTCATGTATCTCCCTCAACCCATTGGCAACATTGGTGCATT 4304  
QY 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGIyValGlnLeuPheLysGIyLysPhe 1438  
Db 4305 TGTGTGCTCTTCTTCATCTTTTGGAAATCTCGGGGTGACGCTCTCAAGGAAAGTTTC 4364  
QY 1439 PheValCysGlnGlyGluLysPheThrArgAsnIleThrAsnLysSerAspCysAlaGluAla 1458  
Db 4365 TTCGTGTGTCAGGGTAGAGCACACAGAAATCATCAACAAATCCACATGCGGTGAGGC 4424  
QY 1459 SerTyArgTrpValArgHisLysTyrlAsnPheAspAsnLeuGIyGlnAlaLeuMetSer 1478  
Db 4425 AGCTTACCGATGGGTCCGGCACAAGTACAACTTTGACAACTGGGCGAGGCTCATGTCTC 4484  
QY 1479 LeuPheValLeuAlaSerLysAspGIyTrpValAspIleMetTyrlAspGIyLeuAspAla 1498  
Db 4485 CTGTGTGTGCTGCTCCCAAGATGGTTGGGTGATCATGTATGATGGGCTGATGCT 4544

QY 1499 ValGIyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuTyrlPheIle 1518  
Db 4545 GTGGGTGTGATCACAGCCCATCATGAAACCAACCCCTGGATCTCTATCTTCACTC 4604  
QY 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGIyValValGIu 1538  
Db 4605 TCTCTCTCTCATGTGTGGCTCTTGTGTCTGAAACATGTTTGTGGGTGGTGGAG 4664  
QY 1539 AsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgArgGIuGlyLys 1558  
Db 4665 AACTTCATTAAGTGCAGACAGCACAGAGAGGAGGAGCGAGCGCGCTGAGAGAG 4724  
QY 1559 ArgLeuArgArgLeuGluLysLysArgArg-----LysAlaGln 1571  
Db 4725 CGACTTACGAGGCTGTGAAGAAAGAGAGACTAAGAGAAAGACAGATGGCCGAACCCAG 4784  
QY 1572 CysLysProTyrlTyrlSerAspTyrlSerArgPheArgLeuLeuValHisIleLeuCysThr 1591  
Db 4785 TGCAGGCCCTTACTCTGACTCATCTGAGATTCCGGCTCTTGTCCACACACTGTATCC 4844  
QY 1592 SerHisTyrlLeuAspLeuPheIleThrGIyValIleGIyLeuAsnValValThrMetAla 1611  
Db 4845 AGCCACTACCTGAGCCTTCTCATCTGATGTCATCGGGCTGAAAGTGTCTCATGTGCC 4904  
QY 1612 MetGIuHisTyrlGlnGlnProGlnIleLeuAspGIuAlaLeuLysIleCysAsnTyrlle 1631  
Db 4905 ATGAAACATTACACAGCCCAAGATCTTGACAGAGCTTGAAAGATTCGACATTATCATC 4964  
QY 1631 PheThrValIlePheValLeuGIuSerValPheLysLeuValAlaPheGIyPheArgArg 1651  
Db 4965 TTTTACCGTCATCTTGTCTTTGAGTCAGTTTCAAACTTGTGGCTTGTGGCTCGCGCT 5024  
QY 1652 PhePheGlnAspArgTrpAsnGluLeuAspLeuAlaIleValLeuLeuSerIleMetGIy 1671  
Db 5025 TTTCTTCCAGACAGGTGAAACCAAGCTGAGCTGTGATGTGCTTGTCTGTCACTATGGC 5084  
QY 1672 IleThrLeuGIuGluIleGIyValAsnAlaSerLeuProIleAsnProThrIleIleArg 1691  
Db 5085 ATCACACTGGAAGAAATGAGTCAATCTGTGCTGCCATCAACCCCACTCATCTCCGT 5144  
QY 1692 IleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGIyMet 1711  
Db 5145 ATCATAGAGGGTCTCGCATCTCGAGTTCTGAAAGCTTGAAGATGGCTGGGCATG 5204  
QY 1712 ArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGIyAsnLeuGIyLeuLeu 1731  
Db 5205 CGGGCACTGCTGCACACGATGATGACAGGCCCTGCCAGGTGGGAAACCTGGGACTTCTC 5264  
QY 1731 PheMetLeuLeuPhePheIlePheAlaAlaLeuGIyValGIuLeuPheGIyAspLeuGIu 1751  
Db 5265 TTTCATGTTATGTTTTCATCTTTCACGCTCTGGGCGTGGAGCTTTTGGAGACTTGGAG 5324  
QY 1752 CysAspGIuThrHisProCysGlnGlyLeuGIyArgHisAlaIleThrPheArgAsnPheGIy 1771  
Db 5325 TGTGATGAGACACACCTTGTGAGGGCTTGGGTGGCATGCCACTTATAGAACTTGGT 5384  
QY 1772 MetAlaPheLeuThrLeuPheArgValIleThrArgIyAspAsnTrpAsnGIyLysMetLys 1791  
Db 5385 ATGGCTTCTGACCCCTCTTCGAGTCTCCACTGTGTCAACTGTGAAGTATGATTAAGAG 5444  
QY 1792 AspThrLeuArgAspCysAspGlnGluSerThrCysTyrlAsnThrValIleSerProIle 1811  
Db 5445 GACACCTCCCGGAGCTGTGACAGAGATCCACTCTCAACACATGTATCTCCCTATC 5504  
QY 1812 TyrPheValIleSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaVal 1831  
Db 5505 TACTTGTGTCTTGTGTGTGTCGAGCGCCAGTTGTGTGTCAAGCTGTGTATTACTGTG 5564  
QY 1832 LeuMetLysHisLeuGluGluSerAsnLysGIuAlaLysGluGluAlaGIuLeuGIuAla 1851  
Db 5565 CTGATGAAGCACCTTGAAAGAAAGCAAAAGAGGCCAAGAGAGGCGAGCTCGAGGCC 5624



Db 733 GATGACTTCATCTTTGCCCTTCTTTGGCGGTGAGATGTTGGTGAAGATGGCGCTTGAGG 792  
QY 141 ILePheGlyLysIleCysTyrIleuGlyAspThrTTPAsnArgIleuAspPhePheIleVal 160  
Db 793 ATCTTTGGGAAAAAGTTTACCTGGGAGACACTTGGAAACCGCGCTTCACTTTTTCATCGTC 852  
QY 161 ILeAlaGlyMetIleuGlyIleTyrSerIleuAspIleuGlnAsnValSerPheSerAlaValArg 180  
Db 853 ATGCAAGGAGTCTGGAGTACTGCTGGACCTGCAAGACGTCAGCTTCTCAAGCTGTCAAG 912  
QY 181 ThrValArgValIleuArgProIleuArgAlaIleAsnArgValProSerMetArgIleu 200  
Db 913 ACAGTCGGTGTGCTGGACCGCTCAAGGCGCATTAACCGGGTGCAGCATGGCGCATCTT 972  
QY 201 ValThrIleuIleuIleuAspThrIleuProMetIleuGlyAsnValIleuIleuIleuCysPhePhe 220  
Db 973 GTCAACCTGTGCTGGATACGCTGCCCATGCTGGGACAGCTCCTGCTGCTCTTCTTC 1032  
QY 221 ValPhePheIlePheGlyIleValGlyValGlnIleuThrAlaGlyIleuIleuArgAsnArg 240  
Db 1033 GTCTTCTTCACTTCGCACTGTCGGCGTCACGTCGTGGGACAGGCTGCTTCGAAACCA 1092  
QY 241 CysPheIleuProGlnAsnPheSerIleuProIleuSerValAspIleuGlnArgTyrTyrGln 260  
Db 1093 TGTCTTCTACCTGAGAAATTCAGCTCCCTCGAGGTGGACCTGAGGCGCTATTACAG 1152  
QY 261 ThrGlnAsnGlnAspGlnSerProPheIleCysSerGlnProArgGlnAsnGlyMetArg 280  
Db 1153 ACAGAAACACAGAGATAGAGAGCCCTTCATCTGCTCCAGCAACGCGAAGACGCAAGCGG 1212  
QY 281 SerCysArgSerValProThrIleuArgGlyAspGlyGlyGlyProProCysGlyIleu 300  
Db 1213 TCTTCGAAAGCGTGGCCACGCTGGCGGGGACGGGGCGGTGGCCACCTTGCGGCTTG 1272  
QY 301 AspTyrGlnAlaTyrAsnSerSerSerAsnThrThrCysValAsnThrAsnGlnTyrTyr 320  
Db 1273 GACTATGAGGCTACAAACAGCTCCAGAACACACACCTGTGTCAACTTGAAACGACTACTAC 1332  
QY 321 ThrAsnCysSerAlaGlyGlyIleAsnProPheIleGlyValAlaIleAsnPheAspAsnIle 340  
Db 1333 ACCAACGTGCTCAGCGGGGAGCAACACCCCTTCAGAGGCGCCATCAACTTTCACACATT 1392  
QY 341 GlyTyrAlaThrIleAlaIlePheGlnValIleThrIleuGlnGlyTyrValAspIleMet 360  
Db 1393 GGCCTATGCTGGATCGCCATCTTCCAGGTATCAACGCTGGAGGCGTGGGTCCACATCATG 1452  
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleIleuIleIle 380  
Db 1453 TACTTTGTATGGATGCTCATTCCTTCAATTCATCAATTCATCACTTCAATCCTCATCATC 1512  
QY 381 ValGlySerPhePheMetIleAsnIleuCysIleuValValIleAlaThrGlnPheSerGln 400  
Db 1513 GTGGGCTCCTTCTTCAATGATCAACCTGTGCTGTGTGATGCCACGCGATTCCTAGAG 1572  
QY 401 ThrIleGlnArgGlnSerGlnIleuMetArgGlnGlnArgValArgPheIleuSerAsnAla 420  
Db 1573 ACCAAGACAGGGAAAGCCAGCTGATGCGGAGACAGCGTGGCTTCCTGTCACACGCC 1632  
QY 421 SerThrIleuAlaSerPheSerGlnProGlySerCysTyrGlnGlnIleuIleuIleuIleu 440  
Db 1633 AGCAACCTGGCTGATCTTCTCTAGGCCCGGCAAGCTGTATAGAGAGCTGCTCAAGTACCTG 1692  
QY 441 ValTyrIleIleuArgIleuAlaAlaArgArgIleuAlaGlnValSerArgAlaAlaGlyVal 460  
Db 1693 GTGTACATCTTGTAAAGGACGCGCGAGGCTGCTCAGGTCTCTCGGGAGACAGGTGTG 1752  
QY 461 ArgValGlyIleuIleuSerSerProAlaProIleuGlyGlyGlnGlnThrGlnProSerSer 480  
Db 1753 CGGGTTGGGCTGCTCAGCAACCCACGACCCCTCGGGGGCCAGAGACCCAGCCACAGCAGC 1812  
QY 481 SerCysSerArgSerHisArgArgIleuSerValHisIleuValHisIleuValHisIleu 500  
Db 1813 AGCTGCTCTGCTCCACCGCGCGCTATCTGTCACACACTGTGTGACCAACCAACCAAC 1872

QY 501 HisIleHisIleTyrHisIleuGlyValAsnGlyThrIleuArgAlaProArgAlaSerProGln 520  
Db 1873 CATCAACCACTTACCACTTGCGCAATGGAGAGCTCAAGGCCCCCGGAGCCAGCCGAGAG 1932  
QY 521 ILeGlnAspArgAspAlaAsnGlySerArgArgIleuMetIleuProProPheSerThrPro 540  
Db 1933 ATCCAGACAGGGAATGCCATATGGTCCCGCGGCTCATGTGCGCACCAACCTCGAGGCT 1992  
QY 541 AlaIleuSerGlyAlaProProGlyGlyValAGlyIleuValHisSerPheTyrHisAlaAsp 560  
Db 1993 GCCCTTCGCGGGGCCCGCTGTGGTGGCCAGATGTGGCAACAGCTTCTTACCATCCAGC 2052  
QY 561 CysHisIleuGlnProValArgCysGlnAlaProProProArgSerProSerGlnAlaSer 580  
Db 2053 TGCACCTTAGACCAAGTCCGCTGCGAGGCGCCCTCCAGGTCCCATCTTAGGCAATCC 2112  
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGln 600  
Db 2113 GGCAGGACTGTGGCAGCGGGAAGGTGTATCCACCGTGCACACACAGCCCTCACCGGAG 2172  
QY 601 ThrIleuLysGlnLysAlaIleuValGluValAlaAlaSerSerGlyProProThrThrThr 620  
Db 2173 ACGCTGAAGAGAAAGCACTAGTAGAGGTGGCTGCAGCTCTGGGCGCCCAACCTCAAC 2232  
QY 621 SerIleuAsnIleProProGlyProThrSerSerMetHisLysIleuIleuGlnThrGlnSer 640  
Db 2233 ACCCTCAACATCCACCGGAGCTTACAGCTTCAATGCACACACACTCTGGAGACACAGACT 2292  
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysIleuLysAlaAspSerGly 660  
Db 2293 ACAGGTGCTGCGCAAGGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGACAGAGTGA 2352  
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyValGlyGlnIleu 680  
Db 2353 GCGTGTGTCAGACAGCTGCCCTTACGTGCGCGGGCGGGGCGAGGAGGTGAGCTC 2412  
QY 681 AlaAspArgGlnMetProAspSerAspSerGlnAlaValTyrGlnPheThrGlnAspAla 700  
Db 2413 GCCAACGTTGAATGCTGACTGACACAGACGAGGAGTTTATGAGTTCAACAGGATGCC 2472  
QY 701 GlnHisSerAspIleuArgAspProHisSerArgArgGlnArgSerIleuGlyProAspAla 720  
Db 2473 CAGCACAGGACCTCGGGAGCCCAACAGCGCGGCGCAACGGAAGCTGGCCCAATGCA 2532  
QY 721 GlnProSerSerValIleuAlaPheThrArgIleuIleCysAspThrPheArgIleVal 740  
Db 2533 GAGCCAGCTGTGTGCTGCTGTGAGGCTAATCTGTGACACCTTCGGAAGATTGTG 2592  
QY 741 AspSerIleTyrPheGlyValArgGlyIleMetIleAlaIleIleuValAsnThrIleuSerMet 760  
Db 2593 GACAGAGATACTTGTGGCCGGGAAATCATGATGCCATCTGTGACACACTCAGCATG 2652  
QY 761 GlyIleGlyTyrHisGlnGlnProGlnGlnIleuThrAsnAlaIleuGlnIleSerAsnIle 780  
Db 2653 GGCATGGAATTAACAAGAGAGCCGAGAGGCTTACCAACGCCCTAGAAATCAGCAACATC 2712  
QY 781 ValPheThrSerIleuPheAlaIleuGlnMetIleuLysIleuIleuValTyrGlyProPhe 800  
Db 2713 GTCTTCACAGGCTCTTGGCCCTGAGATGTGCTGGAAGCTGCTGTGTATGTCCCTTT 2772  
QY 801 GlyTyrIleLysAsnProThrAsnIlePheAspGlyValIleValValIleSerValTyr 820  
Db 2773 GGCATCATTAAGAAATCCCTTAACAATCTTCAATGGTGTCAATTTGTGTATCAGCTGTG 2832  
QY 821 GlnIleValGlyGlnGlnGlyGlyIleuSerValIleuArgThrPheArgIleuMetArg 840  
Db 2833 GAGATGTGGGCAACAAGGGGGGCGGCGTGTGTGTGCGGACCTTCGCGCTGATGCGT 2892  
QY 841 ValIleuLysIleuValArgPheIleuProAlaIleuGlnArgGlnIleuValIleuMetLys 860  
Db 2893 GTGCTGAAGCTGTGTGCTTCTGCGCGGCTGACGCGGCACTGTGTGTCTATGAAG 2952

QY	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer	880
DB	2953	ACCAATGGACCAACGTGGCCACCTTCCTGCATGTGCTTAAGCTTCATCTTCATCTTCAGC	3012
QY	881	IleLeuGlyMetCHisLeuPheGlyCysLeuPheAlaSerGlyValGlyAspGlyAspThrLeu	900
DB	3013	ATCTTGGGCATGCAATCTTCGTGGCTGCAGAGTTTGCTTCAGCGGGATGGGACACCTTG	3072
QY	901	ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	920
DB	3073	CCAGACCGGAAGAATTTGACTCCTTCGTGGGCATCGTCACTGCTTTCAGATCCTG	3132
QY	921	ThrGlnGluAspTrpAsnLysValLeuTyraGlnIleMetAlaSerThrSerSerTrpAla	940
DB	3133	ACCCAGGAGGACTGGACMAAGCTCTTACATGATGTAAAGGCTCCACCTCCTCGGAGC	3192
QY	941	AlaLeuTyrrPheIleAlaLeuMetThrPheGlyAsnTyraIleLeuPheAsnLeuVal	960
DB	3193	GCCCTTAATTCATTTGCCCTCATGACCTTCGGCAACTACGTGCTTTCATTTGCTGTC	3252
QY	961	AlaIleLeuValGluGlyPheGlnAlaGlnGluIleSerLysArgGluAspAlaSerGly	980
DB	3253	GCCATTTCTGGTGGAGGGCTTCAGCGGAG-----	3282
QY	981	GlnLeuSerCysIleGlnLeuProValAspSerGlnIleGlyAspAlaAsnLysSerGln	1000
DB	3283	-----GGAGATGTCCMAAGTCCGAA	3303
QY	1001	SerGlnProAspPhePheSerProSerLeuAspGlyAspArgLysLysCysLeu	1020
DB	3304	TCAGAGCCCGATTCTTCTTCACCCAGCTGGATGTGTATGGAGAACGMAAGTGGCTTG	3363
QY	1021	AlaLeuValSerLeuGlyGlnHisProGlnLeuAspArgLysSerLeuLeuProLeuIle	1040
DB	3364	GCTTGTGTCTCCCTGGAGAGACCCCGAGCTCGGAAGACCTCTCCCTCTCATC	3423
QY	1041	IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGln	1060
DB	3424	ATCCACACGGCGCCACACCCATGTGCTGCCCAAGACACACAGCAGCGGCTGGCGAG	3483
QY	1061	AlaLeuGlyProAlaSerArgArgThrSerSerGlySerAlaGlnProGlyAlaAla	1080
DB	3484	GCGCTGGGCGCTGCTCCGCGCGCACACAGACAGCGGATGGGAGACCTGGGGCGGCGC	3543
QY	1081	HisGlnMetLysSerProSerAlaArgSerSerProHisSerProTrpSerAlaAla	1100
DB	3544	CACGAGATGAACTCACCCGCCAGCCCGCAGCTTCCGCACAGCCCTGGAGGCGCTGCA	3603
QY	1101	SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyValArgAlaProSerLeuLys	1120
DB	3604	AGCAGCTGGACCAAGCAGGCGCTCCAGCCGAAACAGCTTCGCGCGTGCACCCAGCCTGAAAG	3663
QY	1121	ArgAlaGserProSerGlyGlnArgArgSerLeuLeuSerGlyGlnGlnSerGln	1140
DB	3664	CGGAAGAGCCCAAGTGAAGCGGCGGTCCCTGTGTGGGAGAAAGGCAAGAGGCGAG	3723
QY	1141	AspGlnGlnGlnSerSerGlnGlnGlnArgAlaSerProAlaGlySerAspHisArgHis	1160
DB	3724	CATGAAGAGAGAGCTCAGAGAGAGAGCGGCGCAGCTTCGCGGAGAGTGCATCGCAC	3783
QY	1161	ArgGlySerLeuGlnArgGlyAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
DB	3784	AGGGGAGTCCCTGGAGCGGGAGGCCAAAGATGTTCTTTGACCTGCGCAGACACTGCAAGGTG	3843
QY	1181	ProGlyLeuHisAlaArgThrAlaSerGlyValArgGlySerAlaSerGlyHisGlnAspCysAsn	1200
DB	3844	CCAGGCTGCATTCGACCTGCACAGTGCAGAGGCTGTGCTTCGACACACAGGACTGCAT	3903
QY	1201	GlyLysSerAlaSerGlyValArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
DB	3904	GGCAAGTCCGGCTTCAGAGGCGCTGGCGCGGCGCTTCGGCGCTGATGACCCGCCACTGGAT	3963
QY	1221	GlyAspAspAlaAspAspGlnGlyValAsnLeu	1230

[illegible]

QY 155 UnsphepHeIleValIleAlaGlyMetLeuGlyTyrSerLeuAspLeuGlnAsnValSe 175  
 Db 770 GGAATTTCTTCATCGTGTGGCGGGCATGATGAGTACTGTTGGAGGACACACACCTGTAG 829  
 QY 175 rPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValPr 195  
 Db 830 CCTCTGGGCTATACAGAACCGTGGGGTGTGGCCCCCTCCGGCCATCAACCGCGTGGC 889  
 QY 195 oSerMetArgIleLeuValThrLeuLeuAspThrLeuProMetLeuGlyAsnValIle 215  
 Db 890 TAGCATGCGGATCTCGGTCACTCTGCTGCTGATACGCTGCCATCTCTGGGAACTGCTCT 949  
 QY 215 UleuLeuCyPhePheValPhePheIlePheGlyIleValGlyValGlnLeuThrAlaI 235  
 Db 950 TCTGCTGTGCTTCTTGTCTTCTTCAATTTTGGCATCTGTGGCGTCCACTCTGGGCTGG 1009  
 QY 235 YleuLeuArgAsnArgCyPheLeuPProGlnAsnPheSerLeuProLeuSerValAsp-- 254  
 Db 1010 CTTCTGCGGAACCGCTGCTTCTTGAGACAGTGCCTTTGTACGAAACAAACACTGACCTT 1069  
 QY 255 -LeuGluArgTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCySerGlnPr 274  
 Db 1070 CTGCGGCGGTACTACACAGCGAGGAGGCGAGAAACCGTTCATCTGCTCTCACG 1129  
 QY 274 oArgGluAsnGlyMetArgSerCyAspArgSerValPro-----ThrLeuArgGlyAs 291  
 Db 1130 CCGAGCAACCGGATCGAGAGTGTCTGCACATCCCGGCGCGCGAGCTGGC----- 1184  
 QY 291 pGlyGlyGlyGlyProProCySerGlyLeuAspTyrGluAlaTyrAsn----- 306  
 Db 1185 -----ATGCCCTGCACCGCTGGGCTGGAGGCTTACACCGACCGGACGCCA 1231  
 QY 307 -----SerSerSerAsnThrThrCyValAsnTyrPasnGlnTyrTyrThrAsnCySe 324  
 Db 1232 GGGGGTGGGGCTGCACGCAACGCTGCATCACTGAAACAGTACTACAAACGTGTGCCG 1291  
 QY 324 rAlaGlyGluIleAsnProPheGlyValIleAsnPheAspAsnIleGlyTyrTrIaTr 344  
 Db 1292 CTCGGGTGACTCCAAACCCCAACGAGTGCATCACTTGCACAAACATCGGCTACCGCTG 1351  
 QY 344 pIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMe 364  
 Db 1352 GATTGCGATCTTCCAGGTGATCACTGAGAGGCTGGGTGACATCATGTACTACTCAT 1411  
 QY 364 tAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPh 384  
 Db 1412 GAGCGCCCACTCATCTCAACATTCATTAATTCATCTGCTCATCATCGTGGGCTCTT 1471  
 QY 384 ePheMetIleAsnLeuCyLeuValValIleAlaThrGlnPheSerGlnThrIleGlnAr 404  
 Db 1472 CTTCAATGATCAACTGTGTGCTGTGGTGTGATTCACGAGTTTCCGAGACGGAAGCAGG 1531  
 QY 404 gGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAl 424  
 Db 1532 GAGAGATCACTATCGCGGAGCAGCGGACCGCAACCTGTCCAAGACAGACGCGTGGC 1591  
 QY 424 aserPheSerGluProGlySerCyTyrGluGluLeuLeuGlyTyrLeuValTyrIleIe 444  
 Db 1592 CAGCTTCTCCGAGCCTGGCAGCTGTACGAAAGAGCTGTGAAGTACGTGGCGCAATATT 1651  
 QY 444 uArgGlyAlaIleArgArgLeuAlaGlnValSerArgAlaIleGlyValArgValIleGly 464  
 Db 1652 CCGCAAGGTCAACGGCGGCGAGCTTGGCTTACGCGCCGCTGGCAGACCGCGGCGCA 1711  
 QY 464 uLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSerSerCySerAr 484  
 Db 1712 GAAGGTGAGACCCAGTGTCTGTGAAGGCCAG-----GGTCCGGGACCGCCAGGCGCG 1765  
 QY 484 gSerHisArgArg---LeuSerValHisHisLeuVal---HisHisHisHisHisHis 502  
 Db 1766 GCGAGGACGACACACAGCCTCGGTGACCACTGTGTACTACCAACCATATCACACACCA 1825

QY 502 sHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGluIleG 522  
 Db 1826 CCACCACTACCACTTTTCAGCCATGAGCAGCCCCCGCAGGCCCGCCAGACGAGGCGCTG 1885  
 QY 522 nAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProPheSerThrProAlaIe 542  
 Db 1886 CGAC-----ACCAGGCTGTCCAGACTGAGCGGCGCCCCCTGCGCACCTTC 1930  
 QY 542 uSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAspCyHis 562  
 Db 1931 CCCAGCGCGGACCCCGCAGCAGAGTCTGTGCACAGCATCTACATGCCAGCTGGCA 1990  
 QY 562 sLeuGlu-----ProValArgCyGlnAlaProProProArgSerProSerGluAlaSe 580  
 Db 1991 CATAGAGGGGCGCGCAGAGAGGGGCGGGGTGGCAATGCCAGCACTGCCGTGCCAG 2050  
 QY 580 rGlyArg---ThrValGlySerGlyVal---TyrProThrVal----- 593  
 Db 2051 CTTCAAGGCTGGCCACAGGGGCTGGCAGCATATACCCACAGATCTGCTCAGGGGT 2110  
 QY 594 -----HisThrSerPro----- 599  
 Db 2111 GGGCAGCGGCAAGGACAGACCAAGCCCGGAAAGTGGCCGTGACCGCC 2170  
 QY 599 oGluThrLeuGlyGlyValLeuValGluValAlaIleAspSerGlyProProThrIe 619  
 Db 2171 AGGCAC-----GGGGGCGACGGCGCCTTGAGCTT 2200  
 QY 619 tThrSerLeuAsnIleProProGlyProTyrSerSerMetHisValLeuLeuGluThrGl 639  
 Db 2201 GAACAGC-----CTGATCTCCTACGAGAAGATCCCGCATGTGTGCGGGAGCA 2248  
 QY 639 nSerThrGlyAlaCyGlnSer-----SerCyValIleSerSe 652  
 Db 2249 TGAGCTGGGCGAGGCCCTGGCCATCTGTGGGCTCAGTGTGCTGCTGCCCTCCCGCAG 2308  
 QY 652 rProCySleuValAspSerGlyAlaCySerGlyProAspSerCyProTyrCyAlaIar 672  
 Db 2309 CCCC-----CGAGGGGCGACATGACTGTGAGCTGAAAGACTGCCCTACTGACCCG 2362  
 QY 672 gAla---GlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGl 691  
 Db 2363 TCCCTGAGAGACCCGAGGGGTGAGTCACTAGCGGCTCGGAAAGTGGAGACTCAGATGCGCG 2422  
 QY 691 uAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspPro----- 708  
 Db 2422 TGGCTCTATGAAATTACGACAGAGCTCCGACGCTGACCGCTGGAGCCCAACCGAC 2482  
 QY 709 -----HisSerArgGlnArgSe 715  
 Db 2483 ACCCGGTGGACGACACACACAGGCCCGCAGGCCCGCAGGCCCGCGGCGGACAGCA 2542  
 QY 715 rLeuGlyProAspAlaGluProSerSerValLeuAlaPheTyrPArgLeuIleCyAspThr 735  
 Db 2543 GAGGCGAGCCCGGCGAGCCAGGCTGATGGGCGCGCTCTGGGTATTACCTTCAGCGGCA 2602  
 QY 735 rPheArgArgIleValAspSerTyrPheGlyArgGlyIleMetIleAlaIleLeuVal 755  
 Db 2603 GCTGGCGGCATCTGGAGACAGAGTACTTCAAGCGGTGACATCAATGAGCCATCTTGT 2662  
 QY 755 lAsnThrLeuSerMetGlyIleGlyTyrHisGluGlnProGluGluLeuThrAsnAlaIe 775  
 Db 2663 CAACACGCTGACGATGGGGTGTGATCATATGACAGCCCGAGAGCTGATCAATAGTCTT 2722  
 QY 775 uGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuValLeu 795  
 Db 2723 GGAAGTACAGCAATCGTGTTCACACAGATGTTTCCCTGGAGATGCTGTAACCTGCT 2782  
 QY 795 uValTyrGlyProPheGlyTyrIleValAsnProTyrAsnIlePheAspGlyValIleVal 815  
 Db 2783 GGCCTGGCGGCTCTGGGTATATCCGGAACCCGTAACAATCTTTCAGAGGATATATCT 2842  
 QY 815 lValIleSerValTyrGluIleValIleGlyGlnGlnGlyGlyLeuSerValLeuArgTh 835





QY	1532	evalgYValValValGlubenpHeh:slyeCyAsrglHhIsGlnglunGlunl	1552
Db	4898	CGTGGAGGTCTGTGTCGAACCTTCCACAAgTGGCGGACAGCACGAGAGCGGAGAGGC	4957
QY	1552	aATgATgATgIunGlunlYsATgLeuAATgATgLeuGlunlYsYsATgATg-----	1568
Db	4958	GCGGCGGGAGAGAGAGAAAGCGGCTGGCGGCGCTTGAAGAGAGAGGCGAGGACATTTC	5017
QY	1569	-----LysAlInGInCySlySPProTYrTYrSerASPtyrSerpHeATgLeuA	1586
Db	5018	CAGGCCAGAGGCCAGGCGCGGCGCTTACTAGCCGACTACCTCGGCCAAGCGCGCTCAT	5077
QY	1586	lHhIsHsLeuCyThrsSerHsIstYrLeuAspLeuPheHleThrgIYValHleglYLeuAs	1606
Db	5078	TCATTCGCTGTGACCAAGCCACTATCTGCACTCTTCATCACTTCATCACTCTGTGCAA	5137
QY	1606	nValValThrMetAlaMetGluHsIstYrGInGInPProGInHleuAspGluAlaLeuY	1626
Db	5138	CGTCATCACTCCATGTCCATCGAGCACTTAAACCAACCAAGTCGTGAGCGAGCGCCATCA	5197
QY	1626	sAlcYAsnPYrHlePheThrValHlePheValLeuGlnuSerAlPheYsLeuValAl	1646
Db	5198	GTACTGCACATACGCTTCACTACATCGTGTGTGTCTTGAGGCTGCACTGAAGCTGTATG	5257
QY	1646	aPHeGlYpHeATgATgPhepHeGlnAspATgTTPAsnGlnLeuAspLeuAlaIleVal	1666
Db	5258	ATTGGAGGTTCGTGGTTCTTCAAGAGACAGGTGAAACAGCTGGACCTGGCATGTGCT	5317
QY	1666	uLeuSerHleMetGlyHleThrLeuGluGluHleGluValAsnAlaSerLeuProIleAs	1686
Db	5318	GCTGCATCACTATGGGCACTACAGCTGAGAGATGAGATGAGTCGCCCGCGCTCCATCA	5377
QY	1686	nProThrHleHleATgHleMetATgValLeuATgHleAlaIleATgValLeuYsLeuLeuY	1706
Db	5378	CCCAACCACTACATCCGATCATCGCGGTCTTCCGATTTGCCCTGTGCTGAAGCTGCTGA	5437
QY	1706	sMetAlaValGlyMetATgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValAl	1726
Db	5438	GATGGCTAAGGGCAATGGCGCGGCTGCTGGAACATGTGGTGAACCTGCCCCAGAGTGG	5497
QY	1726	YAsnLeuGlyLeuLeuPheMetLeuLeuPheHlePheAlaAlaLeuGlyValGluLe	1746
Db	5498	GAACTCGGGCTTCTTTTCATGCTCTCTGTTTTATCATCTCGCTGCGGAGAGGAGCT	5557
QY	1746	uPheHleYAspLeuGlyCyAspATgHThHsProCyAsGluYLeuGlyATgHsAlaTh	1766
Db	5558	GTTCCGAGGCTGGAGTGCAGTCAAGAACACCCCTGCAGAGGCGCTGAAGAGAGCGGCAC	5617
QY	1766	rPheATgAsnPHeGlyMetAlaPheLeuThrLeuPheATgValSerThrGlyAspAsnTr	1786
Db	5618	CTTCAGCAACTTCGGCATGGCTTCTCAACGCTGTTCGCGCTGTCCAGGGGAGCAACTG	5677
QY	1786	pAsnGlyHleMetYsAspThrLeuATgAspCys-----AspGlnGlnSerThrCy	1803
Db	5678	GAAACGGATCATGAAGAGACAGCTGCGAGAGTCCCGTGAAGAGCAAGCACTGCTGAG	5737
QY	1803	sTYrAsnThrValHleSerProHleTYrPheValSerPheValLeuThraHleGlnPheVa	1823
Db	5738	CTACTCGCGGCGCGCTGCGCGCTTACTTGATGTCCTTCGTGCTGTGGCGCCAGTTGCT	5797
QY	1823	lLeuValAsnValValHleAlaValLeuMetCysHsIleuGlnGlnSerLeuYsGlnAl	1843
Db	5798	GCTGTGTAACTGTGTGTGGCGGTCTCATTAAGCACTGAGAGAGAGCAACAGAGAGC	5857
QY	1843	aLYsGlnGluAlaGluLeuGlnAlaGluLeuGlnLeuGlnMetYsThrHleuSerProG	1863
Db	5858	AACGAGAGATGCGAGCTGCAACCGCAAGATCGAGCTGAGATG-----	5900
QY	1863	nProHsSerProLeuGlySerProPheLeuTrpProGlyValGlnGlyProAspSerPr	1883
Db	5901	-----GCGAGAGGCGCCCGGAGATGC	5920

QY	1883	O-----AspSerProIysProGlyValAlaLeuHisProAlaAlaHisAlaArgSerAl	1900
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Db	5921	ACGCCGGGTGGACGCGACAGGCT-----	5945
QY	1900	aSerHisPheSerLeuLeuHisProThrMetGlnProHisProThrGluLeuProGly--	1919
Db	5946	-----CCTTGGCCCCAGAGAGTCCGGGGCGC	5971
QY	1920	-----ProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLe	1936
		:::	
Db	5972	CAGGAGATGCCCAACTCGTGT---GCACCGAAGGTGTCCGTGTCCAGATGCTCTGCT	6028
QY	1936	uProAsnaBpSerTyMetCysArgHisGlySerThrAlaGluGlyPro-----	1952
Db	6029	GCCCAACGACAGCTACATGTTCCAGGCCCGATGGCTCTGCTCCGGCGGCCCAACCCGCCCC	6088
QY	1953	-----LeuGlyHisArgGlyTyrGlyIleuProIysAlaGlnSerGlySe	1967
		:::	
Db	6089	GCTGCAGAGGTGGAGATGAGACCTATGGGGCGCGACCCCC-----TTGGGGCTC	6139
QY	1967	rValLeuSerValHisSerGlnProAlaAspThrSerTyrIleuGlnLeuProIysAs	1987
Db	6140	CGTTGGCTCTGTGACTCTCCGCCCGAGAGCTGTGGCTCCCTCCAGATCCA-----	6194
QY	1987	pAlaProHisLeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProIysLeuPr	2007
		:::	
Db	6195	-----CTGGCTGTGTGCTCCCGACGAGCGAGCGGCGAGCCCTCCACGCTCTGTCT	6244
QY	2007	oProProGly-----ArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAl	2025
		:::	
Db	6245	CCCTCGGGGGACAGCCCGCTCCCACTCAGCTCAGCCGCTGTCTGCAGACAGAGGCTGT	6304
QY	2025	eArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlnAspLeuLeu-----Al	2043
		:::	
Db	6305	GCACACCGATTCCTTGGAAAGGGAAG---ATTGAAGCGCTTAAGGACACACCTCGATCTCGC	6361
QY	2043	agIuValSerGlyProSerPro-----ProLeuAlaArgAlaTyrSerPheThrGly--	2060
		:::	
Db	6362	AGAGCTGTGTAGAAAAACCCGGTAGAGCGGTAACCCAGGGGGGGCTCCCTGCAGTCCCC	6421
QY	2061	----GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerIysIleSerIysHis	2079
		:::	
Db	6422	ACCAAGCTCCCCACAGCGCCCGCCACAGCTCCGCACTGTAAAGATACC---TTCCGACAGCA	6478
QY	2079	sMetThrProProAlaPro---CysProGlyProGlnuProAsnThrGlyIysGlyProPr	2098
		:::	
Db	6479	CTGGCTCTCCACCGCGCGCGCGGCCCCACAGCGCGAGAG-----	6515
QY	2098	ogIuThrArgSerSerLeuGlnLeuAspThrGluLeuSerThrIleSerGlyAspLeuLe	2118
		:::	
Db	6516	-GAGGCCGAGGCTCCGAGCCAGCGCCAGAGAGATGACACATCACACACTCCGCTCG	6574
QY	2118	uPro-----ProGlyGlyGlnGluGluPro-----SerPr	2129
		:::	
Db	6575	CCCTCGGACAGCCACAGCCGAGCCCATAGGCCCGGAGACCTCTCCGTGGCGCGGCGCA	6634
QY	2129	oAlaAspLeuIysIysCysTyrSerValGlnAlaGlnSerCysGlnArgArgProThrSe	2149
		:::	
Db	6635	GCGGAGCTTGGCGAGGCTCTACAGCGTGAAGAGCTCAAGGGCTTCTCGACAAAGCCG---GG	6691
QY	2149	rTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerG	2168
		:::	
Db	6692	CCGGGCNAACGAGAGTGGCGCCCTCGGCGGAGCTGGGACGCGGAGACTGGGGAAGGC	6751
QY	2169	nProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySe	2188
		:::	
Db	6752	GAAAGCCTCGGGGCGCTGAG-----GCCGAGGCC-----GCTTGGGGTGC	6790
QY	2189	rArgProIysIysIysIysLeuSerProProSerIleThrIleAspProPro---GlnSerG	2208
		:::	
Db	6791	GCGCGAAGAAAGAGATGAGGAGCCCTTCGATCTCGGTGAACCCCTCGGAGAGACGA	6856
QY	2208	ngIProArgThrProProSerPro-----GlyIleCysLeuArgArgArgAlaPr	2255

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Db      6851 GGGCTCTGCGCGGCTCTCCGCGGAGAGGGCGGAGACCACTAGAGGGGAGACCC 6910
QY      2225 oser-----SerAspSerlyAspProLeu-----Alase 2235
Db      6911 GTCTGTGAGGCCACCGCTCAACAGGACTCTCTGAGAGCCACAGAGGGCTCAGGCCGG 6970
QY      2235 rglProAspSerMetAla-----AlaseProSerProlylAspValle 2252
Db      6971 GGGGAGACCTGCGAGCCAGAGGGAGCGCTGGGCGAGGCTCTCGCGGAGGAGCACT 7030
QY      2252 uSerLeuSerGlyLeuSerSerAspProAlaAspLeu-----AspPro 2266
Db      7031 GACCGTCCCGCACTTTGCTTTGAGCGCTGACCTCGGGGTCCCACTGAGAGACCT 7088

RESULT 11
US-10-377-139-8
/ Sequence 8, Application US/10377139
/ Publication No. US20040175761A1
/ GENERAL INFORMATION:
/ APPLICANT: Mackinnon, Roderick
/ APPLICANT: Jiang, Youxing
/ APPLICANT: Lee Mackinnon, Alice
/ APPLICANT: Rute, Vanessa
/ TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
/ FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
/ CURRENT APPLICATION NUMBER: US/10/377,139
/ CURRENT FILING DATE: 2003-03-01
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 8
/ LENGTH: 6990
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-377-139-8

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Alignment Scores:
Pred. No.: 0 Length: 6990
Score: 5496.50 Matches: 1244
Percent Similarity: 60.31% Conservative: 216
Best Local Similarity: 51.38% Mismatches: 525
Query Match: 46.17% Indels: 437
DB: 19 Gaps: 60
US-09-611-257A-37 (1-2266) x US-10-377-139-8 (1-6990)

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QY      31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50
Db      73 CAGCCGCGAGCCCGGAGCCCGCATCTCCCGCCAGAGGCTGTGAGGAGCGCTCTGATGGA 132
QY      51 -----LeuProTyrrProAlaLeuAlaProValAlaPhePheTyrlLeuSerGln 66
Db      133 GCTGATCTCATATGTCACACACCCAGACCTGGCGCTATGCTCTTCTGCTGCGACAG 192
QY      67 AspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgIle 86
Db      193 ACCACGAGCCCGCGAGACTGGTGATCATAGATGCTGCAACCGCTGTTGAATGTGTC 252
QY      87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db      253 AGCATGCTGGTGAATCTGTGAACTGGCGTGACACTTGGAATGTACAGCCCTGCGAGAC 312
QY      107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126
Db      313 ATGACAGCTGCTGCGACCGCTGCAAGATCTGAGAGCTTTGATGACTTCATTATC 372
QY      127 PhePheAlaValGluMetValIleValMetValAlaLeuGlyIlePheGlyIlePheGlyCys 146
Db      373 TTTCTTTGCGATGAGATGTGCTCATAGATGCTGCGCGGATTTTGGCAAGAGTGC 432
QY      147 TyrLeuGlyAspThrTyrPheAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166

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Db      433 TACCTGGGAGACATGAAACCGCTGATTTCTTCATGTCATGAGGAGATGTGAG 492
QY      167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db      493 TACTCCCTGAGACTTCAGAAACATCAACCTGTCAAGCATCCGACCGCTGGCGCTCGAG 552
QY      187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAsp 206
Db      553 CCCCTCAAGCCATCAACCGCGTCCCAATATGGAGATCTGTGAACCTGCTCTTGAC 612
QY      207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly 226
Db      613 ACATGCTCATGCTGGGAGATGTCTGCTGCTGCTGCTTTTGTCTTTCATCTTGGC 672
QY      227 IleValGlyValGlnLeuThrAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
Db      673 ATCATAGTGTGCAAGCTGTGGGCGGCTGTGCTCAACCGCTGCTCTTGAGAGAAAC 732
QY      247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266
Db      733 TTCACCATCAAGAGGATGTGGCTTGGCCCCCATACTACACGCGAGAGAGATGATGAG 792
QY      267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
Db      793 ATGCTCTTATCTGCTCTCTCTGCGGCGACATGGAGATATGGGCTGCCATGAGATCCC 852
QY      287 ThrLeuArgGlyAspGlyGlyProProCysGlyLeu----- 300
Db      853 CGGCTCAAGAGCAG-----GGCGTGAAGTGTGCTGCTGCCAAGACGACGTCTAC 903
QY      301 AspTyrGluAlaIleArgAsnSerSerAsnThrThr-----CysValAsnThrPheAsn 318
Db      904 GACTTTGGGCGGCGGCGGCGACGACTCAATGCGAGCGGCTCTGTGTCAATGGAACCGT 963
QY      319 TyrTyrThrAsnCysSerAlaGlyGlyIleAsnProPheIleGlyAlaIleAsnPheAsp 338
Db      964 TACTTCAATGTGTGCGGACGCGGACGCGCAACCCCAAGAGGTGCCATCACTTTGAC 1023
QY      339 AsnIleGlyTyrAlaThrIleAlaIlePheGlnValIleThrLeuGlnGlyTyrValAsp 358
Db      1024 AACATCGGTTATGCTTGATGTCATCTTCCAGGTATCATCTGGAAGGCTGGGTGAG 1083
QY      359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu 378
Db      1084 ATCATGTACTACCTGTATGATGTCTCACTCTTCTTACAACCTTCACTTCACTGCTT 1143
QY      379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPhe 398
Db      1144 ATCATAGTGGGCTCTTCTTATGATCATCACTGTGCTGCTGTCATAGGACCCAGTTC 1203
QY      399 SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
Db      1204 TCGGAGACCAAGCAAGGAGGACCGGCTGATCTGGAAGAGGCGGACGCTACCTGTC 1263
QY      419 AsnAlaSerThrLeuAlaSerPheSerGlnProGlySerCysTyrTyrGlnGluLeuLys 438
Db      1264 ---TCCAGCACCGGTGGCGACGCTGCGGAGCTGGGAGCTTCAACAGAGATCTTCAG 1320
QY      439 TyrLeuValTyrIleLeuArgLysAlaIleArgArgLeuAlaGlnValSerArgAlaAla 458
Db      1321 TATGTCTGCCATTCCTTCTGCGCAAGGCCAAGCC-----CCGCGCTTG 1362
QY      459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGlnThrGlnPro 478
Db      1363 GGGCTTACAGAGCGCGTGCAGAGCCGGCGGAGCGCTGGGCGGAGGCGCGGCGCC 1422
QY      479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisIleValHisIleHis 498
Db      1423 GCCAAACCT-----GGGCCCCAC 1440
QY      499 HisHisHisHisHisIleTyrHis-----LeuGlyAsnGlyThrLeuArgAlaPro 515
Db      1441 GCCAAGAGGCCCGGCACTTCCATGGGAAGACTTAAGGTTCAGGA----- 1485

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QY 516 ArgAlaSerProGluIleGlnAspArgAlaAsn---GlySerArgArgLeuMet--- 533  
 DB 1486 -----GATGAAGGAGACATCTCGAAGCCGGCATTTGCCAGACT 1524  
 QY 534 LeuProProSerThrProAlaLeuSerGlyAlaProProGlyGlyValGluSerVal 553  
 DB 1525 TTGGATGGGCTGGCTCCCT-----GGAAATGATCACTCGGGAAGAGAG----- 1569  
 QY 554 HisSerPheThrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProPro 573  
 DB 1570 -----CTGTGC-----CCGCCAA 1581  
 QY 574 ArgSerProSerGluAlaSerGlyArgThrValGlySerGlyValValTyrProThrVal 593  
 DB 1582 CATPAGCCCCCTGGATGCGAGCCCAACCCCTG----- 1614  
 QY 594 HisThrSerProProProGluThrLeuLeuValGluValAlaLeuValAlaAsp 613  
 DB 1615 ---GTGCACCCCATCCCGCCAGCGTG----- 1638  
 QY 614 SerGlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHis 633  
 DB 1638 ----- 1638  
 QY 634 LysLeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysAlaValIleSerSerPro 653  
 DB 1638 ----- 1638  
 QY 654 CysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg--- 672  
 DB 1639 -----GTTCCGATCCCGCCAGCTGCCCTTGCTGCACGATGAG 1677  
 QY 673 -----AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAsp 687  
 DB 1678 GACGGCGGCGGCGCTCGGGCTCGGGCAGACCCAGC---TCGGGCGAGAGGGCTCGGGC 1734  
 QY 688 SerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAsp 707  
 DB 1735 TCCGGAGCTCCGCTGTCGGCGAG-----GACGAGCGGATGGGAGCGGGCCCGAGAC 1788  
 QY 708 ProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeu--- 726  
 DB 1789 AGCGAGAGAGAGCCCTCCAGAACTGGGGAAGAGAGAGAGAGAGAGAGAGAGCGGAT 1848  
 QY 727 -----AlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739  
 DB 1849 GGCGCGCTGCTGTGCGGGATGTGTGGCGGAGACCGCAAGCTGGCGGCGATC 1908  
 QY 740 ValAspSerLysPheThrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759  
 DB 1909 GTGGAGAGAGAGTACTTCAACCGGGCATCATGATGAGCATCTGTGTCACACCGTCACG 1968  
 QY 760 MetGlyIleGluTyrHisGlnGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779  
 DB 1969 ATGGGATCGAGACACACGAGAGCGCGAGAGCTACCAACATCTTGAGATCTGCAAT 2028  
 QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuValLeuValTyrGlyPro 799  
 DB 2029 GTGGTCTTCAACGCAATGTTTGGCTCGAGATGATCTGAAGCTGCTCATTTTGGGCTC 2088  
 QY 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerVal 819  
 DB 2089 TTTCGACTACCTGGGTAACCCCTTACAAATCTTGGAGAGATCATTTTTCATCATCAGATC 2148  
 QY 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839  
 DB 2149 TGGGAAATGCTGGGGAGAGCGAGCGGTGGCTGTGCTGTGGAGACTTCCGGCTGCTG 2208  
 QY 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859  
 DB 2209 CCGGTGCTGAAACTGGTGGCTTCATGCTGCTCGGCGGCGCAGCTCGTGGTGTCTCATG 2268

QY 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe 879  
 DB 2269 AAGACCAAGGACAGAGCTGGCCACTTCTGCATGCTGCTCATGCTTATCTTATCTTC 2328  
 QY 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAsp 898  
 DB 2329 AGCATCTTGGGATGCAATATTTTGGCTGCAAGTTCACTCCGCCGACCGACACTGGAGAC 2388  
 QY 899 ThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGln 918  
 DB 2389 ACGGTGCCGAGAGAGAACTTGACCTCCGTGCTGTGGGCGATGCTGATCTGTGTCCAG 2448  
 QY 919 IleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSer 938  
 DB 2449 ATTCCTACCCAGAGAGACTGGAGAGCTGCTCTCATAGATGGATGGCTCCACTTCTCC 2508  
 QY 939 TrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeu 958  
 DB 2509 TGGGCTCCCTCACTTGTGCGCCCTCATGACCTTCGGCAACTATGTCTCTTCAACCTG 2568  
 QY 959 LeuValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAla 978  
 DB 2569 CTGTGGCCATCTGTGTAGAGGCTTCCAGGGCGAG----- 2604  
 QY 979 SerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLys 998  
 DB 2605 -----GTTGACGCCAATCGC 2619  
 QY 999 SerGluSerGluProAspPhePheSerProSer----- 1009  
 DB 2620 TCTCATCTGGAGAGAGACAGAGCTCATCAACATGAGAAGTTGATTAAGCTCCAGAA 2679  
 QY 1010 ---LeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGlnHis 1028  
 DB 2680 GGCCTGAGACAGAGGAGATGCCAGCTGTGCCAATCCCATATGACCCCAATGGGAC 2739  
 QY 1029 ProGluLeuArgLysSerLeuLeuProLeuIleIleHisThrAlaAlaThrProMet 1048  
 DB 2740 -----CTGGAGCCC----- 2748  
 QY 1049 SerLeuProLysSerThrSerThrGlyLeuGlyAlaLeuGlyProAlaSerArgArg 1068  
 DB 2749 AGTCTCCCACTGGTGGGACACTAGTCTCTGTGGGCTGGGGACCTGCCCCCGAGATC 2808  
 QY 1069 Thr-----SerSerSerGlySerAla 1075  
 DB 2809 TCACTGCAAGCGGAGCCCATGCTGTGGCTCGGCTCCGAAAGAGAGATGTCTATCT 2868  
 QY 1076 GluProGlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSerProHisSer 1095  
 DB 2869 CTAGGAGAGATGAGCTATGACGACGCTCCGTGTCCAGCTCCCGAGGCTCTACTAGCGG 2928  
 QY 1096 ProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuArg 1115  
 DB 2929 CCATGGGGCGGAGCGGCGCTGGGCGAGCGCTCGCTCAAGCTGGAAC----- 2976  
 QY 1116 AlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu 1135  
 DB 2977 -----AGCTTAAACAACAAGCGCGTGTGGGCGAGCATGAGTCTCTGTCTCTCGAG 3030  
 QY 1136 ---GlyGlnGluSerGlnAspGluGluGluSerSerGluGlu-----GluArgAlaSer 1152  
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 DB 3091 CCCCTGCAACCCCAACAGCCACACCATTCATCAAGGCGCCCATCTGAGCGACCGCAC 3150  
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Db 3211 GTCGCCGCGTGGCGCCACCCCGGCGCTGGAGGGCGGACGCGCGCGCGG 3270  
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QY 1884 -----AapSerProlyserProly 1889
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QY 1896 -----HisAlaArgSerAlaSer----- 1901
Db 5541 GGTGACAGCTGGCTGAGACGAGGCTTCTCCGAACTGACAGAGCTCTCGTCATCT 5600
QY 1902 -----HisPhSerLeuGluHisProThrmMetGlnPro-----His 1913
Db 5601 GCTGGGTGACGACCTGATCTCGAGACCTCCACAGCTCGCCCACTGGCCGCAAGACAG 5660
QY 1913 sProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly----- 1929
Db 5661 CAAGGTGAGCTGGACCCACCTGACCCCATGCTGTGGAGACCTGGGGAATGCTTCT 5720
QY 1930 ----ValSerArgThrHisSerLeuProAsn--AapSerTyrMetCysArgHisGlySe 1947
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QY 1947 rThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySe 1967
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QY 1967 rValLeuSerValHisSerGlnProAlaAspThrSerTyrLeuGlnLeuProLysAs 1987
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QY 1987 pAlaProHis-----LeuLeuGlnProHisSerAlaProThrTrpGly 2001
Db 5889 GTTCTTCCACCCCTGACGTCTCTCCAGCCAGAAAGGCCAAGAAAGGCACTGGCACTG 5948
QY 2001 yThrTrileProLysLeuProProGly-----ArgSerProLeuAlaGln 2016
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QY 2016 nArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGln 2036
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QY 2076 eSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGln 2096
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QY 2096 yProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpLysSerGlyAs 2116
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QY 2116 pLeuLeuProProGlyGlyGlnGlnGluProProSerProArgAspLeuLysCysTyr 2136
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QY 2136 rSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlnArgArg 2156
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Db 6258 CCACAGACAGCGGGGCTGCTC-----ACCAAGCCCGGCTGACCAACCAAGACTCCATGAGACC 6314
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QY 2210 cArgThrProProSerProGlyIleCysLeuArgArgArgAlaProSerSerAapSer-- 2229
Db 6421 -----CCGCCCGACGCCCGGCTTCAGCCCGCCAGAAATTCAAGACACACAGCAAGCTT 6476
QY 2230 -----LysAapProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSe 2246
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QY 2266 o 2266
Db 6579 G 6579
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## RESULT 12

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US-09-935-541-1
/ Sequence 1, Application US/09935541
/ Patent No. US2002015091A1
/ GENERAL INFORMATION:
/ APPLICANT: Dietrich, Paul S.
/ APPLICANT: McGiven, Joseph G.
/ TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
/ TITLE OF INVENTION: AND USES
/ FILE REFERENCE: R0043B-REG sequence listing
/ CURRENT APPLICATION NUMBER: US/09/935,541
/ PRIOR FILING DATE: 2001-08-23
/ PRIOR APPLICATION NUMBER: 09/404,650
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 6816
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (192)..(6716)
US-09-935-541-1
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## Alignment Scores:

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Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.30% Conservative: 213
Best Local Similarity: 51.44% Mismatches: 506
Query Match: 46.14% Indels: 449
DB: 9 Gaps: 55
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US-09-611-257a-37 (1-2266) X US-09-935-541-1 (1-6816)

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QY 51 -----LeuProTyrProAlaLeuAlaProValAlaPhePheTyrLeuSerGln 66
Db 324 GCTGATCTCATGTCTCCACACCAAGACCTGAGGCTTATGCTTCTTGTGCTGAGACG 383
QY 67 AapSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGlnArgIle 86
Db 384 ACCACAGCGCGCGAAGCTGTGATCAAGATGTGTCAACCCGTGTGTAATGTCTC 443
QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
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QY 805 AenProTyrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValGly 824  
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QY 1260 oProGlnSerArgPheArgLeuLeuGlyCysHisArgGluLeuHisGlySerPheAsp 1280  
Db 3548 TCCCGAAGACAGGTTCGCGGCTCTGTGACACATTAATTGCCCAAACTTTCAGACT 3607  
QY 1280 eValValLeuValIleIlePheLeuAsnGlyIleThrIleAlaMetGluArgProGly 1300  
Db 3608 CGTGGCTCGGCGCTTCATCTTCTCAACTGCATCACCATCGCCCTGAGCGGCTCAGT 3667  
QY 1300 eAspProHisSerAlaGluMetThrValIlePheLeuThrLeuSerAsnTyrlPheThrAla 1320  
Db 3668 CAGGCGCGGACGACCGAAGCATCTTCTCACCGGTCCAACTTAATCTTCAGGCCAT 3727  
QY 1320 IPhelLeuAlaGluMetThrValIleValAlaIleGlyTyrlPheGlyGluGlnAl 1340  
Db 3728 CTTCGTGGGAGATGACATTTGAAGTAAGTCTCGTGGGCTGTACTTCGCGAGCAGGC 3787  
QY 1340 aTyrlLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValIleLeuValIleAs 1360  
Db 3788 GlnACCTACGAGACGATCGAAGCGTGTGATGGCTTCTTGTCTTGTCTTCATTCAT 3847  
QY 1360 PileuValIleSerMetValSerAspSerGlyThrIleGlyIleGluGlyMetLeuArgVal 1380  
Db 3848 CATCGTGGTCTCTGCGCTCACCGCGGAGGACCAAGATCTTGGGGTCTCTCGAATCT 3907  
QY 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuGly 1400  
Db 3908 GCGGCTCTGCGACCTACGCGCCCTGCGTGTCAATCAGCGGCGCGCGGCTGAAGCT 3967  
QY 1400 uValValGluThrLeuMetSerSerLeuGlyProIleGlyAsnIleValValIleCys 1420  
Db 3968 GGTGGTGGAGACATCATCTCTCCCTCAAGCCCATCGCAATCGTCATCTCAGTGG 4027  
QY 1420 sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheGlyGlyAspPheVal 1440  
Db 4028 TGGCTTCTCATCATCTTTGGCATCTCTGGAGATGCAAGCTCTTAAAGGCAAGTTCTACA 4087  
QY 1440 IcyGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460

Db 4088 CTGTCTGGGCGTGGACACCCCGCAATGACCAACCGCTCGGACTGACGCGCCCACTA 4147  
QY 1460 rArgThrValAlaArgHislyrTyrlAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuP 1480  
Db 4148 CCGCTGGGTTCATCAAAATATCACTTGGACACTTGGGCGGAGGCTCTGAATGCTCTCT 4207  
QY 1480 eValLeuAlaSerLysAspGlyTyrlPheAlaAspIleMetTyrlAspGlyLeuAspAlaVal 1500  
Db 4208 TGTCTCTGGATCCAAAGATGGTGGGTGAACATCATGTATCAATGAGACTGGATGCTTGC 4267  
QY 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrlPheIleSerPh 1520  
Db 4268 TGTGACACGACGCTGTGACCAACCAACCCCTGATGTCTGTACTTCATCTCTT 4327  
QY 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPh 1540  
Db 4328 CTGTCTCATGTACACTTCTTGTCTCAATGTTTGTGGGTGTCTGTGGAGAACTT 4387  
QY 1540 eHisLySerCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGlyArgLe 1560  
Db 4388 CCAGAAAGTCCGGGACGACACAGAGAGCTGAAGAGGACGCGCGGTGAAGAAAGCGCT 4447  
QY 1560 uArgArgLeuGluGlyLyArgArgLyArgAlaGlnCysLyProTyrlTyrlSerAspTyrlSe 1580  
Db 4448 GCGGCGCTGGAGAAAGAGCGCGGAGGCGCGGCTGCTTACTATGCGCACTATTG 4507  
QY 1580 rArgPheArgLeuLeuValHisHisLeuGlyThrSerHisTyrlLeuAspLeuPheIleTh 1600  
Db 4508 TCACACCGGCTGTCTATCTCATCTCATGTGACACGACCATCTGACATCTTATCATAC 4567  
QY 1600 rGlyValIleGlyLeuAsnValIleThrMetAlaMetGluHisTyrlGlnGlnProGlnI 1620  
Db 4568 CTTCATTCATCTGCTCCAAAGTGTGATCACCATTGCTCCGAGGACATCAAGCCACGTC 4627  
QY 1620 eLeuAspGluAlaLeuGlyIleCysAsnTyrlPheThrValIlePheValLeuGlySe 1640  
Db 4628 CTTGAGACAGCGCTTCAAGTATCTGCACACTATATGTTCACACTGTCTTGTGCTGAGAGC 4687  
QY 1640 rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspTrpAsnGlnLe 1660  
Db 4688 TGTGCTGAAGCTGTGGCATTTGTGTCTGAGGCGCTTCTTCAAGAACCAATGAAACCACT 4747  
QY 1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs 1680  
Db 4748 GGACCTGGCAATGTGCTACTGTGATGATGAGGATCAACCTGGAGAGATGAGATCA 4807  
QY 1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValIleAlaArg 1700  
Db 4808 TCCGCGCCCTGCCATCAATCCACCATCATCGCATATGAGGGTTCGCGCATTTGCCG 4867  
QY 1700 gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetG 1720  
Db 4868 AATGCTGAAGCTTTGAAGATGGCCACAGAAATGGGGGCTGTGGACACGATGGTGA 4927  
QY 1720 nAlaLeuProGlnValIleGlyAsnLeuGlyLeuLeuPheMetLeuPhePheIlePheAl 1740  
Db 4928 ACTTTGGCCCAAGTGGGGAACCTGGGCTCTCTTCAATGCTGCTCTTCACTCATAGC 4987  
QY 1740 aAlaLeuGlyValGluLeuPheGlyAspLeuGlyCysAspGluThrHisProCysGluG 1760  
Db 4988 TGTCTCTGGGGTGGAGCTCTTGGAGAGCTGTCTGCAAGCAGAAACCCCTGGAGAGG 5047  
QY 1760 yLeuGlyArgHisAlaTrpPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780  
Db 5048 CATGACCGGATGCGACCTTGAAGATCTTGGATGGCTCTTCTCAACATCTTCCAGGT 5107  
QY 1780 IserThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys--AspG 1799  
Db 5108 CTCGACGGGTGACAACTGGAACGGATCATGAAGACACGCTGGGGACTGACCCACGA 5167  
QY 1799 nGluSerThrCysTyrlAsnThrVal-----IleSerProIleTyrlPheValSerPheVal 1817  
Db 5168 CGAGCGCAGCTGCTGAGACAGCTGCAAGTTGTGTGCGCGCTGTACTTCGTGAGCTTGT 5227





QY 727 -----AlaheTPrpAgluLeuIleCyAspThrPheArgLysIleValAspSerLysTyr 744  
 DB 1950 TGGGGGATGTGTGGCGAGACCGGAGCCAAAGCTGTGGCGCATCTGGACAGAACTAC 2009  
 QY 745 PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGlyTyr 764  
 DB 2010 TTCAACGGGGGCATCATGATGGCCATCTGTCTCAACCGCTGACATGGGATGGGAC 2069  
 QY 765 HisGluInProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer 784  
 DB 2070 CAGAGAGACCGGAGAGAGCTGACCAACATCTGGAGATCTGCAATGGTCTTACACAGC 2129  
 QY 785 LeuPheAlaLeuGluMetLeuLeuLeuValTyrGlyProPheGlyTyrIleLys 804  
 DB 2130 ATGTTTCCTCGGAGATGATCTCGAAGCTGGCTGCAATTTGGGCTTTCGACTACCTG 2189  
 QY 805 AsnProTyrAsnIlePheAspGlyValIleValIleSerValTyrGluIleValGly 824  
 DB 2190 AACCTTACACATCTTTCGACAGCATCATTTGTCTCATCAGCATCTGGAGATGTGGGG 2249  
 QY 825 GluGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu 844  
 DB 2250 CAGCGGAGCGGTGGCTGTGGTCTGTGGACCTTCGGGCTGTGGCGGTGCTGAACCTG 2309  
 QY 845 ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn 864  
 DB 2310 GTGGCTTTCATGCTGCTGGCTGGCGGCGCAGCTCGTGGTCTCATGAAGACCATGACAC 2369  
 QY 865 ValAlaIaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMet 884  
 DB 2370 GTGGCCACTTGTGCATGCTGCTCATGCTCTTCACTTTCATCTTCAGATCTTGGAGATG 2429  
 QY 885 HisLeuPheGlyCysLysPheAlaSerGlnArgAsp---GlyAspThrLeuProAspArg 903  
 DB 2430 CATATTTTGGCTGCAAGTTAGCTCCGACGAGACACTGGAGACAGGTGCCGACAGG 2489  
 QY 904 LysAsnPheAspSerLeuLeuTyrAlaIleValIleThrValPheGlnIleLeuThrGlnGlu 923  
 DB 2490 AAGAACTTCCAGCTCCCTGCTGTGGCCATCTGCTGCTTCAGATCTCCACCCAGAGAG 2549  
 QY 924 AsnTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaIleLeuTyr 943  
 DB 2550 GACTGGAACGCTGTTCTTACAAATGAGCGCTCCACTTCTCCCTGGGCTCTCTTAC 2609  
 QY 944 PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeu 963  
 DB 2610 TTTGTCCCTCCATGACCTTGGCAACTATGTCTTCAACCTGTGGTGGCATCTGTG 2669  
 QY 964 ValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSer 983  
 DB 2670 GTGGAGGGCTTCCAGCGGAG----- 2690  
 QY 984 CysIleGlnLeuProValAspSerGlnGlyLysAspAlaAsnLysSerGluPro 1003  
 DB 2691 -----GDTAGCCCAATGCTCTTACTCGGACAG 2720  
 QY 1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013  
 DB 2721 GACCAAGACTATCCAACTAGAAAGTTTGAATGAAGCTCCAGGAAGGCTTGACAGCAGC 2780  
 QY 1014 GlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033  
 DB 2781 GGAATCCCAAGCTCTGCGCAATCCCATGACCCCAATGGGAC----- 2825  
 QY 1034 SerLeuLeuProProLeuIleIleHisThrAlaIaThrPrometSerLeuProLysSer 1053  
 DB 2826 -----CTGGACCC-----AGTCTCCACTGGGT 2849  
 QY 1054 ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThr----- 1069  
 DB 2850 GGGCACTTAAGTCTGCTGGGCTGGGAGACTGCCCCGACTCTCATCTGACCGGAGC 2909  
 QY 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080

DB 2910 CCCATGCTGTGACCTCTGGGCTCCCGAAAGAGAGTCAATGCTCTTACGAGAGATGAC 2969  
 QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100  
 DB 2970 TATGACACAGGCTCTCTGTCCAGCTCCCGAGCTCTTACTACGGGATGGGCGCCAGC 3029  
 QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
 DB 3030 GCGGCTGGGCGGCGGCTGCTCCAGCTGAGAC-----ACCTTCAG 3071  
 QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu---GlyGlnGluSer 1139  
 DB 3072 CACAAGCCCGCTGCGCGGAGCATAGACTCTCTCTCTGCGAGAGCGCGCGCGCGCC 3131  
 QY 1140 GluAspGluGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157  
 DB 3132 CGGATCTGCGAGGTGCGCGGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 3191  
 QY 1158 His-----ArgHisArgGly 1162  
 DB 3192 CAGGCCACCACTTATCATCGGGCCCATCTGGCGACCGCCACCGCACCGCGCG 3251  
 QY 1163 SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182  
 DB 3252 ACGTGTCTCTGCAACAAGAGACTGGTGAACCTTGGCCAGCTGTGCGCGCGCGCGCG 3311  
 QY 1183 LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn 1200  
 DB 3312 GCCACCCCGCA 3371  
 QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAs 1220  
 DB 3372 GCGAGAGAT-GCCACGACTCC---CAAGACGTTCTTACCAAGATGGCGCGCGCGCG 3427  
 QY 1220 PGLYAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240  
 DB 3428 TCGCGGGAGAGATGAGAGAAATCGACTACACCTGTGCTTCCGCGCGCGCGCGCGAG 3487  
 QY 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePr 1260  
 DB 3488 CAGCTGTATTAAGCCGCACTGTGCGAGCTCCGCAAGACTGTGTCTTACTCTTCTC 3547  
 QY 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280  
 DB 3548 TCCCGAAGAACGTTCCGGGTCTGTGTCAAGACATTATGCCCACAACTCTTCACTA 3607  
 QY 1280 sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300  
 DB 3608 CGTGTCTCTGCTTCACTTCTTCACTCACTCACTCACTGCGCTGAGCGGCTCAAGAT 3667  
 QY 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320  
 DB 3668 CAGAGCCGGAGACCGAAGCATCTTCTCAACGTTCCAACTTCAAGTCTTCAAGCGCAT 3727  
 QY 1320 lPheLeuAlaGluMetThrValLysValAlaAlaLeuGlyTyrCysPheGlyGluGlnAl 1340  
 DB 3728 CTTCGTGGCGAGATGACATTTGAAGTATGCTGCTGGGCTGTGACTTTCGCGAGCGGC 3787  
 QY 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360  
 DB 3788 GTACTTACGAGACGCTGGAACGCTGAGATGGCTTCTGTCTTCTGCTGCTGCTCATCA 3847  
 QY 1360 lPheLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe 1380  
 DB 3848 CATGTGTGTCTCTGCGCTCAAGCGGGGAGGCAAGATCTTGGGGGTCTCTCGAGCTT 3907  
 QY 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnIleLysLysLe 1400  
 DB 3908 GCGGCTCTCTGCGACCTTACGCGCCCTGCTGTATCAGCGGCGCGCGCGCGCGCGCT 3967  
 QY 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420



D	b	3368	GGTGGTGGAGACACTCATCTCTCCCTCCACAGCCATGGGCAACATCGTGCATCTGCTG	4027
Q	y	1420	saIaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheGlyIlySerPheVa	1440
D	b	4028	TGCCTTCTTCATCATCTTTGGCATTCTGGAGTCCGAGCTCTTCAAAGGCAAGTTCTAC	4087
Q	y	1440	lCyegInGlyGlnAspThrArganIleThrAsnIlySerAspCysalagIuaIasery	1460
D	b	4088	CTGTCTGGGCGCTGGACACCCCGCAACATCACCAACCGCTCGGACGTGCGCGCACTA	4147
Q	y	1460	rArgTrpValaArgHisIystrYrAsnPheAspAsnLeuGlyGlnIleLeuMetSerLeuP	1480
D	b	4148	CCGCTGGGCTCATCAACAATCAACTTCGACAACTGGGCGAGGCTCTGATGTCCTCTT	4207
Q	y	1480	evaIleuAlaSerIlyAspGlyTrpValAspIleMetYrAspGlyLeuAspAlaValG	1500
D	b	4208	TGTCCTGGCATCCAAAGATGGTGTGGGTAACATCATGACATGGAAGTGGTGTTC	4267
Q	y	1500	yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerP	1520
D	b	4268	TGTGGACACAGCGCTGTGACCAACCAACCCCTGGATGCTGTGATTCATCTCTCT	4327
Q	y	1520	eLeuLeuIleValAlaPhePheValIleuAsnMetPheValGlyValValGlnAsnPh	1540
D	b	4328	CTGTCTCATCTCCAGCTCTTGTGTCTCAACATGTTGTGGTGTCCGGGGGAACTT	4387
Q	y	1540	eHisIySerCysArgGlnHisGInGInGInGInGlnAlaArgArgArgGlnIlyAsArgLe	1560
D	b	4388	CCACAAGTGGCGGCGAGCACCCAGAGGCGTGAAAGAGCAACCGCGGTAGAGGAAGCGGCT	4447
Q	y	1560	uArgArgLeuGlnIlyIlyAsArgArglysaIagInCysIySerProTyrTyrSerAspTyrSe	1580
D	b	4448	GCGCGCGCTGTGAGAAAGAACCCCGGAAGCCCAACGCGCTGCTTCATGACCACTTATGG	4507
Q	y	1580	rArgPheArgLeuLeuValHisIleuCysThrSerHisIyTrpLeuAspPheIleTh	1600
D	b	4508	TCACACCCGCGTGTCTCATTCACATCATGTGACCAAGCACCACTTGACATCTTCATCAC	4567
Q	y	1600	rgIyValIleGlyLeuAsnValValThrMetAlaMetGlyHisIyTrGInGlnProGlnI	1620
D	b	4568	CTTCATCATCTGCTTCAAACGTGTGCATCATCTCCCTGGAGACATCAATGACCCCAAGTC	4627
Q	y	1620	eLeuAspGlnAlaLeuIlyIleCysAsnTyrIlePheThrValIlePheValLeuGlnSe	1640
D	b	4628	CCTGAGACAGACCCCTCAAGTACTGCACTAATATGTCACCACTGTCTTGTGGCTGAGAGC	4687
Q	y	1640	rValPheIlyIleuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe	1660
D	b	4688	TGTCTGTAAGCTGTGTGGCATTTGTGTGTGAGGCGCTTCTCAAGACCGATGTGAACCAAGCT	4747
Q	y	1660	uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGlnIleGlyValAs	1680
D	b	4748	GGACCTGGCCATTGTGTACTGTCACTGATCATGGCATCACCTGGAGAGATCGAGATCA	4807
Q	y	1680	nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaIar	1700
D	b	4808	TGGCGCCCTGGCCATCAATCCCAACATCATCGCATATGAGGGGTCTGGCATTTGCCG	4867
Q	y	1700	gValLeuIlyIleuLeuIlyMetAlaValGlyMetArgAlaLeuLeuAspThrValMetG	1720
D	b	4868	AGTCTGTAAGCTGTGTGAAGATGGCCACAGAAATCGGGCCCTGTGTGACACAGGTGTGAC	4927
Q	y	1720	nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl	1740
D	b	4928	AGCTTTGCCCAAGGTGGCAACTGGGCTCTCTTCATAGCTGCTCTTCTTCATCTATGC	4987
Q	y	1740	aAlaLeuGlyValGlnLeuPheGlyAspLeuGlnCysAspGlnIlyThrHisProCysGlnG	1760
D	b	4988	TGCTCTGGGGTGGAGCTCTTTGGGAAGCTGTGTGCAACGACGAAACCGGTGCGAGGG	5047
Q	y	1760	lyLeuGlyIlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa	1780
D	b	5048	CATGAGCCGCGATGCACCTTCGAGACTTGTGGGATGGCTTCTCTCAACACTTCACAGT	5107

QY	1780	1SerThrGlyAspAsnThrAsnGlyIleMetLysAspThrIleuAlaAspCys---AspGI	1799
Db	5108	CTCCACGGGAGAACAACTGGAAACGGAGTCATGAAGAGCAACGCTCCGGAGCTGCACCCACGA	5167
QY	1799	ngIuSerThrCysArgThrAsnThrVal-----IleSerProIleTyrPheValSerPheVal	1817
Db	5168	CGACGGACAGCTGCCTAGACAGCACTGCAGTGTGTGTGGCCGCTTATCTTGGTAGCTTCGT	5227
QY	1817	lleuThrAlaGlnPheValIleuValAsnValValIleAlaValIleuMetLysHileuGI	1837
Db	5228	GCTACCGCCGACAGTCTGCTCTCAACAGTGTGTGGCTGTCTCATGAAGACCTCGGA	5287
QY	1837	ugIuSerAsnLysGlnAlaLysGluGluValagIuIleuGluAlaGluIleuGluIleuGluMe	1857
Db	5288	CGACGAGAACAGAGAGCGGAGGAGGAGGAGCGCCGAGATGATGATGCCAGCTCGACGTCAGAT	5347
QY	1857	t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGI	1876
Db	5348	GGCCCATGGCTGGAGGCTGGCCCGAGGCTGCCTACCGGCTCCCGGGCGCC---CTGG	5404
QY	1876	YValGluGlyProAsp-----	1881
Db	5405	C---CGAGGGCCGGAGAGGGGCGGGCGGGGCGACACCGAGGGCGGCTTGTGGCGGG	5461
QY	1882	-----SerPro-----	1883
Db	5462	CTGTATATCCCTGCTGCCAGAGAACCTGTGGCTGGACAGCGTCTCTTATATCATCAAGA	5521
QY	1884	-----	1892
Db	5522	CTCTCTGGAGGGGAGCTGACCATCATGACCAACCTGTGGGCTGCATCTTTCACACACTA	5581
QY	1893	-----ProAlaAla-----	1895
Db	5582	CTCTCGGCTGTGGGCTGCAGAGAAGTGTACACAGACACAGAGGTGACGCTGGCTGA	5641
QY	1896	-----HisAlaArgSerAlaSer-----HisPhe	1903
Db	5642	GACGAGGAGCTTCTCCCTGAATCCAGACAGAGTCTCTGCATCTGCTGGTAGACAGACT	5701
QY	1903	eSerLeuGluHileuProThrMetGlnPro-----HisProThrGluLeuPhe	1918
Db	5702	GAGTCTGAGAGAACCCCAACGCTGCCCTGCACCTGGCCGCAAAAGACAGCAAGGTGAGCTGGA	5761
QY	1918	ogIyProAspLeuIleuThrValArgLysSerGly-----ValSerArgThr	1933
Db	5762	CCACGCTGAGCCCACTGCTGTGGGAGACCTGGGGAGATGCTTCTCCCTTGCTGTCTAC	5821
QY	1933	rHisSerLeuProAsn---AspSerTyrMetCysArgHileuGlySerThrAlaGluGlyPhe	1952
Db	5822	GGCGGCTGCCCGGATCCAGAGAACTTCCGTGTGTAGATGAGAGAGATCCCATTCAAACC	5881
QY	1952	oleuGluHileuArgGlyTyrGlyLeuProLysAlaGlnSerGlySerValLeuSerValHileu	1972
Db	5882	TGTCTC-----CGGTCTCTGG-----CTGAACATGACAGCAAGTCACAGACCCCAAGTCC	5929
QY	1972	sSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHis-----	1990
Db	5930	CTTCTCCCGGAGATCCCTCCAGCCCTCTCGGCCATGCCAGCGAGTTCCTTCCAGCCCTCCG	5989
QY	1991	-----LeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProLysIle	2006
Db	5990	AGTGTCTGCCAGCCAGAAAGGCCCAAAAGGAGGCACTGGCACTGGAAACCTCCCAAGAT	6049
QY	2006	uProProProGlyIy-----ArgSerProLeuAlaGlnArgProLeuArgArg	2021
Db	6050	TGGCGTCGAGAGGCTCTGGGCAATCTGTGGGTCAACAGGATCACTGATCCCTCCGCG	6109
QY	2021	gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspIle	2041
Db	6110	GCAGGCCACGGGAGCAGCACTGCCTGGAC-----	6140

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Qy      2041 uleuAaGluValSerGlyProSerProProLeuAlaArgAlaTySerThrProGly 2061
           |||
Db      6141 -----GCCAGCCCGCCAGACCTCCGCGGCGAGCCTGACGACCGCTCGAGGA 6187
           |||
Qy      2061 nserSerThrGluAaGlnGlnHisSerArgSerHisSerLeuIleSerHisMet 2081
           |||
Db      6188 CACCTGACCTGAGCAGACAGCCCGCGGCTGC-----CTGGG 6226
           |||
Qy      2081 rProAlaProCyAspProGlyProGluProAsnThrGlyLySerGlyProProGluThr 2101
           |||
Db      6227 GCCGCGCGCGCTGCTCAAGAACCCGCGGCGCGCTCC-----CCGCGCGCTCG 6277
           |||
Qy      2101 gSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProProG 2121
           |||
Db      6278 CCGCGCGCTGAGCCTG-----6293
           |||
Qy      2121 yGlyGlnGluGluProProSerProArgAspLeuLySerGlySerValGluAaG 2141
           |||
Db      6294 -----CGCGCGCGCGCTCTTCAGCCTCGCGGCGCTGCGGCG-- 6332
           |||
Qy      2141 nserCyGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAlaVal 2161
           |||
Db      6333 -----CATCAGCGCAGCAGCAGCAGCGGCGG 6358
           |||
Qy      2161 lSerCyAlaAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn----- 2178
           |||
Db      6359 CTCG---ACCAAGCGCGGCTGACCCACACAGCTCCATGAGCCCTCGAGCAGAGAGG 6415
           |||
Qy      2179 -LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLySylSylLeuSerProP 2198
           |||
Db      6416 CCGCGGTGGCGCGCGCGCGCGCGCGAGAGCACTCGGAGACCTCGAGAGCCT 6475
           |||
Qy      2198 oSerIleThr-----IleAspProProGluSerGlnGlyProArgThrProProse 2215
           |||
Db      6476 CTGCGCTACCTCTCTCTTCTGCGCGCGCGC-----CCGCGCGCAGC 6517
           |||
Qy      2215 rProGlyIleCyAlaAspArgArgAlaProSerSerAspSer-----LySAs 2231
           |||
Db      6518 CCGCGGCTCAGCGCGCGCAGAGATTACAGCAGCAGCAGCAGCCTGCGCGCGCGCGC 6577
           |||
Qy      2231 pProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLySylSylAsp 2251
           |||
Db      6578 CCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6635
           |||
Qy      2251 lLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
           |||
Db      6636 -----CGCAGCAGAGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6665
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```

## RESULT 15

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US-10-425-800-3
; Sequence 3, Application US/10425800
; Publication No. US20030180866A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McElvorn, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-RG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425, 800
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404, 650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-10-425-800-3

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## Alignment Scores:

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Pred. No.: 0
Score: 5484.00
Percent Similarity: 59.93%
Best Local Similarity: 51.20%
Query Match: 46.07%
DB: 16
Gaps: 56

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US-09-611-257A-37 (1-2266) x US-10-425-800-3 (1-6855)

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Qy      31 ArgProGlyProGlySerAlaGluValAspProGlySerAlaAspSerGluAaGly 50
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Db      264 CACCCGAGACCCCGAGACCCCATCTCCCGCCAGGCTGAGAGAGAGCTCGATGGA 323
           |||
Qy      51 -----LeuProTyProAlaAlaProValAlaPhePheTyLeuSerGln 66
           |||
Db      324 GGTATCTCATGTCTCCACACCCAGACTGGCGCATATTGCTCTTCTGCGCGCAG 383
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Qy      67 AspSerArgProArgSerTrpCySylLeuArgThrValCyAspProThrPheGluArgIle 86
           |||
Db      384 ACCACAGCCCGGAACTGTGCATCAAGATGTGCAACCGGTGTGAATGTGTC 443
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Qy      87 SerMetLeuValIleLeuLeuAsnCyValThrLeuGlyMetPheArgProCySylAsp 106
           |||
Db      444 AGCATGTGTATCTCTGTAACCTGCACTGGCATGTGATACAGCCGTCGAGAC 503
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Qy      107 lLeAlaCyAspSerGlnArgCyArgIleLeuGlnAlaPheAspPheIlePheAla 126
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Db      504 ATGAGCTGCTGTCCAGCCGCTCAAGATCTTCAGATCTTGTATGATCATCTTATTC 563
           |||
Qy      127 PhePheAlaValGluMetValValLySylMetValAlaLeuGlyIlePheGlyLySylCyS 146
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Qy      147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
           |||
Db      624 TACCTGGGAGACATAGAACCCCTGTGATTTTTCATCTCATGCGAGGATGCTGAG 683
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Qy      167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValIleuArg 186
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Db      684 TACTCCCTGAGACCTTGAGAACATCAACCTGTGACCATCGCAGCCGCGCTGTAGG 743
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Qy      187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206
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Db      744 CCGCTCAACCATCAACCCCGTGCAGATCGGATCTGTGTGAACCTGTCTGTGAG 803
           |||
Qy      207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCyAspPheValPhePheIlePheGly 226
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Db      804 ACACTGCCATGTCTGGGAATGTCTGTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTT 863
           |||
Qy      227 lLeValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCySylPheLeuProGluAsn 246
           |||
Db      864 ATCATAGTGTGAGCTGTGGGCGGCTGTCTGTGTAACCGCTGTCTTCTGAGAGAAC 923
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Qy      247 PheSerLeuProLeuSerValAspLeuGluArgTyTrpGlnThrGluAsnGluAspGlu 266
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Qy      267 SerProPheIleCySylSerGlnProArgGluAsnGlyMetArgSerCyAspSerValPro 286
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Db      984 ATGCGCTTCACTGTCTCTGTGTGGGCGGAGAAATGATATGGAGCTCATGATATCCC 1043
           |||
Qy      287 ThrLeuArgIleAspGlyGlyGlyProProCySylLeu-----300
           |||
Db      1044 CCGCTCAAGAGCAG-----GGCGGTGAGTGTGCTGTCAAGAGCAGAGTCTAC 1094
           |||
Qy      301 AspTyTrpAlaValTyTrpAsnSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
           |||
Db      1095 GACTTTGTGGCGCGCGCGCGCAGACCTCAATGTCCAGCGGCTGTGTGTCAACTGAGACCGT 1154
           |||
Qy      319 TyrTyTrpThrAsnCySylSerAlaGlyGluHisAspProPheLySylAlaIleAsnPheAsp 338
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Db      1155 TACTACATGTGTGTGCGCAGCGGCGCGCAGACCCCGCAGAGAGGTGTGCACTTTGAC 1214
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Db 2826 -----CTGGAACCC-----AGTCTCCACATGGGT 2849  
 Qy 1054 ThSerThrGlyLeuGlyGlyAlaLeuGlyProAlaSerArgArgThr----- 1069  
 Db 2850 GGGACACCTAGAGTCTCTGTGGGGCTGGCGGAGCTGCCCCGAGCTCTACACAGCCGGAC 2909  
 Qy 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080  
 Db 2910 CCCATGCTGTGGCCCTGGGCTCCCGAAGAGCAGTCAATGCTCTCAAGGAGGATGAGC 2969  
 Qy 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTTPSerAlaAla 1100  
 Db 2970 TATGACACGAGCTCCCTGTCCAGCTCCCGAGAGCTCTACTACAGGCGGCGGCGGACG 3029  
 Qy 1101 SerSerThrPheSerArgArgSerSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120  
 Db 3030 GCGGCTGGGCGCAGCCGCTCCCTCCAGCTGGAAC-----AGCTCTAAG 3071  
 Qy 1121 ArgArgSerProSerGlyGlyArgArgSerLeuLeuSerGlyLys-----GlyGlnGlnLys 1139  
 Db 3072 CACAAGCCGCGCTGGGCGGAGCAGTCACTCCCTGCTCTCGGAGGCGGCGGCGGCGCC 3131  
 Qy 1140 GlnAspGlnGlnLysSerSerGlyLys-----GlnArgAlaSerProAlaGlySerAsp 1157  
 Db 3132 CGGGTCTGCGAGGTGCGCGGAGCAGAGGGCGCGCGGCGCGCACCCCTGCACACCCCA 3191  
 Qy 1158 His-----ArgHisArgGly 1162  
 Db 3192 CACGCCCCACCATTCATCAGGGGCCCATCTGGCGCACCGCCACCGCCACCGCGCGG 3251  
 Qy 1163 SerLeuGlnArgGlyAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182  
 Db 3252 ACCTGTCCCTCCGACACAGGAGTCCGTGTGACCTGCGCCAGAGCTGTGCGCGGCGGTGG 3311  
 Qy 1183 LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGlnHisGlnAspCysAsn 1200  
 Db 3312 GCCCAACCCCGCGCGCTGGAGGGCGGAGCGCGCGCGCGCGCATGAGAGTGCAT 3371  
 Qy 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeuAs 1220  
 Db 3372 GCGGAGAT-GCCAGCATGCG--CAAAAGCTTTCACCAAGATGGGCGACCGCGGGGA 3427  
 Qy 1220 PGLAspAspAlaAspAspGlnGlyAsnLeuSerGlyGlyLysArgValAlaArgAlaTrp 1240  
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 Qy 1240 eArgAlaArgLeuProAlaCysTyrLeuGlnArgAspSerTrpSerAlaTyrIlePhePr 1260  
 Db 3488 CGACGTCATATAGCCGAGCTGTGCGAGAGTCCGGAAGATGTCGTCTCTCACTTCTC 3547  
 Qy 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIlePheHisLysMetPheAspHis 1280  
 Db 3548 TCCGAGAAACAGGTTCCGGGCTGTGTGACAGCACTATATGCCCACAAACTCTTCGACTA 3607  
 Qy 1280 sValIleValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysI 1300  
 Db 3608 CGTGTCTGTGCTTCATCTTCTCACTGATCACATCCCTGAGCGCGCTCAGAT 3667  
 Qy 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320  
 Db 3668 CGAGCGCGGAGCAGACCGAATCTTCTCACCGGTCCAACTACATCTTCACGCGCAT 3727  
 Qy 1320 lPheLeuAlaGluMetThrValLysValAlaLeuGlyTyrPheCysPheGlyGlyGlnAl 1340  
 Db 3728 CTTGTGTGGCGAGATGACATTTGAAGTAGTCTCGTGGGCTGTACTTCGCGAGCGAGC 3787  
 Qy 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360  
 Db 3788 GTACCTACGACGACCTGAAAGCTGCTGATGCTTTCTTGTCTTCGTCTCATCATCA 3847  
 Qy 1360 pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe 1380

Db 3848 CATCTGTGTCTCCCTGCTCAGCCGCGGAGCCAAAGATCTTGGGGGCTCTCCAGATCTT 3907  
 Qy 1380 uArgLeuLeuArgThrThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysIle 1400  
 Db 3908 GCGGCTCTGGCGACCTTACGCGCCCTGCGTGTATCAGCCGCGGCGCGCGCTGAAAGCT 3967  
 Qy 1400 uValValGlnThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420  
 Db 3968 GGTGTGTGAGAACATCATCTCTCTCCCTCAAGCCCATGGCAATCTGTCTCTCTGCTG 4027  
 Qy 1420 sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440  
 Db 4028 TGCTTCTTCTCATATCTTTGGCATCTCGGAGATGAGCTCTTCAAGGCAAGTTCACCA 4087  
 Qy 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460  
 Db 4088 CTGTCTGGGGGTGACACCCCGAATCAACACCCCTGAGATGATGGCCCAACTA 4147  
 Qy 1460 rArgTrpValArgHisLysTyrAsnPheAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480  
 Db 4148 CCGCTGGTCCATCACAAATACAACTTGCACACCTGGGCGAGGCTGTATGTCTCTG 4207  
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 Db 4208 TGTCCTGGCATCCAGAGATGTTGGGTGAACATCATCTACATGAGACTGATCTGTGC 4267  
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 Qy 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPh 1540  
 Db 4328 CTTGTCTCATCTGTCATCTTCTTGTGTCAACAGTTTGTGGTGTGTGTGTGAAGACTT 4387  
 Qy 1540 eHisLysCysArgGlnHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1560  
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 Qy 1560 uArgArgLeuGlnLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe 1580  
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 Qy 1580 rArgPheArgLeuLeuValHisIleLeuCysThrSerHisTyrLeuAspLeuPheIleTh 1600  
 Db 4508 TCACACCCGCTGCTCATCTCCATGTCACATGTCACACCTACTGACATCTTTCATCAC 4567  
 Qy 1600 rGlyValIleGlyLeuAsnValAlaThrMetAlaMetGlnHisTyrGlnGlnProGlnI 1620  
 Db 4568 CTTTCATCATCTGCTCAACGTCGTGACATGTCCTTGAGACACTACATAGCCCACTC 4627  
 Qy 1620 eLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGlnSe 1640  
 Db 4628 CTGTGAGACAGCCCTCAAGTACTGCAACTATATGTTACACAGCTGTGTGTGCGAGGC 4687  
 Qy 1640 rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe 1660  
 Db 4688 TGTGTCTGAACCTGTGTCATTTGTGTGAGCGCTCTTCAAGACCGAGTGAACCAAGCT 4747  
 Qy 1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGlnIleGluValAs 1680  
 Db 4748 GGAACCTGGCAATGTGTACTGTGATGATGAGGATACCTTGAGAGATTCAGATCA 4807  
 Qy 1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1700  
 Db 4808 TGGCGCCCTGCCATCAATCCACACATCATCCGATCATGAGGGTTCGTGCAATGGCCG 4867  
 Qy 1700 gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetG 1720  
 Db 4868 AGTGTGAAAGCTGTGAAGATGGCCACAGGAATGCGGCGCTCTGGAACGAGTGTGCA 4927  
 Qy 1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl 1740  
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QY 1740 aaAlaLeuGlyValGluLeuPheGlyAspLeuGlyCysAspGluThrHisProCysGluGlu 1760  
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 Db 4988 TGCTCTCGGGGGTGGACCTCTTGGGAAGCTGTCTCAACGAGAGACCCGCGGAGGG 5047  
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 Db 5048 CAGGACCCGGGACGACCTTCGAGAACTTCGGCATGGCTTCTCACTCTCCAGGT 5107  
 QY 1780 lSerThrGlyAspAsnTrpAsnGlyTlleMetLysAspThrLeuArgAspCys--AspGlu 1799  
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 Db 5108 CTCACAGGGGTGACAACTGGAAACGGGATCATGAAGGACACGCTGGGAGATGCCACCA 5167  
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 Db 5168 CAGCGCCAGCTGTCTGAGCAGCTGCACTTTGTGTGCGCTGTACTCTGTAGAGCTTCGT 5227  
 QY 1817 lLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu 1837  
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 Db 5228 GCTCACCGGCGCAGTTGCTGTCTCAACGTGTGTGTGGCTGTGTCTCATGAAGCACTGGA 5287  
 QY 1837 uGluSerAsnLysGlnAlaLysGluGluAlaGluLeuGluValAglyLeuGluGluMet 1857  
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 Db 5288 CGACACCAACAAGAGAGCGCGAGAGAGCGCGAGATGGAATGCCAGCTGAGCTGAGAT 5347  
 QY 1857 t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlu 1876  
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 Db 5348 GGGCCATGGCTGTGGCTGTGGCTGGCCGAGGCTGCTACCGGCTCCCGGGGAGCC--CTGTG 5404  
 QY 1876 yValGluGlyProAsp----- 1881  
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 Db 5405 C---CGAGGGCGGGAGGGGGCGGGCGGGCGGACACCGAGGGGGCTTGTGGCGGGG 5461  
 QY 1882 -----SerPro----- 1883  
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 Db 5462 CTGCTACTGCGCTGCCAGAGAACTGTGGCTGAGCAGCGTCTTTAATCATCAAGGA 5521  
 QY 1884 -----AspSerProLysProGluValLeuHis----- 1892  
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 Db 5522 CTCCTTGAAGGGGAGCTGACATCATCGAACACTGTGGGCTCCATCTTCCACCACTA 5581  
 QY 1893 -----ProAlaAla----- 1895  
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 Db 5582 CTCCTGCGCTGGCGGCTGCAAGAGTGTACACGACGACGAAGAGGTGAGCTGGCTGA 5641  
 QY 1896 -----HisAlaArgSerAlaSer-----HisPh 1903  
 |||||  
 Db 5642 GACGAGGCGCTTCTCCCTGAACTCAGACAGTCTGCTCATCTGCTGGGTGACGACCT 5701  
 QY 1903 eSerLeuGlnHisProThrMetGlnPro-----HisProThrGluLeuPr 1918  
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 Db 5702 GAGTCTCGAGGACCCGACAGCTGCGCCACCTGCGCCGACCAAGAGAGAGGTGAGCTGGA 5761  
 QY 1918 ogLysProAspLeuLeuThrValArgLysSerGly-----ValSerArgTh 1933  
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 Db 5762 CCCACCTGAGCCGATCGTGTGGAGACCTGGGAGATGCTTCTTCCCTGCTCTTAC 5821  
 QY 1933 rHisSerLeuProAsn--AspSerTrpMetCysArgHisGlySerThrAlaGluGlyPr 1952  
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 Db 5822 GGGCGTCTGCGCCGAGATCCAGAACTTCTGTGTGAGATGAGAGAGATCCCATTAACCC 5881  
 QY 1952 olLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHi 1972  
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 Db 5882 TGTC-----CGGTCTCGG-----CTGAACAATGACAGCATCAAGACCCCAAGTCC 5929  
 QY 1972 sSerGlnProAlaAspThrSerTrpLleLeuGlnLeuProLysAspAlaProHis----- 1990  
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 Db 5930 CTCTCTCCCGGAGTGGCTTCAAGCTCTCTGCTGCCATGCGGAGGTGTCTTCCACCTGG 5989  
 QY 1991 -----LeuLeuGlnProHisSerAlaProThrTrpGlyThrLleProLysLle 2006  
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 Db 5990 AGTGTCTGACGACCAAGAAAGGCCCAAGAAAGGCGACTGCGACTGGAACCTTCCCAAGAT 6049

QY 2006 uProProGluGly-----ArgSerProLeuAlaGlnArgProLeuArgAr 2021  
 |||||  
 Db 6050 TGCGCTGACGGGCTCTTGGGATCTCTGCGTACCTACCAAGGATCAACTTACCTCTCCG 6109  
 QY 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe 2041  
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 Db 6110 GCAGGCGCACCGGAGCGACACGTCGCTGAC----- 6140  
 QY 2041 uLeuAlaGluValSerGlyProLeuAspThrProLeuAlaArgAlaTrpSerPheTrpGly 2061  
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 Db 6141 -----GCCACCCCGACAGCTCCGCGGCGAGCTGACAGACCAAGCTTGAAGA 6187  
 QY 2061 nSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetTh 2081  
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 Db 6188 CAGCTTGACCTCGACGACGACGCGCGGCGTGGC-----CTGGG 6226  
 QY 2081 rProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThrAr 2101  
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 Db 6227 GCGGCGCGGCTGCTCCAGAGACCCGCGGCGGCGCTGCC-----CCGCGCGCTCG 6277  
 QY 2101 gSerSerLeuGluLeuAspThrGlnLeuSerTrpLleSerGlyAspLeuLeuProProGlu 2121  
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 Db 6278 CCGCGCGCTGAGCTG----- 6293  
 QY 2121 yGlyGlnGluGluProProSerProArgAspLeuLysCysTrpSerValGluAlaGlu 2141  
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 Db 6294 -----CGGCGCGGGGCTCTTCAAGCTGCGGGGGGCTGGCGGCGG-- 6332  
 QY 2141 nSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAlaVa 2161  
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 Db 6333 -----CATCAGCGCGACCGACAGCGCGGGG 6358  
 QY 2161 lSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn----- 2178  
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 Db 6359 CTC--ACAGACCGGGGCTGCACCACCAAGACTTCAATGAACTCTGTGAGACGAGAGGG 6415  
 QY 2179 -LeuGlyGlnGlnProLeuGlyGlyProGlySerArgProLysLysLeuSerProPr 2198  
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 Db 6416 CCGCGGTGGCGGGGCGGGGCGGGGCGGGGAGCGAGCACTCGAGACCTTCAAGAGCT 6475  
 QY 2198 oSerLleThr-----lLeAspProProGluSerGlnGlyProArgThrProProSe 2215  
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 Db 6476 CTCGCTCACTCTCTTCTGCGCCGCGCCG-----CCGCGCGCGAGC 6517  
 QY 2215 rProGlyLleCysLeuArgArgArgAlaProSerSerAspSer-----LysAs 2231  
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 Db 6518 CCCGAGCTTCAAGCGCCGAGAGATTCAAGCAACGACAGCTGGCGCGCGCGCGCGG 6577  
 QY 2231 pProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspVa 2251  
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 Db 6578 CCCCAAGCGCGCGCGCTGGGCCCAAGGCTGGCGCGGAGCCCTGTGTGGGCGGAGAC-- 6635  
 QY 2251 lLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266  
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 Db 6636 -----CGACGCAAGAGACCCCGCGCGCGGAGCAG 6665

Search completed: September 19, 2005, 17:30:37  
 Job time : 3453.66 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 18, 2005, 17:44:07 ; Search time 14254.4 Seconds  
(without alignments)  
6050.997 Million cell updates/sec

Title: US-09-611-257a-37  
Perfect score: 11904  
Sequence: 1 MDEEDDQAGAESGQPRSFM.....PKKDVLSLGLSSDPADLDP 2266

Scoring table:  
BLASTSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cgm2\_1/USPTO.spool/US09611257/runat.15092005.134301.25185/app.query.fasta\_1.4878  
-DB=EST -QPM=faetacp -SUFFIX=rec -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=DIOSUM62 -TRANS=human40.cdi -LIST=45  
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-USER=US09611257 @CGN 1.1 23209 @runat.15092005.134301.25185 -NCPU=6 -ICPU=3  
-NO\_MMAP -IARGOUTDIR -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -MAXN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_ncc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gesl1:\*  
9: gb\_gesl2:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1703.5	14.3	6636	3	BC043482 Mus muscu
2	1683.5	14.1	6035	3	BC051413 Mus muscu
3	1382.5	11.6	1076	4	BM479323 AGENCOURT
4	1314.5	11.0	879	7	CF548698 AGENCOURT
5	1290.5	10.8	5666	9	AY416501 Mus muscu
6	1281.5	10.6	1064	4	BM451648 AGENCOURT
7	1257	10.3	793	6	CA319705 UI-M-FW0
8	1223.5	10.3	5943	9	AY416499 Homo sapi
9	1216	10.2	711	5	BM950154 UI-M-EH0P

10	1215.5	10.2	771	5	BU058818 UI-M-FR0-
11	1215.5	10.2	990	4	BI905383 603167426
12	1212.5	10.2	784	7	CF742232 UI-M-HB0-
13	1187.5	10.0	810	5	BU709095 UI-M-BW0-
14	1185	10.0	736	4	BI160856 602864778
15	1183	9.9	939	4	BI736618 603361089
16	1178	9.9	973	2	BF783704 602109506
17	1174	9.9	4675	3	AK083220 Mus muscu
18	1140.5	9.6	777	6	CA945335 UI-M-FD0-
19	1136	9.5	6822	9	AY406058 Mus muscu
20	1132	9.5	715	7	CF745071 UI-M-GV0-
21	1130	9.5	676	4	BI917129 603181539
22	1130	9.5	843	5	BO180375 UI-M-EX0-
23	1129.5	9.5	6813	9	AY406056 Homo sapi
24	1116.5	9.4	770	5	BU708898 UI-M-FI0-
25	1107.5	9.3	717	5	BU704267 UI-M-FD0-
26	1104	9.3	952	7	CF584866 AGENCOURT
27	1103.5	9.3	845	6	CA327685 UI-M-FY0-
28	1101	9.2	707	7	CN216936 RJAO02G02
29	1092.5	9.2	918	6	CD557381 AGENCOURT
30	1084	9.1	647	6	CB518482 UI-M-GH0-
31	1081	9.1	693	5	BM949227 UI-M-EG0P
32	1074	9.0	708	5	BO179746 UI-M-BW0-
33	1068.5	9.0	710	7	CR576255 CR576255
34	1065.5	9.0	727	5	BO443110 UI-M-EV0-
35	1058.5	8.9	731	7	CN534628 UI-M-HS0-
36	1055.5	8.9	803	6	CB245297 UI-M-FY0-
37	1051	8.8	773	4	BI249987 602995228
38	1025	8.6	640	6	CB056097 NISC J112
39	1024	8.6	588	2	BE781203 601469131
40	1018.5	8.6	684	5	BU262763 603374462
41	1012	8.5	726	6	BQ042267 UI-M-RD0-
42	1012	8.5	772	6	CB524438 UI-M-FY0-
43	1006	8.5	707	6	BU612176 UI-M-BW0-
44	995	8.4	1134	2	BF179657 601806048
45	993	8.3	957	4	BG298038 602396253

## ALIGNMENTS

RESULT 1	BC043482	6636 bp	mRNA	linear	HTC 19-NOV-2003
LOCUS	BC043482		Mus musculus	calcium channel, voltage-dependent, alpha 1f subunit,	
DEFINITION	BC043482		mRNA (CDNA clone IMAGE:536391), containing frame-shift errors.		
ACCESSION	BC043482.1	GI:28175783			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
1 (bases 1 to 6636)					
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,					
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schlier, G.D.,					
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,					
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,					
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,					
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,					
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,					
Carninci, P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J.,					
Adams, R.D., Mullaly, S.J., Bosak, S.A., McGowan, P.J.,					
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,					
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huiyik, S.W.,					
Vallilon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,					
Pahy, J., Helton, E., Keteeman, M., Madan, A., Rodriguez, S.,					
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,					
Dickson, M.C., Blakesley, R.W., Touchman, J.W., Green, E.D.,					
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E.,					
Schmech, A., Schein, J.E., Jones, S.J., and Marra, M.A.					
Generation and initial analysis of more than 15,000 full-length					
human and mouse cDNA sequences					

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
MEDLINE 22388257  
PUBMED 12477932  
REFERENCE 2 (bases 1 to 6636)  
AUTHORS Strausberg, R.  
TITLE Direct Substitution  
JOURNAL Submitted (09-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Offices, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
REMARK Contact: MGC help desk  
COMMENT Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
[info@bgsc.bc.ca](mailto:info@bgsc.bc.ca)  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeay, Steven Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalusz, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Series: IRAX Plate: 86 Row: o Column: 1  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9624972  
This clone has the following problem: frame shifted.  
Location/Qualifiers  
FEATURES  
source  
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/db\_xref="taxon:10090"  
/clone="IMAGE:5369391"  
/cissue\_type="Eye, retina, mouse strain C57BL/6"  
/clone\_lib="NIH MGC\_94"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORTc"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.4e-107 Length: 6636  
Score: 1703.50 Matches: 665  
Percent Similarity: 38.49% Conservative: 331  
Best Local Similarity: 25.70% Mismatches: 805  
Query Match: 14.31% Indels: 792  
DB: 3 Gaps: 98  
US-09-611-257a-37 (1-2266) x BC043482 (1-6636)  
QY 1 MetAaSpGluGluGluAaSpGlyAlaGlyAlaGluGluSerGlyInProAArgSerPheMet 20  
DB 3 ATGTCGGAATCTGCAAGTCGGGAAGATACAAACCCAGAGCCCAAGTCACACCAAT----- 56  
QY 21 ArgLeuAaAaSpLeuSerGlyAlaGlyGlyArgProGlyPro-----GlySerAlaGlu 38  
DB 57 -----GGGACTGGGCGCTGGGCGCTGAATGGGGGCTCTGTCT 92  
QY 39 LysAaSPPro-----GlySerAlaAaSPSerGluAlaGluGlyLeuProTyrrPro----- 54  
DB 93 GGGCGCTCCAACTGTGGGACTATACACAGGGGGCGCTCAGGGCTGGGAGACCCCAAGAAGA 152  
QY 55 -----AlaLeuAlaProValValPhePheTyrrLeu 64  
DB 153 AGGACCCAGACAAACAACAACAAGACTGTGGCGGTGGCC----- 191  
QY 65 SerGlnAaSPSerArgProAArgSerTyrrCySLeuAArgThrValCyAaSPPro----- 81

DB 192 AGTGTCTAGAGATATCATCTCGAGCGGCTCTTGTGCTCACCTTACTATATCCATTGTGCG 251  
QY 82 -----Trp-----PheGluAArgIleSerMetLeuValIleLeu 92  
DB 252 TCCTTCATCAGCATTTGTAGAGAGAGCCCTTGTATATTCATCTCCTGACATCTTT 311  
QY 93 LeuAaSPValThrLeuGlyMetPheAArgProCys-----GluAaSP 106  
DB 312 GCCAATCGGTGAGCATTTGGGGGTATATTCCTTCTCTGAGAGACTCCACACTGCT 371  
QY 106 ----- 106  
DB 372 AACCAACTTGTGAGGTCTAACCCCATCCCAACAGACTGCAGTTCCCTTAGAGCTA 431  
QY 107 ---IleAlaCyAaSPSerGlnAArg----- 113  
DB 432 CAGATAAACCAACCCAGCCAGACCCACCCCTCGGGGCTTACCTTACCTTGTGT 491  
QY 114 -----Cys--- 114  
DB 492 CCTGCCAAAGCAACCTTAACTGTGCTTACGACTCACCCAGGGGTGTACCTGCC 551  
QY 115 ArgIle-LeuGlnAlaPheAaSP-----AaSP 123  
DB 552 GAAATTAATTCAGAGCGCTTACAGCCCGCCCTGCTCGCCCTCAGAGAAAGGTAGATA 611  
QY 123 eIlePhe---AlaPhePheAlaValGluMetValValIysMetValAlaLeuGly---Il 141  
DB 612 CGTGTCTCTGTGATTTTACCGTGTGAGACAGTGTCAAGATCTGTAAGCTTGTGGCTGT 671  
QY 141 ePheGlyIysIysCysTyrrLeuGlyAaSPThrTryAaSPArgLeuAaSPPheIleValIl 161  
DB 672 GTCATATCCAGAGCGCTTATTCGCAATGGCTGGAACCTGCTGACTTATCATGTGTGT 731  
QY 161 eAlaGlyMetLeuGluTyrrSerLeuAaSPLeu----- 171  
DB 732 GGTGGGCGTTCACAGCGTGTGCTGGAACAAGACTGGGCGGCCAGAGATGCCCGCA 791  
QY 172 -----GlnAaSPSerPheSerAlaValArgThrValArgValLeuA 186  
DB 792 TACTGAGAGAAAGCCAGAGGCTTGATGTAAAGCACTGGGCGCATTTAGGTCACG 851  
QY 186 pThrLeuPrgAlaIleAaAArgValProSerMetArgIleLeuValThrLeuLeuAa 206  
DB 852 ACCTTAAGGCTAGTGTCTGGGCTCCAGATCTGCACATAGTCTCAATTTCATATGA 911  
QY 206 pThrLeuProMetLeuGlyAaSPValLeuLeuLeuCysPhePheValPhePheIlePheG 226  
DB 912 GGGCGTTGTGGCGCGTGCACATTCGCCCTGTGTGTCCTTCGTATATCATTTAGCG 971  
QY 226 yIleValGlyValGluLeuTrrPalAGlyLeuLeuAArgAaSPCysPheLeuProGluAa 246  
DB 972 CATCATCGGACTCGACTATTCCTCGAGCAATGACAAACATCACTTCTTC----- 1023  
QY 246 nPheSerLeuProLeuSerValAaSPLeuGluAArgTyrrTyrrGlnThrGluAaSPGl 266  
DB 1024 -----CTGGGATCTGATATGAA-----GCAAGAGAGAGACC 1055  
QY 266 uSerProPheIleCysSerGlnProAArgLysnGlyMetAArgSerCysAArgSerValPr 286  
DB 1056 ATCACCT-----TGTGACTT----- 1071  
QY 286 oThrLeuAArgIyaSPGlyGlyGlyProProCysGlyLeuAaSPTyrrGluAlaTyrrAa 306  
DB 1072 -----TCTGGCTCTGGGCGTTCAGACACATGAAAC----- 1101  
QY 306 nSerSerSerAaSPThrThrCysValAaSPTrpAaSPGlnTyrrThrAaSPSerAlaG 326  
DB 1102 -----CATACGAGTGGCGGGCG 1121  
QY 326 yGluHisAaSPProPheIysGlyAlaIleAaSPPheAaSPAnIleGlyTyrrAlaTrpIleAl 346



Db 1122 CTGGCCAGACCCAGCGTGCATCAGAACTTGCAATTTTCTTCCATGCTAAC 1181  
 Qy 346 ailepeginvalilethleugluglytrpvalaspilemettyrphervalmetaspa 366  
 Db 1182 TGTGTTCCAGTGTATTATCATGAGAGCGTGCAGACGCTCTACTCATGATGACGATGC 1241  
 Qy 366 ahlsasrpe---tyrasnphelietyrphelleuleullelevalglyserperph 385  
 Db 1242 CATGGGGTATAGACGTGCTGGGGTACTTGTGAGCGCTTGTCATCTTTGGGCTCTTCT 1301  
 Qy 385 emetileanleucyaleuvalvallealathnglnpheserghluthrlysgln--- 403  
 Db 1302 TGCTCTCAACCTTGCTGCTGAGGCTTACGCGGGAGCTTCTCAAGGAAAGAGAAAGC 1361  
 Qy 404 -----Argluserglnleumecarglgnargva 414  
 Db 1362 AAAAGCAGAGTGACTTTGAGAAAGCTTGGGAGAACGACAGATGGAAAGACCTTCG 1421  
 Qy 414 larpheleu-----Serasn1 420  
 Db 1422 GGGCTACCTGAGCTGATCACAAGCTGAGAGTTAGACCTTCATGACCTCAGTAGA 1481  
 Qy 420 aserthleualaserpheserghluproglysercytyrghluleuleulystyle 440  
 Db 1482 CGGCAACTTGGCTTCTTCTGTAAGAGGA----- 1512  
 Qy 440 uvaltyrleleuarglyalaalargargleualaglnvalserarglaalaglyva 460  
 Db 1513 -----CGGGCGGGCCA 1523  
 Qy 460 larpvalglyleuleuserproalaproleuglyly-----Glnghluth 476  
 Db 1524 TCGTAGGCAACTCAATCTGGCCCCCTTATCTTACCTTGAGCCCTGATGGCTCTCTG 1583  
 Qy 476 rgluproseserCyseraserghisargargleuservalhishisleuvalh1 496  
 Db 1584 AAACCCAGACCAAGCCTGC-----AGCCACCTTAGGCTTTGGCCCAAACT--- 1629  
 Qy 496 shishishishishishishishityrhishleuglyasnghlythreularglaProAr 516  
 Db 1630 -----GANTCAGGG-----CACAG 1643  
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 Db 1686 TTGTCCCTAGATTGACCTTAATTTGCGCACCAAG-----CACTCT-- 1728  
 Qy 556 etyrhishalaaarCyhishleugluprovalargCyaglnalaproproargserpr 576  
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 Qy 576 oserglualaserglyargthryvalgly--serglyysvaltyrpro-----ThVal 593  
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 Qy 594 Hisheserproproprogluithleulysglulysalaleuvalgluvalalalaser 613  
 Db 1824 CACACACT-CCACCAGACGACG-----CCAGCC 1852  
 Qy 614 serglyproprothleuthrserleuasnileproproglyprotyrsersermetchis 633  
 Db 1853 TCCACAGCAAGTGAACACTGC-TCATATGACAGACACCCCTGAGAT----- 1896  
 Qy 634 lyaleuleugluthrghlnserthrglyalacyglinserserCylyslleserSerpro 653  
 Db 1897 -----GAGGATGAAGAGAGGAGCGCATGGCTAGCTGTACACGCTGCTTAAACAG 1947  
 Qy 654 cyaleuleuysalaaasrserglyalacyseglyproasrserCyprotyrCyalaalargla 673  
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 Db 1987 AACCGGGGT----- 1995  
 Qy 694 tyrgluphethrghlnaspaalaglnhiserasrleuargasrprohiserargargln 713  
 Db 1996 -----CTCCG-----GCAGGCTGCCGC 2013  
 Qy 714 ArgserleuglyproaspaalagluoproserSerValleualpheThpargleuleCy 733  
 Db 2014 CGGGCGGTGACAGCCAACGCC-----TGCTACTCG----- 2043  
 Qy 734 asrthrphearglysllevalasrserlytyrphleglyargglyleuethlealeale 753  
 Db 2044 -----GCTGTACTGTGCTGTC 2061  
 Qy 754 leuvalasnThrleusermetglyilegityrhishleugluproglyluleuthraan 773  
 Db 2062 TTCTCAACACGTTGACATAGCTTCAGACACACATGGGCAAGCTTTGGCTCACCCAG 2121  
 Qy 774 Alaleugluilesasrasnilevalpethrserleuphealaleugluleuleulys 793  
 Db 2122 ACCAAGAGATGCCAACAAGTTCTGCTGCTGCTCTTCACTGAGATGCTCTCAAA 2181  
 Qy 794 leuleuvaltyrglyprophleglytyrilelyasnpProtyrAsnlelpeasr----- 811  
 Db 2182 CTGTACGGCGCTGGCCCCCTCTGTACGTTGCTCTTTTCAACCGCTTTGACTGCTTC 2241  
 Qy 812 -----glyValilevalilleservalITrgluilevalglylnglnglyly 828  
 Db 2242 GTGCTGTGGGGGATCTCTAAGAAACACTTTGTGTGAGGTGGGGCCATGACGCTTT 2301  
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 Qy 929 leuTyrasnglywethlaser-----ThserSertrpalaaleu 942  
 Db 2593 ATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2652  
 Qy 943 TyrPheilealeuumeetThrpheglyasnTyValleupheasnleuvalalale 962  
 Db 2653 TATTTCAATCACTCTTCACTGTGGCACTATCATCTGTGAACGTTTCTTGCCATT 2712  
 Qy 963 leuvalgluglypheglnalaglugluileserlyahrglunasralsasrglyglnleu 982  
 Db 2713 GCGGTGATTAACCTTACGAC----- 2733  
 Qy 983 serCyaleileglnleuprovalasrserglnglyasrpalasnyserSerghluserglu 1002  
 Db 2734 -----GGGATGACGACACTGCAAA----- 2754  
 Qy 1003 proasrpheserProserleuasnarglyasrarglyalysCyaleualaleu 1022  
 Db 2755 -----GACAGAGGAGAGAGAGAGAG----- 2775



Db 4554 GGAACATTCATCAAGCTTCCAGGCTTCCCTCATGTG-----GCACTTCTCATAG 4604  
 Qy 1733 eteLeuPhePheIlePheAlaIleuGlyValIleuPheGlyAspLeuGlyCys- 1752  
 Db 4605 CAAATGATATCTTCATCATGAGTCATGTCATGCAATGAGATGTTGGCAAGTGGCTCTTC 4664  
 Qy 1753 --AapGluThrHisProCysGlyLeuGlyValArgHisAlaThrPheArgAspNheGlyM 1772  
 Db 4665 AGAAGCGCAGCAGC-----ATTAATCCAAACAAACAAATTTCCAGACCTTCCGC 4712  
 Qy 1772 etAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnThrPheAsnGlyIleMetLysA 1792  
 Db 4713 AGGCTGCTGCTCTTCTGTCTGAGGTGCTCACTGCTGAGGCTGGCAAGATTAAGCTAG 4772  
 Qy 1792 sPThrLeu-----ArgAspCysAspGlnGlySer-----T 1802  
 Db 4773 CCAAGCTTCCAGGAATTCAGATGTGACCTGTGACTTGGCCCAAGGAGAAATTTA 4832  
 Qy 1802 hrcYsTyraNthrValIleSerProIleTyPheValSerPheValLeuThrAlaGlnP 1822  
 Db 4833 CCTGT--GGTAGAGATTGTTGCCATCGCTCACTTCATCAGCTCTTATGCTGTGCTCT 4889  
 Qy 1822 heValLeuValAsnValValIleAlaValLeuMet----- 1833  
 Db 4890 TCCGATTATTAATCTCTTGTGCTGTATCATGATTAACCTTGATTAACCTTAACCAAG 4949  
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 Db 4950 ATTGCTATTCCTGGAGACCCCAACCACTTGATGAATTC--AAGAGATCTGCTGAT 5006  
 Qy 1847 laGluLeuGlnAlaGluLeuGlnLeuLys-----MetLysThrL 1860  
 Db 5007 ATGACCCCGGAGCCAAAGGCGCATCAAGCACTTGATGTGTTGCCCTGCTGAGACGA 5066  
 Qy 1860 euserProGln-----ProHisSer----- 1866  
 Db 5067 TCCAGCCCATTTGGATTTGGAAAGCTATGCCCACACCGAGTGGCTGCAGAGACTCG 5126  
 Qy 1867 -----ProLeuGlySerProPhe-----LeuT 1874  
 Db 5127 TGGCAATGATGTGCTCCCTCACTCAGCAG-TCGAACAGTACATTCACACGCTACTT 5185  
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 Db 5186 GCCCTGTGCGGACATCCCTGAAGATCAAGACAGAAAGGAACTGGATCAAGCCCAACAG 5245  
 Qy 1894 laAla-----HisAlaArgSerAlaSerHisPheSerLeuGlu----- 1906  
 Db 5246 GAGCTTCCGATGTATCAAAAAGATCTGAAAGCGGATTAACAGAAATTTGTTGATGAG 5305  
 Qy 1907 --HisProThrMetGln-----ProH 1913  
 Db 5306 GTCTATCCCTCTCCCGATGAGGAGAGAGTCACTGGGAAATTTCTATGCCACACTTCTCT 5365  
 Qy 1913 isPProthGlnLeuProGlyProAspLeuThrValArgLysSerGlyValAsnArgT 1933  
 Db 5366 ATCCAAAGTATATT-----CCGAAATTTCCGAGAAAGAAAGAAAGGCGCTACTGAGA 5419  
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 Db 5420 AGAAGAGC--CCCAACAAAGACATCTCTGCTCCAGGCTGTGATTAAGAG--CCTG 5473  
 Qy 1953 eu-----GlyHisArgGlyT 1958  
 Db 5474 CAGAGCTTGGGTCTCTGAGATCCGTCAGACCTCTACCTATGACACTGAGGAAGAAAGAGA 5533  
 Qy 1958 rPgLyLeuProLysAlaGlnSerGly-----SerV 1968  
 Db 5534 GAGGAAGAGCAGTGGGTGTCAGAGGCTGAGAGAAAGAAAGCTGAGAACCAACCAAGCA 5593  
 Qy 1968 alleuSerValHisSerGlnProAlaAspThrSerTy-----Ile- 1981  
 Db 5594 TACAAGACTCTCATGACTCCACGCCCAATCTGATGAGAACTTAGATTTCCGATGCT 5653

Qy 1982 LeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGly 2001  
 Db 5654 CTACCTGTTAAGAGAAACTTCCAGATTCCTTCAACTGGGCGGATGATGATGAG 5713  
 Qy 2002 ThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArg 2021  
 Db 5714 CTGGCTCCCACTCCAGGACGCCAAGTGTGATACAGGCTGGCTCCCAACCAACAGAGA 5773  
 Qy 2022 GlnAlaAlaIle-----ArgThrAspSerLeuAspValGlnGlyLeu 2035  
 Db 5774 AGCTCGGGGTTTTCATGTTCACTATCCCGAAAGAAAGATTTACGCTCAAGGGAAC 5833  
 Qy 2036 GlySerArgGlu-----AspLeuLeu 2042  
 Db 5834 CAAAGGACAGACATACAGATGAGAAAGAAAGTCCCTGACTGACCTCTGCTGAGAT 5893  
 Qy 2043 AlaGlnValSerGlyProSerProProLeuAlaArgAlaTySerPheTrpGlyGlnSer 2062  
 Db 5894 GAGACAGCGGAGACTCTTCGAACCAAGTCTTTTACCA--CTTCACCTG----- 5941  
 Qy 2063 SerThrGlnAlaGlnHisSerArgSerHisSerLysIleSerLysHisMetThrPro 2082  
 Db 5942 -----TCCAGCAACACGTAACCGGACCATGTGCGACAGCGGACGTTGCTGCC 5992  
 Qy 2083 ProAlaProCysProGlyProGlyProAsnTrpGlyLysGlyProProGluThrArgSer 2102  
 Db 5993 CCCACCTGCA-----GTTCCGAAGCCCTTCCTACCATTCAG 6031  
 Qy 2103 SerLeuGlnLeuAspThrGlnLeuSerTrpIleSerGlyAspLeuLeuProProGly 2121  
 Db 6032 TGTCTGCAGACGCAAGGCGAGTTGTGA-----GATTACTTATCCAGGACCC 6079  
 Qy 2122 -----GlyGlnGlnGluProProSerProArgAspLeuLysCysTySerVal 2138  
 Db 6080 TACCATCTGAGAGGACCTCAGACCAAGC----- 6109  
 Qy 2139 GlnAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlnAlaArgHisSer 2158  
 Db 6110 -----AGGGCTCAGGTTCTCTGGACAGCCCTCTCGAAAGGGTGA 6151  
 Qy 2159 IleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn 2178  
 Db 6152 CTGCTATATACC-----CCCTGTGTTGGTGAAGAAATCTACA 6190  
 Qy 2179 LeuGlyGlyInProLeuGlyGlyProGlySerArgProLysValLysLeuSerProPro 2198  
 Db 6191 GTGGGTGAAGATACCTTGC-----AAACTTGGCGGCCCA 6226  
 Qy 2199 SerIleThr-----IleAspProProGlnSerGlnGlyProAspThrProProSer 2215  
 Db 6227 CTGCGTACCTTCACTGCTGTGCAAGTGCCTGG--AGCTCATCCGAATCCAGCAAGCGCA 6285  
 Qy 2216 ProGlyTleCys-----LeuArgArgAlaProSer 2226  
 Db 6286 GAGGGAGAGTGTGACAGATTGTGAGAGCTGTGCTCATCTCCAGAG-----CTTAGG 6339  
 Qy 2227 SerAspSerLysAspProLeuAlaSerGlyPro-----ProAspSerMetAlaAla 2243  
 Db 6340 TCTCTTTGCCCAAGACCAAGATTTGTGGCTCGGCCAAGCAGAGATTCAGATGCATG 6399  
 Qy 2244 SerProSerPro 2247  
 Db 6400 TCACCTGACCT 6411

RESULT 2  
 BC051413 6035 bp mRNA linear HTC 19-NOV-2003  
 LOCUS  
 DEFINITION  
 Mus musculus calcium channel, voltage-dependent, alpha 1F subunit,  
 mRNA (CDNA clone IMAGE:6493332), containing frame-shift errors.  
 ACCESSION  
 BC051413.1 GI:30802106  
 KEYWORDS  
 HTC.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 6035)  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, K.H., Schefer, C.F., Bhat, N.K., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Mak, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Statchenko, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wexler, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hultky, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E., Schermer, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE human and mouse cDNA sequences  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16699-16903 (2002)  
MEDLINE 22388257  
PUBMED 12477932

REFERENCE 2 (bases 1 to 6035)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [gcgabs-remail.nih.gov](mailto:gcgabs-remail.nih.gov)

Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@ngri.nih.gov](mailto:nisc_mgc@ngri.nih.gov)  
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granter, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Madeno, Q.L., Mastaglio, C., Maskeri, B., Maestrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantirip, S., Thomas, P.J., Touchman, J.W., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Series: IRK Plate: 108 Row: O Column: 13  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9624972  
This clone has the following problem: frame shifted.

FEATURES  
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/db\_xref="taxon:10090"  
/clone="IMAGE:6493332"  
/issue\_type="Eye, retina, mouse strain C57Bl/6"  
/clone\_id="NIH\_MGC\_94"  
/lab\_host="DH10B"  
/note="Vector: PCMV-SPORT6"

## Alignment Scores:

Prod. No.: 1.99e-105 Length: 6035  
Score: 1683.50 Matches: 616  
Percent Similarity: 38.15% Conservative: 331  
Best Local Similarity: 24.82% Mismatches: 752  
Query Match: 14.14% Indels: 786  
DB: 3 Gaps: 86

US-09-611-257a-37 (1-2266) x BC051413 (1-6035)

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QY 21 ArgLeuAanPleuSerGlyAlaGlyGlyArgProGlyPro-----GlySerLaglu 38  
DB 72 -----GGAGCTGGCCCTGGCCCTGAATGGGGCTCTGCTCT 107  
QY 39 LysAapPro-----GlySerLAspSerGluAgluGluGlyLeuProTyPro----- 54  
DB 108 GGGCTTCACATCTGGGAGCATGATCCAGCGGGGCTGAGGCTTGGGAGCCCAAGAGA 167  
QY 55 -----AlaIeuAlaProValValPhePheTyLeu 64  
DB 168 AGGACCCAGACCAACAAACAAAGACTGTGGCGGTGGCC----- 206  
QY 65 SerGlnAapSerArgProArgSerTrpCysLeuArgThrValCysAsnPro----- 81  
DB 207 AGTGCTCAGAGATCAGCTCGAGCGCTTCTTGCTCCTCACCCTTACTATCCATTCCTCGG 266  
QY 82 -----Trp-----PheGluAglIserMetLeuValIleLeu 92  
DB 267 TCCGTCATCAGCATGTGATGAGTGAAGCTTTTGTATATTCATCTCTCTGCAATCTTT 326  
QY 93 LeuAanCysValThrLeuGlyMetPheArgProCysGluAapIleAlaCysAapSerGln 112  
DB 327 GCCAATCGGTGGCAATTCGGGGGTATATATCCCTTCCCTGAGGAGACTCCAACTCTCT 386  
QY 113 ArgCysArgIleLeuGlnAlaPheAapPheIlePhe-----AlaPhePheAlaValGlu 131  
DB 387 AACCAACATTCGAAACAGGTA-----GAATACGTTCTCGTGATTTTCCGTTGGAG 440  
QY 132 MetValValIysMetValAlaLeuGly--IlePheGlyLysCysTyLeuGlyAap 150  
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QY 151 ThrTrpAanArgLeuAapPhePheIleValIleAlaGlyMetLeuGluTySerLeuAap 170  
DB 501 GCGTGGAACTGCTGACATTCATCGTCGTGGGCTGTTCCAGCGTGTCTGGAA 560  
QY 171 Leu-----GluAanValSer 175  
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QY 256 GluArgTyTrpGlnThrGluAanGluAapGluSerProPheIleCysSerGlnProArg 275  
DB 840 GAA-----GCAGAGAGAGAGCCATCCT----- 863

OY	276	GLU	ANG	LEU	ME	T	ARG	SER	VAL	PRO	THR	LEU	ARG	GLY	GLY	GLY	295					
DB	864	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	884					
OY	296	PRO	PRO	CYS	GLY	LEU	ASP	TYR	GLU	ALA	LEU	TYR	ASN	SER	SER	ASN	THR	CYS	VAL	ASN	315	
DB	885	CGT	T	C	A	T	C	A	C	T	G	A	C	T	G	A	C	T	G	A	C	902
OY	316	TRP	ASN	GLY	TYR	THR	ASN	CYS	SER	ALA	GLY	LEU	HI	ASN	PRO	PHENY	GLY	ALA	LE	335		
DB	903	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	950		
OY	336	ASN	PHEN	ASN	LEU	LEU	TYR	ALA	LEU	TRP	LEU	ALA	LEU	PHEN	GLY	VAL	LEU	THR	LEU	GLY	355	
DB	951	AAC	TTC	G	CA	A	AT	T	T	T	T	T	T	T	T	T	T	T	T	T	1010	
OY	356	TRP	VAL	ASP	LEU	ME	TYR	PHEN	VAL	ME	ASN	ALA	HI	SER	PHEN	---	TYR	ASN	PHEN	LEU	TYR	374
DB	1011	TGG	A	C	A	G	A	G	C	T	T	A	C	T	G	A	T	G	A	T	G	1070
OY	375	PHEN	LEU	LEU	LEU	LEU	LEU	LEU	GLY	SER	PHEN	ME	LEU	LEU	ASN	CYS	LEU	VAL	VAL	LE	394	
DB	1071	TTT	T	G	A	C	C	T	T	G	A	C	T	T	T	T	T	T	T	T	1130	
OY	395	ALA	THR	GLY	ASN	SER	GLY	THR	LEU	ASN	ARG	GLY	USER	GLY	ASN	LEU	ME	ARG	GLY	GLY	414	
DB	1131	AGC	G	G	G	G	A	G	T	T	C	C	A	A	A	A	A	A	A	A	1190	
OY	415	ARG	PHEN	LEU	SER	ASN	ALA	SER	THR	LEU	ALA	SER	PHEN	SER	GLY	PRO	GLY	SER	CYS	TYR	GLY	434
DB	1191	CGG	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1214		
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DB	1275	TC	A	G	T	A	G	A	C	G	G	A	C	T	T	G	C	T	T	G	1334	
OY	465	USER	SER	PRO	ALA	PRO	LEU	GLY	GLY	LEU	GLY	THR	GLY	PRO	SER	SER	SER	CYS	SER	TYR	485	
DB	1335	CTG	T	A	G	A	G	C	T	G	A	C	A	T	A	T	A	G	A	G	1374	
OY	485	THR	ALA	ARG	LEU	SER	VAL	HI	ASN	LEU	VAL	HI	SHI	SHI	SHI	SHI	SHI	SHI	SHI	SHI	505	
DB	1374	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1374		
OY	505	THR	IS	LEU	GLY	ASN	GLY	THR	LEU	ARG	ALA	PRO	ARG	ALA	SER	PRO	GLY	LEU	LEU	ASN	ARG	525
DB	1375	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1404		
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DB	1405	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1425		
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DB	1425	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1425		
OY	565	VAL	ARG	CYS																		

QY	625	oProGlyProtyrserSermethtsluylsleuLeuGlnThrGlnSerThrGlyAlaCysGI	645
DB	1460	CCCTGGAGAT-----GAGATGAAAGAGGGGACCATGGC	1495
QY	645	nSerSerCysAluylleSerSerProCysleuLysAlaasPserGIAlaCysGIProAs	665
DB	1496	TAGCTGTACACGCTGCCCTMAACAGATTATGAAACA-----AG	1534
QY	665	pSerCysProTyrrCysAlaAlaArgAlaGlyAlaGlyGluValGluLeuAlaAspArgGlu	685
DB	1535	GATCTGCGCGACCTTCGCCGAGGCAACCGGGGT-----	1568
QY	685	cProAspSerAspSerGluAlaValTyrrGluPheThrGlnAspAlaGlnHisSerAspLe	705
DB	1569	-----CT	1570
QY	705	uArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerVa	725
DB	1571	CCGT-----GCACGCTGCCCGCGCGGTCAAGTCCAGGCC-----	1607
QY	725	lleuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrrh	745
DB	1608	----TGCTACTGG-----	1616
QY	745	eGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGlyTyrrhI	765
DB	1617	-----GCTGTACTGGTGTGCTGCTTCCTTCAACAGCTTGACCAATGCTTCAGGACCA	1669
QY	765	sGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLe	785
DB	1670	TGGGACAGCTTTGGCTGACCTCACCCAGACCCAGAGATAGCCAAAGTTGCTGCTGCT	1729
QY	785	uPheAlaLeuGlnMetLeuLeuIleuLysleuLeuValTyrrGlyProPheGlyTyrrIleLysAs	805
DB	1730	CTTCACTGTGAGATGCTCTCAACAGTGTACGCGCTGGGCGCCCTGCTGCTCACTGTGCTC	1789
QY	805	nProTyrrAsnIlePheAsp-----GlyValIleValIleSerValTr	820
DB	1790	CTTTTTCACCGCTTGTGACTGCTTCGTGCTGTGGGGGCATCTTCAAGAACCATCTTGCT	1849
QY	820	pGluIleValGlyGlnGlnIlyGlyIleuSerValLeuArgThrPheArgLeuMetAr	840
DB	1850	GAGGGTGGGGGCATGCAGCCTCTTGGCATTCAGTGTCTCCGATGTGTACGTCTCTCAG	1900
QY	840	gValLeuIysleuValArgPheLeuProAlaLeuGlnArgIleuValIleuMetLys	860
DB	1910	GATCTTCAAGGTCAACGACGACGACTGGGCACTCCGTAGCAATCGGTGGCATCTTGGCTCA	1965
QY	860	sThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSe	880
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QY	900	uProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLe	920
DB	2081	CACCAAGAGGACGACCTTGTGATTACTTCCCCCAAGCCCTCTCAGCTGCTTTCAGATCT	2144
QY	920	uThrGlnIleuAspTrpAsnLysValLeuTyrrAsnGlyMetAlaSer-----	935
DB	2141	GACTGTGTAGGATTTGGAACGTGTTCATCATGATCATGTGTCAATGGCTTACGAGTGGCCCTT	2200
QY	936	-----ThrsSerSerTrpAlaAlaLeuTyrrPheIleAlaMetThrPheGlyAsnTyrrVa	954
DB	2201	CTTCCACGAGATGCTGCTGTGTGTATTATTTATCATCTCTTTCATCTGTGGCACTACAT	2266
QY	954	lleuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLys	974
DB	2261	CCTGTGTGAACGTGTTCTTGTCCATTTGCCGTGGATTAACCTAGCAGC-----	2306
QY	974	sArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGI	994



Oy	1701	ValLeuLysValLeuLysValMetAlaValGlyMetArgAlaLeuLeuAspThrValMet---	1713
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Oy	1720	-----GlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePhe	1737
Db	3965	TCTTTCCAGGCGCTTGCCCTATGTG-----GCATCTTCATAGCAATGATTTCTTC	4015
Oy	1738	IlePheAlaAlaLeuGlyValGlyLeuPheGlyAspLeuGlyCys---AspGlyThrHis	1756
Db	4016	ATCTATGACGATCATTTGGCATGCATGATGTTTGGCAAGGATGCTCTTCAGACGACCCAG	4075
Oy	1757	ProCysGlyGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThr	1776
Db	4076	-----ATTAATCGAAACCAACATTTCCAGACTTTCCGAGGCTGTCTGCTT	4123
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Oy	1795	ArgAspCysAspGlyGlySer-----ThrCysTyrAsnThr	1806
Db	4184	AATGATGTGACCCGTGACTGTGACTTTGGCCAGCGAGATTTACTCTG---GGTAGC	4240
Oy	1807	ValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsn	1826
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Oy	1827	ValValIleAlaValLeuMet-----	1833
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Oy	1834	-----LysHisLeuGlyGlySerAsnLysGlyAlaLysGlyAlaGlyLeuGlyAla	1851
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Oy	1852	GlyLeuGlyLeuGlyL--	1863
Db	4418	AAGGCCGCATCAACCACTTGATGTGTGCTGCTGACGATCCAGCCCCCATTTG	4477
Oy	1864	-----ProHisSer-----	1866
Db	4478	GGATTTGGAAACCTATGCCACACCCAGATGGCCTGCAGAAAGACTGTGGCAATGATGTC	4537
Oy	1867	ProLeuGlySerProPhe-----LeuThrProGlyValGly	1878
Db	4538	CCCTTCACATCGA-TGGAAACGTGACATTCACACGTACACTCTTTGGCCGTGGTGGAC	4596
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Db	4597	ATCCCTGAAGATCAAGACAGAAAGGAACTGTGATCAACCAACGAGAGCTTGGATGT	4656
Oy	1896	HisAlaArgSerAlaSerHisPheSerLeuGly-----HisProThrMet	1910
Db	4657	CATCAAAAGATCTGGAAGCGGATTAAGACAAATTTGGATGAGGTCAATCCCTCTCC	4716
Oy	1911	Gln-----	1917
Db	4717	CGATGAGGAGGAGTCACTGTGGAAAAATTCTATGCSAATTTCCGATTCGAAGATTATTT	4776
Oy	1918	ProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro	1937
Db	4777	-----CCGAAAAATTCGAGAGAGAAAGAAAGGGCTACTACTAGAGAGAGC---CCC	4827
Oy	1938	AsnAspSerTyrMetCysArgHisGlySerThrAlaGlyGlyProLeu-----	1953
Db	4828	AACAAAGCACATCTCTGCTCCCTCAAGCTGTCTTAAGAG---CTGCAGAGACTTGGTTC	4884
Oy	1954	-----GlyHisArgGlyTyrProGlyLeuProLys	1962
Db	4885	TGAGATTCGTCAAAGCCCTCACTATGACACTGAGGAAGAGGAAAGGAAAGGAGCAGT	4944

QY	1963	AlaGlnSerGly	-----	SerValLeuSerValHis	1972
Db	4945	GGGTCCAGAGAGCTAGGAGAGAGAGCTGAGAACCAACCAAGAACCAATCAACAAAGACTCAT			5004
QY	1973	SerGlnProAlaAspThrSerGly	-----Ile-LeuGlnLeuProGly 1986		
Db	5005	AGACTCCACAGCCCCAATCTCGATGGAACCTGAGATTTCGGTGTCTTCACTGTGTTAAGGA			5064
QY	1986	AspAlaProHisValLeuLeuGlnProHisIleSerAlaProThrTrpGlyThrIleProGlyVal			2006
Db	5065	GAACATTCACGAAATTCCTCTCTCACTGGGCGAGAGATGATGATGGGGCTGGCTCCAACTC			5124
QY	2006	uProProProGlyValArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIle			2025
Db	5125	CAGCAGAGCCAGTGTGATACAGGCTGGCTCCCAACACACAGAGAAAGCTCTGGGGTTTT			5184
QY	2026	-----ArgThrAspSerLeuAspValGlnGlyLeuGlySerArgVal			2039
Db	5185	CATGTTCACTATCCCGGAAGAGAAAGATATTCACTCAAGGAACTCAAGGGCCAGAAC			5244
QY	2040	-----AspLeuValGlnValSerGly			2047
Db	5245	TCAGAAATGAGAAACAGAAAGTCCCTGACTGAGACTCTCGACTGGATGAGCAGGGCGGGAC			5304
QY	2047	YProSerProProLeuAlaArgAlaTySerPheTrpGlyGlnSerSerThrGlnAlaGly			2067
Db	5305	TCCTTCGAACCCAGACCTCTTTACCA--CTCACTG--			5343
QY	2067	nglnHisSerArgSerHisSerGlyIleSerGlyHisMetThrProProAlaProCysPyr			2087
Db	5344	GCAACACCTTAAACGGGACCAATGTGCCACCGCCGAGTTGTGCTGCCCCCAGCCCTGCA-			5401
QY	2087	oglyProGluProAlaAsnTrpGlyIlyGlyProProGluIlyThrArgSerSerLeuGluLeuAs			2107
Db	5402	-----GATCGAAGCCCTCTTCAACATCCAGTGTCTGCAACGGCA			5442
QY	2107	pThrGlyLeuSerTrpIleSerGlyAspLeuLeuProGly			2123
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Db	5507	---AGGGCTCAGGGTCTCTGGAGACCCCTCTCAGAAAGGCTGACTGCTATATGCC--			5566
QY	2163	sLeuAspSerGlySerGlnProHisIleGlyIlyThrAspProSerAsnLeuGlyGlnPyr			2183
Db	5561	-----CCCTGTGTGTGGTGAAGAACTCAAGTGGGGTGAAGAGATA			5601
QY	2183	oLeuGlyGlyProGlySerArgProGlyValGlyValGlyLeuSerProProSerIleThr			2201
Db	5602	CCTTGGC-----AAACTTGCGCGGCCCACTGCGTACCTTCAC			5631
QY	2202	---IleAspProProGluSerGlnGlyProArgThrProProSerProGlyIlyLeuGly-			2215
Db	5638	CTGTCTGCAAGTGCCTGG-AGCTCATCCGAATCCAGGACCCGCAAGAGGGGAGCTGCTG			5696
QY	2220	-----LeuArgArgArgAlaProSerSerAspSerLeuAsp			2231
Db	5697	ACAAGTTTGATGAGAGCTGTGCTCATCTCCGAAG--CCTAGGTCTCTTTGGCCAAAG			5755
QY	2231	pProLeuAlaSerGlyPro-----ProAspSerMetAlaAlaSerProSerPro			2247
Db	5751	ACCCACAGATTGTGTGGCCTGGCCAAAGCAGAGATTCAGATGTCATGTCACCTGACCTT			5808

RESULT 3

LOCUS BM479323

DEFINITION AGENCECOURT 6418725 NIH\_MGC\_67 Homo sapiens cDNA clone IMAGE:5502230

5', mRNA sequence.

1076 bp

linear

EST 05-FEB-2002

IMAGE:5502230



ACCESSION BM479323  
VERSION BM479323.1 GI:18528365  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1076)  
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
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CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLNL12140 row: a column: 15  
High quality sequence stop: 692.  
Location/Qualifiers  
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT;  
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Technologies."  
ORIGIN  
Alignment Scores:  
Pred. No.: 1,13e-85 Length: 1076  
Score: 1362.50 Matches: 286  
Percent Similarity: 90.37% Conservative: 5  
Best Local Similarity: 88.82% Mismatches: 15  
Query Match: 11.61% Indels: 16  
DB: 4 Gaps: 3  
US-09-611-257A-37 (1-2266) x BM479323 (1-1076)  
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DB 3 AGGAACATCAACCAATTAATCGACTGTGCGAGGCCAGTTACCGGTGGGTCGGCACAAG 62  
QY 1467 TyrAsnPhaSpAnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAap 1486  
DB 63 TACAACTTTCACAACCTTGGCCAGGCGCTGATGTCTCTTTGGCTTCCACAAGAT 122  
QY 1487 GLTTPVaLaSpIleMetTyRAspGlyLeuAspLaValaGlyValaSpGInGInPcoIle 1506  
DB 123 GGTGGGTGACATCATGTAAGAGGCTGAGTGTGGCTTGAACCAAGCCCAATC 182  
QY 1507 MetAsnHisAnProTTPMetLeuLeuTyRPhelISeSPheLeuLeuIleValaIaPhe 1526  
DB 183 ATGAACCAACAACCCCGAGATGCTGCTATTCATCTCGTTCGTCATGTGGCTTC 242  
QY 1527 PheValLeuAsnMetPheValaGlyValaValaGluAsnPhelIsLysCySaRgInHis 1546  
DB 243 TTGTGCTCTGAACATGTTGTGGGTGTGGTGTGAAGAATCTTCACAAGTGTCCGACAG 302  
QY 1547 GInGluGluGluGluLaArgArgArgGInGluLysArgLeuArgLeuGInLysLys 1566  
DB 303 CAGAGAGAAAGAGAGGCGCGCGGAGAGAAAGGCTTACGAAGACTTGGAGAAAG 362  
QY 1567 ArgArgLysAlaGInLysLysProTyTyRSeSPtyrSeSPtyrPheArgLeuLeuVal 1586  
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DB 423 CACCACTTGTGACACGACCACTTGAACCTTTCATCAACAGGTGATCGGCTGAAC 482  
QY 1607 ValIaIleThnMetAlaMetGluHisTyRgInGInPcoGInIleLeuAspGluAlaLeuLys 1626  
DB 483 GTGTCAACATGCGCATGAGAGCATACCAAGAGCCCAAGATTTCGATGAGGCTTGAAG 542  
QY 1627 IleCySaenTyRlePheThrValIlePheValaLeuGInSerValPheLysLeuValaIa 1646  
DB 543 ATCTCAACTACATCTTCATCTTCATCTTGTCTTGTGGAGTCAAGTTTCAACTTGTGCG 602  
QY 1647 PheGlyPheArgArgPhePheGInAspArgTTPAsnGInLeuAspLeuAlaIleValLeu 1666  
DB 603 TTTGGTTTCGGGTCTTCTTCCAGACAGGTGAACCAAGCTGACCTGACCTGTGTCTG 662  
QY 1667 LeuSerIleMetGlyIleThrLeuGInGInIleGluValaAsnAlaSerLeuProIleAsn 1686  
DB 663 CTGTCAATCATGCGCATCAAGCTGAAGGAATCGAGTCAAGCCTCGCTGCCATCAAC 722  
QY 1687 ProThrIleIleArgIle-MetArgValaLeuArgIleAlaArgValaLeuLysLeuLeu-L 1706  
DB 723 CCACCATCATCCGATCATTAAGGAGGTGTGCGCATTTGCCCAAGTCTGAACCTCTGA 782  
QY 1706 yMetAlaValaGlyMet-ArgAlaLeuLeuAspTTPrrValMetGluAla--LeuProGInV 1725  
DB 783 AAATGGTGTGGGACATGCCGCGCTGTGACACAGGATGACAGCCCTGTCTCCCGGT 842  
QY 1725 aIGlyAsnLeuGlyLeuLeuPheMet-----LeuLeuPhePheIlePheAlaIaLeuG 1743  
DB 843 GGGAAACCTGGGACCTTTTCTCCAGGCGCTGTGTTTTCATCCCTCGCGCTCG 902  
QY 1743 lyVal-----GluLeuPheGlyAspLeuGluCyAspGluThrHisProCysGlu 1759  
DB 903 GCGCGTGAAGCCTCTTTTGGAGAA-----CCTTGCAAG 937  
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CF548698  
ACCESSION CF548698.1 GI:34885530  
VERSION  
KEYWORDS EST.  
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Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
1 (bases 1 to 879)  
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
AUTHORS Contact: Daniela S. Gerhard, Ph.D.  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLNL14738 row: j column: 24  
High quality sequence stop: 646.  
Location/Qualifiers  
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Email: c9abbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA library arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/BLNT at:  
<http://image.llnl.gov>  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)

Seq primer: pyx-5.  
 Location/Qualifiers

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/notes="Organ: Brain; Vector: pyx-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
to Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction. ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP), supported by National
Institute of Mental Health (NIMH), Hemm Chn, Ph.D.,
program coordinator."
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## ORIGIN

## Alignment Scores:

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Pred. No.: 3,85e-77 Length: 793
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Best Local Similarity: 91.63% Mismatches: 2
Query Match: 10.56% Indels: 18
DB: 6 Gaps: 1
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US-09-611-257A-37 (1-2266) x CA319705 (1-793)

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QY 1453 SerAspCysAlaGluAlaSerTyrArgTTPValArgHisIleTyrAnpPheAspAnleu 1472
DB 63 TCCGACTGTCTCAGGCCAGATTACCGGTGGTCCGACACAAGTCAACTTTGCAACCTG 122
QY 1473 GlyGlnAlaIleuMetSerLeuPheValIleuAlaSerTyrAspGlyTTPValAspIleMet 1492
DB 123 GGCACAGGCTCTGATGTCCTGTTGTGCTGCTCCAGAGATGGCTGGGTGACATCAG 182
QY 1493 TyrAspGlyLeuAspAlaValGlyAlaAspGlnGlnProIleMetAsnHisAsnProTTP 1512
DB 183 TATGATGGAGTGAATGCTGTGGAGTGGACCAACGCCATCTGAAACCAACCTTGG 242
QY 1513 MetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPhe 1532
DB 243 ATCTGCTCTACTTCACTCTCTCTCTCATCATGTGGCTTCTTCTGCTGAAACATGTTT 302
QY 1533 ValGlyValValValGluAnpPheHisIleCysArgGlnHisGlnGlnGluGluGlu 1552
DB 303 GTGGGCGTGTGTGTGAGAACTTCATTAAGTGCAGGACACAGAGAGAGAGAGGCG 362
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DB 363 CGGCGCGCGGAGAGAGACGACTTAAGAGAGGCTGGAGAAAAAGAGAGAACTTAATGTTG 422
QY 1569 -----LysAlaGlnCysIlePro 1574
DB 423 GACGATGTAATTGCTTCGCGAGCTCAGCCAGCCGTGGCTGACAGAGCCAGGCAAAACC 482
QY 1575 TyrTyrSerAspTyrSerArgPheArgLeuValHisIleCysThrSerHisTyr 1594
DB 483 TACTACTGTGACTTCTCGGCTTCGCGCTCTCGTCCACCACTGTGTACGCCACTAC 542
QY 1595 LeuAspLeuPheIleThrGlyValIleGlyLeuAnValValThrMetAlaMetGluHis 1614
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QY 1615 TyrGlnGlnProGlnIleLeuAspGluAlaLeuValIleCysAsnTyrIlePheThrVal 1634
DB 603 TACCAAGCAGCCCAAGATCCTGGACGAGGCTGGAAGATCTGCACATCAATCTTACCCGTC 662
QY 1635 IlePheValLeuGluSerValPheIleValAlaPheGlyPheArgArgPheGln 1654
DB 663 ATCTTGTCTTGGATCGATTCATTCANACTTGTGGCTTCGCTTCGCCGCTTCTCCAG 722
QY 1655 AspArgTTPAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeu 1674
DB 723 GACAGGTGAACCACTGGAAGCTGTATGTGCTTGTGTCCATCATGATGATGATGATGATG 782
QY 1675 GluGluIle 1677
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 VERSION  
 AY416499.1 GI:3972459  
 SOURCE  
 GSS.  
 ORGANISM  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 (bases 1 to 5943)  
 Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.O.,  
 Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 TITLE  
 JOURNAL  
 PUMED  
 14671302  
 2 (bases 1 to 5943)  
 Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.O.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT  
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## ORIGIN



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Best Local Similarity:	23.04%	Mismatches:	862
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		Gaps:	79

US-09-611-257a-37 (1-2266) x AY416499 (1-5943)

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QY 28 ALAGLGLVARGPRGGLY---PROGLYSERAGLULYSAPPROGLYSERALAASER 46
DB 132 TCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 191
QY 47 GLUALAGLULYEU-----PROTYRPROALALEUALA-PROVALVALPHEPH 62
DB 192 TTTTGCCCTTCATCAGCGGAGACATCCCCCAAGGCTGTGCAGTTCCCTCGAGACTT 251
QY 62 e-----TyrluSerGln----- 66
DB 252 TGACCCATCTATTGACGAGAGAAACCTTTGATGATTAAACAGAGGAGAAACTCTT 311
QY 67 -----AapSerArgPro-----ArgSerTr 73
DB 312 CAGATTGATGCGACGCTGCTTGACATTTAACTCTTTAACTGATTAAGAGAAAT 371
QY 73 pCysLeuArgThrValCysAsnProTrpPheGluArgIleSerMetLeuValIleLeu 93
DB 372 AGCATTAATAATTTTGATACATTCATTATTTAGCATGATCATTTGCGACTATTTGAC 431
QY 93 uAsnCysValThrLeuGlyMetPheArgPro-----CysGluAspIleAlaCysAs 110
DB 432 CAACCTGTGTATTCACCTTTAGTAAACCTCTGACTGTGCAAGATGTG----- 483
QY 110 pSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePhe--AlaPhePheAl 129
DB 484 -----GAGAACGCTTCACAGGAGATTATAC 509
QY 129 aValGluMetValAllyMetValAlaLeuGlyIlePheGlyIlybysCys----- 146
DB 510 ATTGGAATCACTAGTAAATCATTCAGAGAGGTTTC-----TGCATAGATCG 557
QY 147 -----TyrluGlnArgThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMe 164
DB 558 CTTTACCTTTTACGGAGCCATCGAACTGGTATTCAGTTCATCATCAATGAGGCTA 617
QY 164 tLeuGlnTyrsLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgVa 184
DB 618 TATTAACAGAGTTTGTAACTTAACTGAGCAATGTT-----TCAGCTCTACGCACTTTCAGGCT 671
QY 184 lLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeu 204
DB 672 ACTAGAGGCTTTGAAACTATTTTCGTRATCCAGGCTGAAACAAATGTGGGTGCCCT 731
QY 224 ePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeu-- 243
DB 792 TTTTGCCCTTGATCGAGCTGAGCTGTTTCATGAGGAACTTGAACAAAGTGTGTGTG 851
QY 244 -ProGluAsnPheSerLeuProLeuSerValAspLeuGluArgIlyrTrpGln-----Th 261
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QY 261 rGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSe 281
DB 891 CAAGGCTTTGATGGAGAGATATATC-----AACATATTAACAAACA 932
QY 281 rCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProPro-----CysG 299
DB 933 TTTCTACACAGTTCCT-----GGCATGCTGGAACCTTTACTCTGTGG 974

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QY 319 rTyThrAsnCysSerAlaGlyIlybysAsnPropheylsGlyAlaIleAsnPheAspAs 339
DB 1015 -----TGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1064
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DB 1185 CTTTGAGGTTCTTCTATCTGATGAACTTGATCTTGCTGTGTGGCTGATGCA 1244
QY 399 -----SerGlnTrpGlnArgGluSerGlnLeu 409
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QY 409 tArgGlnGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGlnP 429
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QY 429 oGlySerCysTyrluGlnLeuLeuLeuTyrluValTrileuArglybAlaIla 449
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QY 449 gArgLeuAlaGlnValSerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAl 469
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QY 489 uSerValHisIleValHisIleHisIleHisIleHisIleHisIleHisIleHisIle 509
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QY 529 r-ArgArgLeuMetLeuProProProSerThrProAlaLeuSerGlyAlaProProGly 548
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QY 549 -----GlyAlaGluSerValHisSerPheTyrluAlaAspCysHisIleLeuGluP 565
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QY 603 ybGlybysAlaLeuValGluValAlaAlaSerSerGlyProProThrThrLeuThrSerLeu 623
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Db 5650 -----GAGCCAAATGACAACACACTGGCGTCCGCAAG 5679  
QY 2007 ProProProGlyIArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIleLeu 2026  
Db 5680 CAGAGAGAGTACTCTGCTGCTCCAGCGCTACCGCTTACGATTTGGCAAGCGG 5739  
QY 2027 -----ThrAspSerLeuAspValGlnGlyLeuGlySerArgGlnAsp 2040  
Db 5740 GCGTTATCTGCAGAAAAGACACTTTTAATAGCTGGAAGAGGACACACCGGAG 5799  
QY 2041 LeuLeuAlaGlnValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTyrGly 2060  
Db 5800 -----AAAAAGAGACACCCCATCTACAGCTCCCTCCGCTATGACAGTGAAT 5853  
QY 2061 GlnSerSerThrGlnAlaGlnGlnHisSer-----ArgSerHisSerLysIle 2076  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapds-remail.nih.gov  
Tissue Procurement: Dr. James Lin, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/BLNt at:  
http://image.llnl.gov  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)  
Seq primer: pyx-5

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Site 2: Not I; The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured mRNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded

cDNA was size selected according to mRNA size fraction,  
ligated with EcoR I adaptor, digested with Not I, and then  
cloned directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA  
tail, is CAGCCAGCAGC. This library was created for the  
University of Iowa Mouse Brain Molecular Anatomy Project  
(BMAP): 'Gene Discovery in the Developing Mouse Nervous  
System', supported by National Institute of Mental Health  
(NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

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Score: 1216.00 Matches: 236  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 10.22% Indels: 0  
DB: Gaps: 0

US-09-611-257A-37 (1-2266) x BM950154 (1-711)

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QY 1622 AspGlnAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGlnSerVal 1641  
Db 123 GACGAGGCTCTGAAGATCTGCAACTATCATCTTACCGTCATCTTGTCTGGAGTCAGTA 182  
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Db 243 CTGGCTATTGTCTCTTCTGTCCATCATGGGCATCACGCTGGAAAGATTCAGGTCAATGT 302  
QY 1682 SerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgVal 1701  
Db 303 TCACGCGCCATCAACCCGACCATCATCCGATCATGAGGCTCTCCGCAATGCTCGAGTT 362  
QY 1702 LeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAla 1721  
Db 363 CTGAAGCTGTGTAAGATGGCTGTGGCATGCGGACCTGTGAGACACGGTATGACGGCC 422  
QY 1722 LeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuPhePheIlePheAlaAla 1741  
Db 423 CTGCCCGAGTGGGAACTGGGACTTCTTTCATGCTATTATTTTTCATCTTTCAGAGT 482  
QY 1742 LeuGlyValGlnLeuPheGlyAspLeuGlnCysAspGlnThrHisProCysGlnGlyLeu 1761  
Db 483 CTGGGGGTGAGACTCTTTTGAGACCTGGAGGTGTATGAGACACACCTGTGAGGGCTTGG 542  
QY 1762 GlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSer 1781  
Db 543 GGC CGGCAATGCCACTTTAGAACTTTGTATGAGGCTTTTGTGACCTCTTCCGAGCTTC 602  
QY 1782 ThrGlyAspAsnTyrAsnGlyIleMetCysAspThrLeuArgAspCysAspGlnGlnSer 1801  
Db 603 ACTGGTACACTGGAAATGTATTATTGAAAGACACCTCCGGGACCTGTGACAGAGATCC 662  
QY 1802 ThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheVal 1817  
Db 663 ACTGCTACACACCGTATCTCACCCATCTACTCGTCTCTTCTGTTG 710

RESULT 10  
BU058818 771 bp mRNA linear EST 26-AUG-2002  
LOCUS BU058818  
DEFINITION UI-M-FRO-cak-a-11-0-UI\_r1 NIH\_BMAP\_FRO Mus musculus cDNA clone



/strain="CZECCH 11"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5255383"  
 /issue\_type="pooled lung tumors"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NCI CGAP Lu33"  
 /note="Organ: lung; Vector: pTR7D-Pac (Pharmacia) with a modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5].  
 TGTACCATCTGAGTGGAGCGCGCTCTGTTTCTTTTCTTTT 3'.  
 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia). digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

## Alignment Scores:

Pred. No.: 4,32e-74 Length: 990  
 Score: 1215.50 Matches: 261  
 Percent Similarity: 83.03% Conservative: 13  
 Best Local Similarity: 79.09% Mismatches: 45  
 Query Match: 10.21% Indels: 12  
 DB: 4 Gaps: 3

US-09-611-257a-37 (1-2266) x BI905383 (1-990)

QY 1805 AsnThrValIleSerProIle-TyrPheValSerPheValLeuThrAlaGlnPheValIle 1824  
 DB 1 AACACCGTCATCTCACCCATCGACTTCGTGCTTCCTTCGTGACGCGCCAGTTTGTGCT 60  
 QY 1824 uValaenValaIleAlaValleuMetIyHsleuGluIuSerAsnIyGluAlaIy 1844  
 DB 61 GGTCAACGGTGCATGCGCGTGTGTAAGCACTCGAAGAGAGCAACAAAGAGGCCAA 120  
 QY 1844 sGIuGIuAlaGluLeuGluAlaGluLeuGluMetIyThLeuSerProGlnIy 1864  
 DB 121 GAGAGGGGGAGCTTGAAGCGGAGCTGAGCTGAGTGAAGACACTAGCCCGAGCC 180  
 QY 1864 oHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSerProAs 1884  
 DB 181 CCACTCCCGGTGGAGAGCCCTTCCTTCGCTGGGGTGAAGGTGATATGACCTCA 240  
 QY 1884 pSerProLyProGlyValaLeuHsIperAlaAlaHsIalAagSerAlaSerHis---Ph 1903  
 DB 241 CAGCCCTTAAGCCCTGGGCTCCACACCAAGGCCCATTTGAGCAGCCTTCACAGCTT 300  
 QY 1903 eSerLeuGluHsIProThrMetGlnProHsIProThrGluLeuPro-----GlyPr 1920  
 DB 301 CTCCTTGAAGACCCCAACATGATGACTCACTGAGAGGGGCCAGTCCCTTAGGACC 360  
 QY 1920 oAspLeuLeuThrValIArgIySersGlyValSerArgThrHsIserLeuProAsnAspSe 1940  
 DB 361 AGACCTGTGACTGTAGAGAAAGCTGTGTGACGCGGACACACTCTCTGCCAATACAG 420  
 QY 1940 rTyMetCyAaGhIyGlySerThrIaGluGlyProLeuGluHsIArgGlyTyrGlyIy 1960  
 DB 421 CTACATGTGTCCCAAGAGGAGCACTGCCAGAGATCCCTAAGACACAGGGGCTGGGGCT 480  
 QY 1960 uProLyAlaGlnSerGlySerValLeuSerValHsIserGlnProAlaAspThrSerty 1980  
 DB 481 CCCCAAGCCAGTCAAGCTTCATCTTGTCTTCACTCCCAACACGACAGACACGAGCTG 540  
 QY 1980 rIleLeuGlnLeuProLyAspAlaProHsIleuLeuGlnProHsIserAlaProThrTr 2000  
 DB 541 CATCTACAGCTTCCCAAGATGACACATATGCTTCAGACCTCATGGGCTCCACAGT 600  
 QY 2000 pGIyThrIleProLyLeuProProProGlyIyAagSerProLeuAlaGlnArgProleu 2020  
 DB 601 GGGCGGCATCTCCCAACTACCCACACCTGGCCGCTCCCTGGCTCAAGAGGCTCTTCA 660  
 QY 2020 gATgGlnAlaIaIaIaArgThrAspSerLeuAspValGlnGlyIySerArgGluAs 2040

DB 661 GCGCCAGCAGAAATAAAGACTGACTCCCTGAGCGTGAAGGCGCTGGTAGCGGAGAGA 720  
 QY 2040 pLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpG 2060  
 DB 721 CTTGTTTCAGAGGGAGTGGGCGCTCTGCTGACCGGTCTCA-TCTTCTTGGGG 779  
 QY 2060 yGln---SerSerThrGlnAlaGlnGlnHsIser-ArgSerHsIserLySleSertyS- 2078  
 DB 780 GGGGTTCAGATCATGTGCTCAGCAGGCGCTCCGCGACAGACGAAAGTCTCAAGG 839  
 QY 2079 HisMetThrProPro-AlaProCySProGlyPro-GluProAsnTrpGlyIyProp 2098  
 DB 840 CACATCCGGCTGCGAGGCGCTTGGCCAGGGCTGGAACAGAGCTGGCGCAAGGACCTC 899  
 QY 2098 roGlu-ThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117  
 DB 900 AAGAGAACCCAGAAACACTTAACCTTGAACCGGAGCTGAAGCTGGATCAGGGGAACCTC 959  
 QY 2118 LeuProProGlyGlyGln 2123  
 DB 960 TTGGCAGAAAGTCGGAAGA 977  
 RESULT 12  
 CF742232  
 LOCUS  
 DEFINITION  
 UI-M-HB0-Clk-j-06-0-UI.r1 NIH\_BMAP\_HB0 Mus musculus cDNA clone  
 IMAGE:30619901 5', mRNA sequence.  
 CF742232  
 CF742232.1 GI:37638571  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Email: cga@bme-mail.nih.gov  
 Tissue Procurement: Dr. James Lin University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clome Distribution: Distribution information can be found at  
 http://genome.uiowa.edu/distribution/mouse1.html  
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)  
 Seq primer: pYX-5.  
 FEATURES  
 source  
 location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="CS7BL/6"  
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 /clone="IMAGE:30619901"  
 /issue\_type="whole eye"  
 /dev\_stage="embryo 12.5,13.5,14.5 dpc"  
 /lab\_host="DH10B (T1 phage resistant)"  
 /clone\_lib="NIH BMAP HB0"  
 /note="Organ: Eye; Vector: pYX-Aac; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction. Ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Aac vector. The library tag sequence located between the Not I site and the polyA tail is TTAATGAAGT. This library was created for the University Iowa Brain Anatomy Project (BMAP). Gene Discovery in the

ORIGIN

Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH). "

Alignment Scores:

Pred. No.:	4.78e-74	Length:	784
Score:	1212.50	Matches:	243
Percent Similarity:	95.40%	Conservative:	6
Best Local Similarity:	93.10%	Mismatches:	10
Query Match:	10.19%	Indels:	2
DB:	7	Gaps:	1

US-09-611-257a-37 (1-2266) x CF742232 (1-784)

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DB 2 TCATCTTGGGCTGCTCTTACTTCAATGCGCTCAATGCTTTGGCAACTACGTGCTCTT 61
QY 957 AsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLYsArgGlu 976
DB 62 AACCTGCTTCCGCAATTCCTGTGAGGGTTTCCAGGCAAGAAATCGGCAAAACGGGAA 121
QY 977 AspAlaSerLYsGlnLeuSerCYsIleGlnLeuProAlaAspSerGln-GLYGlyAspAl 996
DB 122 GATACGAGTGAACAGTTAACCTGATTACAGCTGCTGTCACTCCAGGGAGAGATGC 181
QY 996 AaAnLYsSerGlySerGluProAspPhePheSerProSerLeuAspLYsArgLYsAspAl 1016
DB 182 CACCAAGTCTGAGTCAAGAGCTGATTTCTTCCGCCAGGTGTGATGTGGAGGACAG 241
QY 1016 gLyLYsCYsAlaLeuAlaLeuValSerLeuGlyGluHisProGlnLeuArgLYsSerLeu 1036
DB 242 GAAGAAGCGCTGAGCCCTGGTGGCTTGGAGAAACCTCGAACTACGAAAGAGCCTTTT 301
QY 1036 uPProProLeuIleIleIleHisThrAlaAlaThrProMetSerLeuProLYsSerThr 1056
DB 302 GCCACCTCTATCATCTACACAGCTGCTACACCATATCACTGCCAAGAGCTTCACAG 361
QY 1056 rGlyLYsGlyValAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaG 1076
DB 362 AGGTGTGGGGAGAACATGCGGCTGCTGCTCGCGGACCAAGTACAGTGGGTCCGCTGA 421
QY 1076 uProGlyAlaAla--HisGluMetLYsSerProProSerAlaArgSerSerProHis 1095
DB 422 GCGTGAAGTGCCTCATCATGATGAATACACCCCAAGTGCAGGAGCTCCCGCACAG 481
QY 1095 rProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgSerSerLeuGly 1115
DB 482 TTCCTGAGGCGACAAAGCAGCTGGACAGAGCGCTCCAGCCGGAACAGCTGGGCGG 541
QY 1115 gAlaProSerLeuLYsArgArgSerProSerGlyLYsArgArgSerLeuSerGlyG 1135
DB 542 GGGCCCCAGAGCTGAAGGCTAGAGAGCCCAAGCGGAGAGCGAGGTCCTGCTGTGAGA 601
QY 1135 uGlyGlnGlnLYsSerGlnAspGlnGlnGlnLYsSerGlnGlnGlnArgLYsSerProAla 1155
DB 602 GGGTCAAGAGAGCCAGATGAGGAGAGTTCAGAAAGAGACCGGGCCAGCCACAGAG 661
QY 1155 ySerAspHisArgHisArgGlySerLeuGluArgGluAlaLYsSerSerPheAspLeuPr 1175
DB 662 CAGGATCATCTGCGACAGGGGTTCTTGGAACTGAGAGGCAAGAGTTCCTTGAAGCTGCC 721
QY 1175 cAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyLYsArgLYsSerAlaSerG 1195
DB 722 TGACACCTTCAAGATGCTCCGGGCTTCAATCGAACAGCAGCGGTGAGAGCTGTGCTGA 781
QY 1195 u 1195
DB 782 A 782
RESULT 13
BUT09095 810 bp mRNA linear EST 15-JUL-2003
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DEFINITION

UI-M-EMO-csz-e-20-0-UI.r1 NIH\_BMAP\_EMO Mus musculus cDNA clone  
IMAGE:6419323 5', mRNA sequence.

ACCESSION

UI-M-EMO-csz-e-20-0-UI.r1 NIH\_BMAP\_EMO

VERSION

UI-M-EMO-csz-e-20-0-UI.r1 NIH\_BMAP\_EMO

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 810)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

FEATURES

Seq primer: pYX-5.

source

Location/Qualifiers

1. 810

/organism="Mus musculus"

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/clone="IMAGS:6419323"

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/dev\_stage="embryo 15.5 dpc"

/lab\_host="DH10B (T1 phage resistant)"

/note="Organ: brain"

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Qy	1417	111ecysCysa1aPhephe11e11epheg1y11eleug1yVal1GlnleuPhe1yG1y1y	1437
Db	181	CATCTGCTCTGCTCTCTTCATCATTTTGGAAATCTTTGGGGTGCAGCTCTTCAAGGGAA	240
Qy	1437	gPhepheVal1CysGlnG1y1uAspThrArgAsn1eThraSn1ySeserPAspCysa1aG1	1457
Db	241	GTCTCTTGCTGTGTCAGGAGGAGACACCGAACAATCATCTAACAGTCCGACTGTGCTTA	300
Qy	1457	u1aSerTyraTgTrrpVala1ArgH1s1yS1yraSnPheaPAsnLeuG1yGlna1aLeuW	1477
Db	301	GGCGAGTTACCGGTGGTCCGGACAAAGTACAATTGACAACCTTGCCGACAGGCTTGAT	360
Qy	1477	tSerleuPheVal1LeuA1Ser1ySAspG1yTrrpVala1P1eMeTyrAspG1yLeuAs	1497
Db	361	GTCCCTGTTGCTGCTGCTCCAGAGATGGCTGGGTTGACATCATGTATGATGACTGGA	420
Qy	1497	pAlaVala1G1yVala1ArgG1nGlnPro11eMeTAsnH1sAsnProTrrMeTleuTyrPh	1517
Db	421	TGCTGTGGAGTGGACGACGACCATCAATGAACCAACCTTGATGCTGCTACTT	480
Qy	1517	e11eSerPheLeuLeu11eVala1aPhePheVal1euaSnMetPheVala1yVala1yA	1537
Db	481	CATCTCTCTCTCTCATGCTGGCTCTTTCGTTCGTAACATGTTTGTGGCGTGGTGT	540
Qy	1537	1G1uAsnPheH1s1yCysArgG1nH1sGlnG1uG1uG1uA1aArgTArgG1uG1	1557
Db	541	GGAGAACTTCCATTAATGACGACGACCAAGAGAGAGAGAGCGCGCGGAGAGA	600
Qy	1557	u1ySaArgLeuArgArgLeuG1u1yS1ySaArgArg-----	1568
Db	601	GAAAGCACTTAAGAGGCTGGAGAAAGAGAGAAATCTTAATGTTGGAGATGAATTCG	660
Qy	1568	-----Lysa1aGlnCys1ySProTrrTyrSeserP1y	1579
Db	661	TTCCGCGAGTCAAGCAGCGCTGCGTCAAGAGCCAGTGCANACCTTAAGTACTGACTA	720
Qy	1579	rSerArgPheVala1gLeuLeuVala1H1s1leuCysTrrSerH1sTyrLeuAspLeuPhe11	1599
Db	721	CTCGGCTCTCCGCTCTCC--TCGTCACACCTGTGTACAGC-CACTACTGNA-CTCTTCAT	777
Qy	1599	eThrg1yVal11eG1yLeuAsnVala1Thr	1609
Db	778	CACCTGATCATCGGCTGATATGTGTACG	808
RESULT 14			
LOCUS	B1160856	736 bp	mRNA
DEFINITION	602864778F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019018 5',	linear	EST 05-JUL-2001
ACCESSION	B1160856		
VERSION	B1160856.1	GI:14620857	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	NIH-MGC http://mgs.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLCM1833 row: k column: 19		
	High quality sequence stop: 710.		

FEATURES		Location/Qualifiers	
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		/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." "	
ORIGIN			
Alignment Scores:			
Pred. No.:		3.56e-72	
Score:		1185.00	
Percent Similarity:		97.15%	
Best Local Similarity:		95.93%	
Query Match:		9.95%	
DB:		4	
US-09-611-257A-37 (1-2266) x B1160856 (1-736)			
Qy	1268	LeuCySH1sArg1e11eThH1s1ySMeCpheaPhe1sVala1leuVal11e11ephe	1287
Db	2	CTGTGTACCCGATATATACCCACAAGATGTTGACACAGTGTCTTGATCATCTTC	61
Qy	1288	1euaSnCys11eTh11a1aMeT1uArgPro1yS11eAspProH1sSera1aG1uArg	1307
Db	62	CTTAATCATATACATGAGCGCATGGAGCGCCCAAAATTTGACCCCAAGCGCTTAAGCG	121
Qy	1308	11ePheLeuTrr1eSerAsnTrr11ePheThra1aVala1PheLeuA1g1uMeTThra1	1327
Db	122	ATCTTCCTGACCTTCCAAATTAATCTTCAACCGAGTCTTGTGGTGAATGACAGTG	181
Qy	1328	1ySVala1a1aLeuG1yTrrCysPheG1yGlna1aTyrLeuArgSerSerTrrpAsn	1347
Db	182	AAGGTGTGTGCACTGGCTGTGTGCTCGGAGACAGGGGTACCTCGAGACAGTTGGAAC	241
Qy	1348	Val1euaPAspG1yLeuLeuVal1eul1eSerVal11eAsp11eLeuVal1eSerMeTVal1Ser	1367
Db	242	GTGTGTGAGAGGCTGTGTGTCTCATCTTCGTCATCGACATTTGTTGTTCCATGTTCT	301
Qy	1368	AspSerG1yThTrrG11eLeuG1yMeTleuArgVal1leuaArgLeuLeuArgThTrrLeuArg	1387
Db	302	GACAGCGCACCAAAATCTCTGGCAYGTGAGGGGTGTGGGCTGTGCGACCTTGCGC	361
Qy	1388	Pro1euaArgVal11eSerArg1aGlnG1yLeu1yS1euaVala1G1uThTrrLeuMeTSer	1407
Db	362	CGGCTCAAGGTATATAGCCGGGCGAGGGGCTGAAGCTGTGTGTGAACGTGATGTCC	421
Qy	1408	Ser1eua1ySPro11eG1yAsn11eVala11eCysCysa1aPhePhe11e11epheG1y	1427
Db	422	TCACTGAACCATCGGCAACATTTAGTATCATCTGCTGCTTCATCATCTTTCCGCG	481
Qy	1428	11eLeuG1yVala1GlnleuPhe1yG1y1ySPhPheVala1CysGlnG1yGlna1sPThArg	1447
Db	482	ATCTTGGGGGTGCACTCTTCAAGGAAATTTTGTGTGTCAGAGGCGAGATTCACAGG	541
Qy	1448	Asn11eThraSn1ySAspCysa1aG1uA1aSerTyraTgTrrpVala1ArgH1s1yTyr	1467
Db	542	AACATCACCAATTAATCGGACGTGTCCGAGCGCAATTAACCGTGGTCCGGACAAAGTAC	601
Qy	1468	AsnPheaPAsnLeuG1yGlna1aLeuMeTser1euaPheVala1leua1aSerTyraSAspG1	1487
Db	602	AACTTGACAACTTGGCCAGGCTGTGATGTCCGTGACGATATAGGCTTCCAAAGATGG	661

QY 1487 YTPVAlaAspIleMetTyrAspGly-LeuAapAlaValGlyAlaAspGlnProIleM 1507  
 DB 662 TAGGCTGACATCATGATGACATGCGCTGATGCTGCGGCGTGCAGACAGAGCCCATCA 721  
 QY 1507 eLanHhSaenPro 1511  
 DB 722 TGAACCAACACCT 735

RESULT 15  
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 BI736618 60361089F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:5367862 5',  
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 ACCESSION BI736618  
 VERSION BI736618.1 GI:15713631  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 939)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 http://image.lnll.gov  
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 /clone\_id="NIH\_MGC\_94"  
 /note="Organ: eye; Vector: PCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI. Cloned unidirectionally; oligo-dT primed.  
 Average insert size 3.3 Kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

FEATURES  
 source

ORIGIN

Alignment Scores:  
 Pred. No: 7.31e-72 Length: 939  
 Score: 1183.00 Matches: 247  
 Percent Similarity: 84.69% Conservative: 13  
 Best Local Similarity: 80.46% Mismatches: 41  
 Query Match: 9.94% Indels: 9  
 Gaps: 3

US-09-611-257a-37 (1-2266) x BI736618 (1-939)

QY 1929 G1YValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr 1948  
 DB 3 GGTCTCAGCCGCGACACACTCTCTGCCCAATGACAGTACATGATGCCGCAATGGAGCACT 62  
 QY 1949 AlaGlnGlyProLeuGlyHisArgGlyTyrGlyLeuProGlyAlaGlnSerGlySerVal 1968  
 DB 63 GCCAGAGATCCCTAAGACACAGGAGGCTGCGCCCAAGCCCAATCAGCTCCTCATC 122  
 QY 1969 LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProGlyAspAla 1988  
 DB 123 TTGCTGTTACTCCCAACAGACACAGAGCTGATCTTACAGCTTCCCAAGATGCA 182

QY 1989 ProHisLeuLeuGlnProHisSerAlaProThrTrrpGlyThrIleProGlyLeuProPro 2008  
 DB 183 CACTATCTCTCCAGCTTATGAGGCTCCACCTGGGCGCCATCTCTTAACCTACCCCA 242  
 QY 2009 ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIleArgThrAsp 2028  
 DB 243 CTGGCCGCTCCCTTGGCTCAGAGGCTCTCAGGCGCCAGGACCAATAGAGCTGAC 302  
 QY 2029 SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuAlaGlnValSerGlyPro 2048  
 DB 303 TCCCTGAGAGTGAAGGCTGGGTAGCCGGAAGACTTGTTCAGAGGTGAGTGGGCC 362  
 QY 2049 SerProProLeuAlaArgAlaTyrSerPheTrrpGlyGlnSerSerThrGlnIleGln 2068  
 DB 363 TCTGCGCTTGAACCGCTTCATCTTGGGCGGCTGAGCATCCAGGTGCAGACG 422  
 QY 2069 HisSerArgSerHisSerIleSerIleSerIleMetThrProProAlaProCysProGly 2088  
 DB 423 CGCTCCGCGACGACAGCAAGCTCTCCAGACATCCGCTGCACCCCTTCCAGAG 482  
 QY 2089 ProGluProAsnTrrpGlyTyrGlyProProGluThrArgSerSerLeuGluLeuAspThr 2108  
 DB 483 CTGAAACCCAGCTGGGCCAAGACCTCAAGAGACCAAGACGTTAGAGCTGCAGACG 542  
 QY 2109 GlnLeuSerTrrpIleSerGlyAspLeuLeuProProGlyGlyGlnGlnGluProProSer 2128  
 DB 543 GACCTAGCTGATTCAGAGACCTCTCG--CCAGCAGTCAAGAAAGACCTCTGTC 599  
 QY 2129 ProArgAspLeuGlySerTyrSerValGlnAlaGlnSerCysGlnArgArgProThr 2148  
 DB 600 CCAAGGACTTGAAGAAATGCTCACTGAGAGGCCCAAGCTGCCGCGCCAGGCTGG 659  
 QY 2149 SerTrrpLeuAspGlnGlnArgArgHisSerIleAla-ValSerCysLeuAspSerGlySe 2168  
 DB 660 TCCTGGCTAGACAGACAGAGACACTCATGCTTGTCACTGCTGCAGAGGCTG 719  
 QY 2168 rGlnProHisLeuGlyThrAspProSerAsnLeu-GlyGlyGlnProLeuGlyGlyProG 2188  
 DB 720 CCAAGCCCGCTTATGTCCAAGCCCTCAAGCCTCGGCGGCCCAACTTGGGCGCCCTGG 779  
 QY 2188 lYSerArgProGlyGlySerLeuSerProProSerIleThrIleAspProProGluSerG 2208  
 DB 780 GAGAGCGGCTTAAGAAATCTAG-CAACCCAGTATCTTAAGACCCCGAGAGCA- 837  
 QY 2208 InGlyProArgThrProProSerProGlyTleCysLeuArgArgAlaPro-SerSer 2227  
 DB 838 --GAGCCCTGGGCCCATGCAGTCT-GGCGTGTGCC-AGAGAGAGG---CCGCGGCAAG 890  
 QY 2228 AspSerIleAspPro 2232  
 DB 891 GACTCGAAGATCCT 905

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